

A-1937-WO-PCT\_ST25  
SEQUENCE LISTING

<110> AMGEN INC.  
HSU, Hailing  
KANNAN, Gunasekaran  
WALKER, Kenneth W.  
HORTTER, Michelle  
BELOUSKI, Edward J.

<120> ANTI-TL1A/ANTI-TNF-ALPHA BISPECIFIC ANTIGEN BINDING PROTEINS AND  
USES THEREOF

<130> A-1937-WO-PCT

<150> 62/268,432  
<151> 2015-12-16

<150> 62/333,063  
<151> 2016-05-06

<150> PCT/US2016/052006  
<151> 2016-09-15

<160> 2136

<170> PatentIn version 3.5

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

Tyr Ala Ala Ser Thr Leu Gln 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  
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cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300

A-1937-W0-PCT\_ST25

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

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

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

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser  
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| gggaaagccc ctaagcgctt gatctatgat gcatccagtt tgcaaagtgg ggtcccatca | 180 |
| aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct | 240 |
| gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa | 300 |
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|                                                                 |    |
|-----------------------------------------------------------------|----|
| Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Arg Asp Asp |    |
| 20                                                              | 30 |

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile |    |
| 35                                                              | 45 |

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly |    |
| 50                                                              | 60 |

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro |    |
| 65                                                              | 80 |

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro |    |
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr

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Ala Arg Asp Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
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<213> Homo sapiens
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<210> 10
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<212> PRT
<213> Homo sapiens
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 11  
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ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240  
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<400> 12

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

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| 1   | 5   | 10  | 15  |
| Thr | Leu | Ser | Leu |
|     | 20  | Thr | Cys |
|     |     | Thr | Val |
|     |     | 25  | Ser |
|     |     |     | Gly |
|     |     |     | Gly |
|     |     |     | Ser |
|     |     |     | Ile |
|     |     |     | 30  |
|     |     |     | Ser |
|     |     |     | Ser |
|     |     |     | Tyr |
| Phe | Trp | Ser | Trp |
|     | 35  | Ile | Arg |
|     |     | Gln | Pro |
|     |     | 40  | Pro |
|     |     |     | Gly |
|     |     |     | Lys |
|     |     |     | Gly |
|     |     |     | Leu |
|     |     |     | 45  |
|     |     |     | Glu |
|     |     |     | Trp |
|     |     |     | Ile |
| Gly | Tyr | Ile | Tyr |
|     | 50  | Tyr | Ser |
|     |     | Gly | Ser |
|     |     | 55  | Thr |
|     |     |     | Asn |
|     |     |     | Tyr |
|     |     |     | 60  |
|     |     |     | Asn |
|     |     |     | Pro |
|     |     |     | Ser |
|     |     |     | Leu |
|     |     |     | Lys |
| Ser | Arg | Val | Thr |
|     | 65  | Met | Ser |
|     |     | 70  | Ile |
|     |     |     | Asp |
|     |     |     | Thr |
|     |     |     | Ser |
|     |     |     | 75  |
|     |     |     | Lys |
|     |     |     | Asn |
|     |     |     | Gln |
|     |     |     | Phe |
|     |     |     | Ser |
|     |     |     | 80  |
|     |     |     | Leu |
| Lys | Leu | Ser | Ser |
|     |     | 85  | Val |
|     |     |     | Thr |
|     |     |     | Ala |
|     |     |     | Ala |
|     |     |     | Asp |
|     |     |     | 90  |
|     |     |     | Thr |
|     |     |     | Ala |
|     |     |     | Val |
|     |     |     | Tyr |
|     |     |     | Tyr |
|     |     |     | 95  |
|     |     |     | Cys |
|     |     |     | Ala |
| Arg | Glu | Ile | Gly |
|     |     | 100 | Ser |
|     |     |     | Tyr |
|     |     |     | Tyr |
|     |     |     | Gly |
|     |     |     | 105 |
|     |     |     | Phe |
|     |     |     | Asp |
|     |     |     | Tyr |
|     |     |     | Trp |
|     |     |     | Gly |
|     |     |     | 110 |
|     |     |     | Gln |
|     |     |     | Gly |
|     |     |     | Ala |
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|     |     |     | 115 |
|     |     |     | Ser |
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 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln 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

Gly Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
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 ccaggtaagg gactggagtg gattggctat atctattaca gtgggaacac caaatacaac 180

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ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
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20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
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Leu Val Thr Val Ser Ser  
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<213> Homo sapiens

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tggtaccagc agaaaccagg acagcctcct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctgatcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttataagact      300
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<213> Homo sapiens

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
          20           25           30

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Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
          35           40           45

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```

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50           55           60

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Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80

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Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
          85           90           95

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 100 105 110

Lys

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 cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggat 180  
 aatgattatg cagtttctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240  
 cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300  
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<400> 20

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Thr Leu Ser Leu Thr Cys Val Ile Ser Gly Asp Ser Val Ser Thr Asn  
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Ser Val Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
 35 40 45

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

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 21  
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
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gggacacgac tggagattaa acga 324

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<400> 22

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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| 1                                                               | 5   | 10  | 15 |
| Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser | 20  | 25  | 30 |
| Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu | 35  | 40  | 45 |
| Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser | 50  | 55  | 60 |
| Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu | 65  | 70  | 75 |
| Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro | 85  | 90  | 95 |
| Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys                     | 100 | 105 |    |

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| ccagggaagg ggctggagtg gattggggaa atcaatcatg ctggaaacac caactacaac | 180 |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg | 240 |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt | 300 |
| agaagtacca cctgctactt tgactactgg ggccaggga ccttggtcac cgtctcctca  | 360 |

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Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

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

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 25

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<212> DNA

<213> Homo sapiens

<400> 25

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tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 180

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gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
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<400> 26

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys

<210> 27



A-1937-W0-PCT\_ST25

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<212> DNA

<213> Homo sapiens

<400> 27

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cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtgggtat      180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac      240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca      300
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<400> 28

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
20           25           30
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```
Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35           40           45
```

```
Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50           55           60
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Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn
65           70           75           80
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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
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85

90

95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 29  
<211> 342  
<212> DNA  
<213> Homo sapiens

<400> 29  
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tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatttcgca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga 342

<210> 30  
<211> 113  
<212> PRT  
<213> Homo sapiens

<400> 30

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

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Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

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

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys

<210> 31  
<211> 375  
<212> DNA  
<213> Homo sapiens

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caggccccag ggaaaggcct tgagtgggtg agcaggacat actacaggtc caagtgggtat 180  
aatgattatg cagtttctgt gaaaggctga ttcaccatca gccagacac atccaagaac 240  
acgttctacc tgcagatgaa ctctctgaga gccgaggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctca 375

<210> 32  
<211> 125  
<212> PRT  
<213> Homo sapiens

<400> 32

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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 Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

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

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

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

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

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 33  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 33  
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atcacttgcc gggcaagtca ggacatcaga aatgatttag gctggtatca gcagaaacca 120  
gggaaaagccc ctaagcgcct gatctatgct gcgtccagtt tgcaaagtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggccagaa ttactctca caatcagcag cctgcagcct 240  
gaagattttg caacttatta ctgtctacaa cataatagtt atccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acgt

324

<210> 34  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 34

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 Arg Ala Ser Gln Asp Ile Arg Asn Asp  
 20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105

<210> 35  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

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tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct 120

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ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc 300  
cgtagtggga gctactacta ttactacagt atggacgtct ggggccaagg gaccacggtc 360  
accgtctcta gt 372

<210> 36  
<211> 124  
<212> PRT  
<213> Homo sapiens

<400> 36

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

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

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 37  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

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 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggt 336

<210> 38  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 38

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 39  
<211> 348  
<212> DNA  
<213> Homo sapiens

<400> 39  
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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
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tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagt 348

<210> 40  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 40

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

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

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

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe



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50

55

60

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

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

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

Thr Val Ser Ser  
115

<210> 41  
<211> 324  
<212> DNA  
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<400> 41  
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ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180  
aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240  
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300  
ggtactaaag tagaaatcaa acgt 324

<210> 42  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 42

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr 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 Tyr Asn Ile Tyr Pro Leu  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 43  
<211> 354  
<212> DNA  
<213> Homo sapiens

<400> 43  
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ccgggaaagg gcctggaatg gatgggttgg attaatactt acattggaga gcctatttat 180  
gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240  
ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300  
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<210> 44  
<211> 118  
<212> PRT  
<213> Homo sapiens

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<400> 44

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 Tyr Val Phe Thr Asp Tyr  
20 25 30

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

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

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
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<210> 45

<211> 708

<212> DNA

<213> Homo sapiens

<400> 45

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gtgacgatta cctgtcgcgc gtcccaggga atccggaatt acctcgcatg gtatcagcaa 180

aaacccggaa aagcaccgaa gctcctgatc tatgccgcct cgactcttca gagggtgtg 240

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ccgtcgaggt ttagcgggtc cgggtcaggt acggacttta ctctcacaat ttccagcctg      300
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ggacaaggga caaaagtcga gatcaagcgt acggtggctg caccatctgt cttcatcttc      420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac      480
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tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc      600
ctgacgctga gcaaagcaga ctacgagaaa cacaagctct acgcctgcga agtcacccat      660
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<210> 46  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 46

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

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

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 47  
<211> 1419  
<212> DNA  
<213> Homo sapiens

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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180  
caagcgcctg gaaaagggtt cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300

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|                                                                      |      |
|----------------------------------------------------------------------|------|
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa    | 360  |
| gtctcctact tgtctacagc ttcgctcgctc gactattggg gtcaaggaac gttgggtcacc  | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtctttcccc tggcaccctc ctccaagagc    | 480  |
| acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actactttccc cgaaccgggtg | 540  |
| acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acacctttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc   | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa     | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc    | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc caaaaacca aggacaccct catgatctcc   | 840  |
| cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagaccc tgagggtcaag | 900  |
| ttcaactgggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gcgggaggag  | 960  |
| cagtacaaca gcacgtaccg tgtgggtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagtg caaggctctcc aacaaagccc tcccagcccc catcgagaaa   | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc     | 1140 |
| cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc   | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg    | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag    | 1320 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac   | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtaaa                           | 1419 |

<210> 48

<211> 451

<212> PRT

<213> Homo sapiens

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

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| Ser | Leu | Arg | Leu |
|     | 20  |     |     |
| Ser | Cys | Ala | Ala |
|     |     | 25  |     |
| Ser | Gly | Phe | Thr |
|     |     |     | Phe |
| Asp | Asp | Tyr |     |
|     |     |     | 30  |
| Ala | Met | His | Trp |
|     | 35  |     |     |
| Val | Arg | Gln | Ala |
|     |     | 40  |     |
| Pro | Gly | Lys | Gly |
|     |     |     | 45  |
| Leu | Glu | Trp | Val |
|     |     |     |     |
| Ser | Ala | Ile | Thr |
|     | 50  |     |     |
| Trp | Asn | Ser | Gly |
|     |     | 55  |     |
| His | Ile | Asp | Tyr |
|     |     |     | 60  |
| Ala | Asp | Ser | Val |
|     |     |     |     |
| Glu | Gly | Arg | Phe |
|     |     |     | 70  |
| Thr | Ile | Ser | Arg |
|     |     |     |     |
| Asp | Asn | Ala | Lys |
|     |     | 75  |     |
| Asn | Ser | Leu | Tyr |
|     |     |     | 80  |
| Leu | Gln | Met | Asn |
|     |     |     | 85  |
| Ser | Leu | Arg | Ala |
|     |     |     |     |
| Glu | Asp | Thr | Ala |
|     |     |     | 90  |
| Val | Tyr | Tyr | Cys |
|     |     |     | 95  |
| Ala | Lys | Val | Ser |
|     |     |     | 100 |
| Tyr | Leu | Ser | Thr |
|     |     |     |     |
| Ala | Ser | Ser | Leu |
|     |     |     | 105 |
| Asp | Tyr | Trp | Gly |
|     |     |     | 110 |
| Gln | Gly | Thr | Leu |
|     |     |     | 115 |
| Val | Thr | Val | Ser |
|     |     |     | 120 |
| Ser | Ser | Ala | Ser |
|     |     |     |     |
| Thr | Lys | Gly | Pro |
|     |     |     | 125 |
| Val | Phe | Pro | Leu |
|     |     |     | 130 |
| Ala | Pro | Ser | Ser |
|     |     |     | 135 |
| Lys | Ser | Thr | Ser |
|     |     |     | 140 |
| Gly | Gly | Thr | Ala |
|     |     |     |     |
| Ala | Leu | Gly | Cys |
|     |     |     | 145 |
| Leu | Val | Lys | Asp |
|     |     |     | 150 |
| Tyr | Phe | Pro | Glu |
|     |     |     | 155 |
| Pro | Val | Thr | Val |
|     |     |     | 160 |
| Ser | Trp | Asn | Ser |
|     |     |     | 165 |
| Gly | Ala | Leu | Thr |
|     |     |     |     |
| Ser | Gly | Val | His |
|     |     |     | 170 |
| Thr | Phe | Pro | Ala |
|     |     |     | 175 |
| Val | Leu | Gln | Ser |
|     |     |     | 180 |
| Ser | Ser | Gly | Leu |
|     |     |     |     |
| Tyr | Ser | Leu | Ser |
|     |     |     | 185 |
| Ser | Ser | Val | Val |
|     |     |     | 190 |
| Thr | Val | Thr | Val |
|     |     |     |     |
| Pro | Ser | Ser | Ser |
|     |     |     |     |
| Leu | Gly | Thr | Gln |
|     |     |     |     |
| Thr | Tyr | Ile | Cys |
|     |     |     |     |
| Asn | Val | Asn | His |
|     |     |     |     |

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195

200

205

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

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

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

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

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

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

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

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

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro



385 390 395 400

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

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

Pro Gly Lys  
450

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<210> 49
<211> 708
<212> DNA
<213> Homo sapiens
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| agatgcgaca | tccagatgac  | ccagttctcca | tcctccctgt  | ctgcatctgt | aggagacaga  |  | 120 |
| gtcaccatca | cttgccggac  | aagtcaggac  | attagagatg  | atttaggctg | gtatcagcag  |  | 180 |
| aaaccagggg | aagcccctaa  | gcgcctgata  | tatgatgcat  | ccagtttgca | aagtgggggtc |  | 240 |
| ccatcaaggt | tcagcggcag  | tggatctggg  | acagaattca  | ctctcacaat | cagcagcctg  |  | 300 |
| cagcctgaag | attttgcaac  | ttattactgt  | ctacagcata  | atagttaccc | tccgacgttc  |  | 360 |
| ggccaagggg | ccaaggtgga  | aatcaaacga  | acggctggctg | caccatctgt | cttcatcttc  |  | 420 |
| ccgccatctg | atgagcagtt  | gaaatctgga  | actgcctctg  | ttgtgtgcct | gctgaataac  |  | 480 |
| ttctatccca | gagaggccaa  | agtacagttg  | aaggctggata | acgccctcca | atcgggtaac  |  | 540 |
| ttccaggaga | gtgtcacaga  | gcaggacagc  | aaggacagca  | cctacagcct | cagcagcacc  |  | 600 |
| ctgacgctga | gcaaagcaga  | ctacgagaaa  | cacaaagtct  | acgcctgcga | agtcacccat  |  | 660 |
| cagggcctga | gctcgcccgt  | cacaaagagc  | ttcaacaggg  | gagagtgt   |             |  | 708 |

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<210> 50  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 50

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
 20 25 30

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

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
 85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 51

<211> 1425

<212> DNA

<213> Homo sapiens

<400> 51

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc  | 60  |
| agatgccagg tgcagctggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg  | 120 |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc  | 180 |
| caggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa  | 240 |
| ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg  | 300 |
| ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga  | 360 |
| gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg  | 420 |
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc | 480 |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 540 |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 600 |
| gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc  | 660 |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 720 |
| aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct  | 780 |

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```

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg      840
atctccccgga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag      900
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg      960
gaggagcagt acggcagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac     1020
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc     1080
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc     1140
ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc     1200
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag     1260
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg     1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg     1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa                      1425

```

<210> 52  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 52

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Pro | Thr | Val | Thr | Leu | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Gly | Gln | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val |

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260

265

270

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Pro Gly Lys

450

<210> 53  
 <211> 708  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
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 agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120  
 gtcacatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180  
 aaaccaggga tagcccctaa gctcctgac tatgctacat ccagtttgca aagtggggtc 240  
 ccatcaaggt tcagtggcag tggatctggg acagatttct ctctcaccat cagcagtctg 300  
 caacctgaag attttgcaac ttacttctgt caacagagtt acagtacccc tcggacgttc 360  
 ggccaaggga ccaaggtgga gatcaaacga acgggtggctg caccatctgt cttcatcttc 420  
 ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
 ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600  
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
 cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 54  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 54

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210



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<210> 55  
 <211> 1401  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
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 gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120  
 tgcactgtct ctggtggctc catcagtagt tacttctgga gctggatccg gcagccccca 180  
 gggaagggac tggagtggat tgggtatatc tattacagtg ggagcaccaa ctacaacccc 240  
 tccctcaaga gtcgagtcac catgtcaata gacacgtcca agaaccagtt ctccctgaag 300  
 ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aattgggagc 360  
 tactacggct ttgactactg gggccaggga gccctgggtca ccgtctcctc agcctccacc 420  
 aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540  
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600  
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 660  
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
 gacaaaactc acacatgccc accgtgcccc gcacctgaac tcctggggggg accgtcagtc 780  
 ttctcttctc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840  
 tgcgtgggtg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 900  
 ggctgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacgg cagcacgtac 960  
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1020  
 tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1080  
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1140  
 aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1200  
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1260

A-1937-W0-PCT\_ST25

gacggctcct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 1320  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1380  
ctctccctgt ctccgggtaa a 1401

<210> 56  
<211> 448  
<212> PRT  
<213> Homo sapiens

<400> 56

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Glu Ile Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Ala  
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

## A-1937-W0-PCT\_ST25

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Gly 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

## A-1937-W0-PCT\_ST25

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 Glu Glu Met 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 Lys  
 435 440 445

&lt;210&gt; 57

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120

gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180

agaccaggga aagcccctaa gtcctgatc tatgctgcat ccagtttgca aagtggggtc 240

ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 300

caacctggag attttgcaac ttactactgt caacagagtt acagtacccc tcggacgttc 360

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```

ggccaaggga ccaagctgga aatcaaacga acggtggctg caccatctgt cttcatcttc      420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac      480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac      540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc      600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat      660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt      708

```

<210> 58  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 58

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20           25           30

```

```

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

```

```

Tyr Ala Ala Ser Ser Leu Gln 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

```

```

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

```

```

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

```

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 59

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 59

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120

ccaggtaagg gactggagtg gattggctat atctattaca gtgggaacac caaataacaac 180

ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300

agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggctctt ccccttgga cctcctcca agagcacctc tgggggcaca 420

A-1937-W0-PCT\_ST25

gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc 540  
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccttgagggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta cggcagcacg 900  
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080  
aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct cttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg taaa 1344

<210> 60  
<211> 448  
<212> PRT  
<213> Homo sapiens

<400> 60

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

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Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

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



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His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Gly 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 Lys 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 Glu Glu Met 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

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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 Lys  
 435 440 445

<210> 61  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 atggtgttgc agaccaggt cttcatttct ctgttgctct ggatctctgg tgcctacggg 60  
 gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 120  
 atcaattgca agtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 180  
 tggtagcagc agaaaccagg acagcctcct aaactgctca ttactgggc atctaccgg 240  
 gaatccgggg tccctgatcg attcagtggc agcgggtctg ggacagattt cactctcacc 300  
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttataagact 360  
 cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 420  
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480  
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 540  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600  
 ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720

<210> 62  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<400> 62

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

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|     |     |     |     |
|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Gly | Ala | Tyr | Gly |
| 20  | Asp | Ile | Val |
| Met | Thr | Gln | Ser |
| Pro | Asp | Ser | Leu |
| 30  | Ala |     |     |
| Val | Ser | Leu | Gly |
| 35  | Glu | Arg | Ala |
| Thr | Ile | Asn | Cys |
| 40  | Lys | Ser | Ser |
| 45  | Gln | Ser |     |
| Val | Leu | Tyr | Ser |
| 50  | Ser | Asn | Asn |
| 55  | Lys | Asn | Tyr |
| 60  | Leu | Val | Trp |
| Tyr | Gln | Gln |     |
| Lys | Pro | Gly | Gln |
| 65  | Pro | Pro | Lys |
| 70  | Leu | Leu | Ile |
| 75  | Tyr | Trp | Ala |
| 80  | Ser | Thr | Arg |
| Glu | Ser | Gly | Val |
| 85  | Pro | Asp | Arg |
| 90  | Phe | Ser | Gly |
| 95  | Ser | Gly | Ser |
| Thr | Asp |     |     |
| Phe | Thr | Leu | Thr |
| 100 | Ile | Ser | Ser |
| 105 | Leu | Gln | Ala |
| 110 | Glu | Asp | Val |
| Ala | Val | Tyr |     |
| Tyr | Cys | Gln | Gln |
| 115 | Tyr | Tyr | Lys |
| 120 | Thr | Pro | Leu |
| 125 | Phe | Gly | Gly |
| Gly | Thr |     |     |
| Lys | Val | Glu | Ile |
| 130 | Lys | Arg | Thr |
| 135 | Val | Ala | Ala |
| 140 | Pro | Ser | Val |
| Phe | Ile | Phe |     |
| Pro | Pro | Ser | Asp |
| 145 | Glu | Gln | Leu |
| 150 | Lys | Ser | Gly |
| 155 | Thr | Ala | Ser |
| 160 | Val | Val | Cys |
| Leu | Leu | Asn | Asn |
| 165 | Phe | Tyr | Pro |
| 170 | Arg | Glu | Ala |
| 175 | Lys | Val | Gln |
| Trp | Lys | Val |     |
| Asp | Asn | Ala | Leu |
| 180 | Gln | Ser | Gly |
| 185 | Asn | Ser | Gln |
| 190 | Glu | Ser | Val |
| Thr | Glu | Gln |     |
| Asp | Ser | Lys | Asp |
| Ser | Thr | Tyr | Ser |
| Leu | Ser | Ser | Thr |
| Leu | Thr | Leu | Ser |

195

200

205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
 210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235 240

&lt;210&gt; 63

&lt;211&gt; 1431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

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atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc      60
agatgccagg tacagttgca gcagtcaggt ccaggactgg tgaagccctc gcagaccctc      120
tcactcacct gtgtcatctc cggggacagt gtctctacca acagtgttgc ttggaactgg      180
atcaggcagt ccccatcgag aggccttgag tggctgggaa ggacatacta caggtccaag      240
tggtataatg attatgcagt ttctgtgaaa agtcgaataa ccatcaaccc agacacatcc      300
aagaaccagt tctccctgca gctgaactct gtgactcccg aggacacggc tgtgtattac      360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg      420
accacggtca ccgctctctc agcctccacc aagggcccat cggtcttccc cctggcaccc      480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc      540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc      600
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc      660
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag      720
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca      780
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc      840
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac      900
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag      960

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ccgcgggagg agcagtacgg cagcacgtac cgtgtgggtca gcgtcctcac cgtcctgcac      1020
caggactggc tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc      1080
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc      1140
ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa      1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac      1260
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc      1320
accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag      1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a              1431

```

<210> 64  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens

<400> 64

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

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

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

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

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
 85 90 95

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Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro Gly Lys  
450 455

<210> 65  
<211> 642  
<212> DNA

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<213> Homo sapiens

<400> 65

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgccaa      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

<210> 66

<211> 214

<212> PRT

<213> Homo sapiens

<400> 66

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

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20          25          30

```

```

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

```

```

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

```



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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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 67

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 67

cagggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc

60

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| acctgcgctg tccatggtgg gtccttcagt gggtactact ggaactggat ccgccagccc   | 120  |
| ccagggaagg ggctggagtg gattggggaa atcaatcatg ctggaaacac caactacaac   | 180  |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca  | 360  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 420  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 480  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 540  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 660  |
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga  | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct   | 780  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggc   | 900  |
| agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 960  |
| gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aacctctcc    | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc  | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg   | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1320 |
| cagaagagcc tctccctgtc tccgggtaaa                                    | 1350 |

<210> 68

<211> 450

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<212> PRT

<213> Homo sapiens

<400> 68

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

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

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

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys  
450

<210> 69  
<211> 726  
<212> DNA  
<213> Homo sapiens

<400> 69  
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
agatgcgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120  
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180  
ttagtttggt accagcagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240  
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360  
aagactcctc tcactttcgg cggagggacc aaggtggaga tcaaacgaac ggtggctgca 420  
ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac tgcctctggt 480  
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540

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gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600  
 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660  
 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720  
 gagtgt 726

<210> 70  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 70

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

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

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

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

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

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

<210> 71  
<211> 1365  
<212> DNA  
<213> Homo sapiens

<400> 71  
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcctc caccaagggc ccacgtgtct tccccctggc accctcctcc 420  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

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gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660  
 aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720  
 gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aaccaagga caccctcatg 780  
 atctccccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840  
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900  
 gaggagcagt acggcagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960  
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc 1020  
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080  
 ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140  
 tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200  
 accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1260  
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320  
 cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1365

<210> 72  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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

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

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



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

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

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

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

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

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

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

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

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

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

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Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro Gly Lys  
 450 455

<210> 73  
 <211> 726  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtggtgcc 60  
 cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120  
 gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180  
 ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240  
 acccggggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
 ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360  
 aagactcctc tcactttcgg cggaggggacc aagggtggaga tcaaacgaac ggtggctgca 420  
 ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtag cgcctctgtt 480  
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540  
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600  
 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660  
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 gagtgt 726

<210> 74  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 74

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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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

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

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

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

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

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

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

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

<210> 75  
<211> 1431  
<212> DNA  
<213> Homo sapiens

<400> 75  
atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60  
agatgagagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120  
cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
atcaggcagg cccagggaa aggccttgag tgggtgagca ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctgtgaaa ggtcgattca ccatcagccc agacacatcc 300  
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
accacggtca ccgtctctc agcctccacc aagggcccat cggtcttccc cctggcaccc 480  
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600  
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660  
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720  
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc 780  
gcacctgaac tcctgggggg accgtcagtc ttctcttcc cccaaaacc caaggacacc 840  
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900  
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 960  
ccgcgggagg agcagtacgg cagcacgtac cgtgtgggtc gcgtcctcac cgtcctgcac 1020

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caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1080  
 cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140  
 ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa 1200  
 ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260  
 tacaagacca cgcctcccggt gctggactcc gacggctcct tcttcctcta tagcaagctc 1320  
 accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380  
 gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1431

<210> 76  
 <211> 455  
 <212> PRT  
 <213> Homo sapiens  
 <400> 76

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 Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

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

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

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

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

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met

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100

105

110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 245 250 255

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

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr

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290

295

300

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro Gly Lys  
450 455

<210> 77

<211> 708

<212> DNA

<213> Homo sapiens



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<400> 77

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg  | 60  |
| cgctgtgaca tccagatgac ccagtcctcca tcctccctgt ctgcatctgt aggagacaga  | 120 |
| gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag   | 180 |
| aaaccaggga aagcccctaa gcgcctgac tatgctgcgt ccagtttgca aagtggggtc    | 240 |
| ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg   | 300 |
| cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc   | 360 |
| ggcggaggga ccaagggtgga gatcaaacgt acgggtggctg caccatctgt cttcatcttc | 420 |
| ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac   | 480 |
| ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac  | 540 |
| tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc   | 600 |
| ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat   | 660 |
| cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt               | 708 |

<210> 78

<211> 214

<212> PRT

<213> Homo sapiens

<400> 78

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Asp | Ile | Arg | Asn | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 79

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 79

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg

60

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg   | 120  |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc   | 180  |
| caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa   | 240  |
| tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg   | 300  |
| ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga   | 360  |
| gagggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc  | 420  |
| acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc   | 480  |
| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc    | 540  |
| gaaccgggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg | 600  |
| gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc   | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg   | 720  |
| gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca  | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc   | 840  |
| atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct   | 900  |
| gagggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg   | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag   | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggctctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac   | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cggtgtaaa               | 1428 |

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<210> 80  
 <211> 454  
 <212> PRT  
 <213> Homo sapiens

<400> 80

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

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

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

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

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr

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165

170

175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 180 185 190

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

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

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

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

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

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

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

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

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355

360

365

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

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

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

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

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

Ser Leu Ser Pro Gly Lys  
450

<210> 81  
<211> 2166  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 81  
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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180  
caagcgcttg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300  
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgccaaa 360

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc   | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtcttcccc ttggcaccctc ctccaagagc   | 480  |
| acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccggtg  | 540  |
| acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta   | 600  |
| cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc  | 660  |
| acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa   | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctggggggac cgtcagtctt cctcttcccc ccaaaacca aggacaccct catgatctcc    | 840  |
| cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag    | 900  |
| ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa    | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1140 |
| cgaggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1440 |
| tcccagggtgc agctgcagga gtcgggcccc ggactgggtga agccttcgga gaccctgtcc | 1500 |
| ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag   | 1560 |
| ccccaggta agggactgga gtggattggc tatacttatt acagtgggca gaccaaatac    | 1620 |
| aaccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc    | 1680 |
| ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact   | 1740 |
| gggagctact acggctttga ctactggggc cagggaaccc tggtcaccgt ctctcagga    | 1800 |

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ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag 1860  
tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt 1920  
cagagcatta acaactatth aaattggtat cagcagagac cagggaaagc ccctaagctc 1980  
ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga 2040  
tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2100  
tactgtcaac agagttacag taccctcgg acgttcggcc aagggaacaa gctggaaatc 2160  
aaacga 2166

<210> 82  
<211> 700  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 82

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1 5 10 15

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

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

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

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

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



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Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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

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

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

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

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

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

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

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

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

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

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

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Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

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

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

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

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

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

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

Tyr Ala Ala Ser Ser Leu Gln 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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
690 695 700

<210> 83  
<211> 717  
<212> DNA  
<213> Homo sapiens

<400> 83  
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cgctgtcagt ctgtgtgac gcagccgccc tcagtgtctg gggccccagg gcagagggtc 120  
accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aacttggtac 180  
cagcagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240  
ggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300  
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360  
ggttcgggtg tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420  
tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactggtg 480  
tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540  
cccgtaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600  
gccagcagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660  
caggtcacgc atgaaggag caccgtggag aagacagtgg cccctacaga atgttca 717

<210> 84  
<211> 217  
<212> PRT  
<213> Homo sapiens

<400> 84

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln

## A-1937-W0-PCT\_ST25

|                 |                                                 |                         |         |
|-----------------|-------------------------------------------------|-------------------------|---------|
| 1               | 5                                               | 10                      | 15      |
| Arg Val Thr     | Ile Ser Cys Thr Gly                             | Ser Ser Ser Asn Ile Gly | Ala Gly |
|                 | 20                                              | 25                      | 30      |
| Tyr Asp Val     | His Trp Tyr Gln Gln Phe Pro Gly                 | Thr Ala Pro Lys Leu     |         |
|                 | 35                                              | 40                      | 45      |
| Leu Ile Gln Gly | Asn Ser Asn Arg Pro Ser Gly                     | Val Pro Asp Arg Phe     |         |
|                 | 50                                              | 55                      | 60      |
| Ser Gly Ser Lys | Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly     | Leu                     |         |
| 65              | 70                                              | 75                      | 80      |
| Gln Ala Glu Asp | Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp         | Ser Ser                 |         |
|                 | 85                                              | 90                      | 95      |
| Leu Ser Gly Ser | Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly |                         |         |
|                 | 100                                             | 105                     | 110     |
| Gln Pro Lys Ala | Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu |                         |         |
|                 | 115                                             | 120                     | 125     |
| Glu Leu Gln Ala | Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe |                         |         |
|                 | 130                                             | 135                     | 140     |
| Tyr Pro Gly Ala | Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val |                         |         |
| 145             | 150                                             | 155                     | 160     |
| Lys Ala Gly Val | Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys |                         |         |
|                 | 165                                             | 170                     | 175     |
| Tyr Ala Ala Ser | Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser |                         |         |
|                 | 180                                             | 185                     | 190     |
| His Arg Ser Tyr | Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu |                         |         |

195

200

205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
 210 215

<210> 85  
 <211> 1404  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 cgctgtgagg tgcagctggg gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120  
 aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgctg 180  
 cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttgggtga ctgagatacc 240  
 agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc 300  
 gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
 agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
 accaagggcc catcggctct cccctggca cctcctcca agagcacctc tgggggcaca 480  
 gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctgaggactc 600  
 tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660  
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc 720  
 tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780  
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgagggtc 840  
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900  
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 960  
 taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020  
 aagtgaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1080

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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1140  
aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct atcccagcga catcgccgtg 1200  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260  
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1320  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380  
agcctctccc tgtctccggg taaa 1404

<210> 86  
<211> 446  
<212> PRT  
<213> Homo sapiens  
<400> 86

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

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

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

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

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val  
290 295 300



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

Lys 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 Glu Glu Met 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 Lys  
435 440 445

<210> 87

<211> 642

<212> DNA

<213> Homo sapiens

<400> 87

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atcacttgta aagccagtca gaacgtaggt actaacgtag cctggtatca gcaaaaacca 120

ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180

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aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca      240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag      300
ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccacca      360
tctgatgagc agttgaaatc tggaactgcc tctgttggtg gcctgctgaa taactttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt                          642

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<210> 88  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 88

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr 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 Tyr Asn Ile Tyr Pro Leu  
 85 90 95

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys  
210

<210> 89  
<211> 1434  
<212> DNA  
<213> Homo sapiens

<400> 89  
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agatgcgagg ttcagctggg cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg 120  
agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca 300

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gcataacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga  | 360  |
| ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac agtctcctca   | 420  |
| gcttccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tcgacaagaa agttgagccc   | 720  |
| aaatcttgtg acaaaaactca cacatgcgcc gcggacgaag tggatggctg cccaccgtgc  | 780  |
| ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac    | 840  |
| accctcatga tctcccgac ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa   | 900  |
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 960  |
| aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg   | 1020 |
| caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca    | 1080 |
| gccccatcg agaaaaccat ctcaaagcc aaagggcagc cccgagaacc acaggtgtac     | 1140 |
| accctgcccc catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc    | 1200 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac   | 1260 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttctt ctatagcaag   | 1320 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat   | 1380 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa         | 1434 |

<210> 90

<211> 456

<212> PRT

<213> Homo sapiens

<400> 90

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

## A-1937-W0-PCT\_ST25

|     |     |     |     |
|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Ser | Leu | Arg | Leu |
|     | 20  |     |     |
| Ser | Cys | Ala | Ala |
|     |     | 25  |     |
| Ser | Gly | Tyr | Val |
|     |     |     | 30  |
| Phe | Thr | Asp | Tyr |
|     |     |     |     |
| Gly | Met | Asn | Trp |
|     | 35  |     |     |
| Val | Arg | Gln | Ala |
|     |     | 40  |     |
| Pro | Gly | Lys | Gly |
|     |     |     | 45  |
| Leu | Glu | Trp | Met |
|     |     |     |     |
| Gly | Trp | Ile | Asn |
|     | 50  |     |     |
| Thr | Tyr | Ile | Gly |
|     |     | 55  |     |
| Glu | Pro | Ile | Tyr |
|     |     |     | 60  |
| Ala | Asp | Ser | Val |
|     |     |     |     |
| Lys | Gly | Arg | Phe |
|     | 65  |     |     |
| Thr | Phe | Ser | Leu |
|     | 70  |     |     |
| Asp | Thr | Ser | Lys |
|     |     | 75  |     |
| Ser | Lys | Ser | Thr |
|     |     |     | 80  |
| Ala | Tyr | Cys |     |
|     |     |     |     |
| Leu | Gln | Met | Asn |
|     |     | 85  |     |
| Ser | Leu | Arg | Ala |
|     |     |     | 90  |
| Glu | Asp | Thr | Ala |
|     |     |     | 95  |
| Val | Tyr | Tyr | Cys |
|     |     |     |     |
| Ala | Arg | Gly | Tyr |
|     | 100 |     |     |
| Arg | Ser | Tyr | Ala |
|     |     |     | 105 |
| Met | Asp | Tyr | Trp |
|     |     |     | 110 |
| Gly | Gln | Gly | Thr |
|     |     |     |     |
| Leu | Val | Thr | Val |
|     | 115 |     |     |
| Ser | Ser | Ala | Ser |
|     |     |     | 120 |
| Thr | Lys | Gly | Pro |
|     |     |     | 125 |
| Ser | Val | Phe | Pro |
|     |     |     |     |
| Leu | Ala | Pro | Ser |
|     | 130 |     |     |
| Ser | Ser | Lys | Ser |
|     |     | 135 |     |
| Thr | Ser | Gly | Gly |
|     |     |     | 140 |
| Thr | Ala | Ala | Leu |
|     |     |     |     |
| Cys | Leu | Val | Lys |
|     | 145 |     |     |
| Asp | Tyr | Phe | Pro |
|     | 150 |     |     |
| Glu | Pro | Val | Thr |
|     |     | 155 |     |
| Val | Thr | Val | Ser |
|     |     |     | 160 |
| Trp | Asn |     |     |
|     |     |     |     |
| Ser | Gly | Ala | Leu |
|     | 165 |     |     |
| Thr | Ser | Gly | Val |
|     |     |     | 170 |
| His | Thr | Phe | Pro |
|     |     |     | 175 |
| Ala | Val | Leu | Gln |
|     |     |     |     |
| Ser | Ser | Gly | Leu |
|     | 180 |     |     |
| Tyr | Ser | Leu | Ser |
|     |     | 185 |     |
| Val | Val | Thr | Val |
|     |     |     | 190 |
| Pro | Ser | Ser |     |
|     |     |     |     |
| Ser | Leu | Gly | Thr |
|     |     |     |     |
| Gln | Thr | Tyr | Ile |
|     |     |     |     |
| Cys | Asn | Val | Asn |
|     |     |     |     |
| His | Lys | Pro | Ser |
|     |     |     |     |

## A-1937-W0-PCT\_ST25

195

200

205

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

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
 245 250 255

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

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

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 290 295 300

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

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

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

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

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 370 375 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

385 390 395 400

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

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

Ser Leu Ser Leu Ser Pro Gly Lys  
450 455

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<210> 91
<211> 33
<212> DNA
<213> Homo sapiens
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<400> 91
cgcgcggtccc aggggaatccg gaattacctc gca 33
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<210> 92
<211> 11
<212> PRT
<213> Homo sapiens
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<400> 92

Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala  
1 5 10

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<210> 93
<211> 21
<212> DNA
<213> Homo sapiens
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<400> 93  
gccgcctcga ctcttcagag t 21

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<210> 94  
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<220>  
 <223> Synthetic oligonucleotide

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<210> 95  
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<400> 95  
 cagagataca accgagcgcc ttacaca 27

<210> 96  
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 <212> PRT  
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<400> 96

Gln Arg Tyr Asn Arg Ala Pro Tyr Thr  
 1 5

<210> 97  
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<400> 97  
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<210> 98  
 <211> 11  
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<400> 98



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Arg Thr Ser Gln Asp Ile Arg Asp Asp Leu Gly  
1 5 10

<210> 99  
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<400> 99  
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21

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<400> 100

Asp Ala Ser Ser Leu Gln Ser  
1 5

<210> 101  
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<400> 101  
ctacagcata atagttaccc tccgacg

27

<210> 102  
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<400> 102

Leu Gln His Asn Ser Tyr Pro Pro Thr  
1 5

<210> 103  
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<400> 103  
cgggcaagtc agagcattaa caactattta aat 33

<210> 104  
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<400> 104  
cagcagtatg gtagctcacc tacc 24

<210> 105  
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<400> 105  
gctacatcca gtttgcaaag t 21

<210> 106  
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<400> 106

Ala Thr Ser Ser Leu Gln Ser  
1 5

<210> 107  
<211> 27  
<212> DNA  
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<400> 107  
caacagagtt acagtacccc tcggacg 27

<210> 108  
<211> 9

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<212> PRT

<213> Homo sapiens

<400> 108

Gln Gln Ser Tyr Ser Thr Pro Arg Thr  
1 5

<210> 109

<211> 33

<212> DNA

<213> Homo sapiens

<400> 109

cgggcaagtc agagcattaa caactattta aat 33

<210> 110

<211> 11

<212> PRT

<213> Homo sapiens

<400> 110

Arg Ala Ser Gln Ser Ile Asn Asn Tyr Leu Asn  
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<210> 111

<211> 21

<212> DNA

<213> Homo sapiens

<400> 111

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<210> 112

<211> 7

<212> PRT

<213> Homo sapiens

<400> 112

Ala Ala Ser Ser Leu Gln Ser  
1 5

<210> 113  
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 <212> DNA  
 <213> Homo sapiens

<400> 113  
 caacagagtt acagtacccc tcggacg

27

<210> 114  
 <211> 16  
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<220>  
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<220>  
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 <222> (2)..(2)  
 <223> Xaa may independently be M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(7)  
 <223> Xaa may independently be M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(14)  
 <223> Xaa may independently be M, G, A, V, I, or L

<400> 114

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Asn | Xaa | Ser | Xaa | Xaa | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 115  
 <211> 51  
 <212> DNA

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<213> Homo sapiens

<400> 115

aagtcagcc agagtgtgtt atacagctcc aacaataaga actacttagt t

51

<210> 116

<211> 17

<212> PRT

<213> Homo sapiens

<400> 116

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  
1 5 10 15

Val

<210> 117

<211> 21

<212> DNA

<213> Homo sapiens

<400> 117

tgggcatcta cccgggaatc c

21

<210> 118

<211> 7

<212> PRT

<213> Homo sapiens

<400> 118

Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 119

<211> 27

<212> DNA

<213> Homo sapiens

<400> 119

cagcaatatt ataagactcc tctcact

27

<210> 120  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 120

Gln Gln Tyr Tyr Lys Thr Pro Leu Thr  
 1 5

<210> 121  
 <211> 36  
 <212> DNA  
 <213> Homo sapiens

<400> 121  
 agggccagtc agagtgttag aagcagttac ttagcc

36

<210> 122  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 122

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

<210> 123  
 <211> 21  
 <212> DNA  
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<400> 123  
 ggtgcatcca gcagggccac t

21

<210> 124  
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 <212> PRT  
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<400> 124

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Gly Ala Ser Ser Arg Ala Thr  
1 5

<210> 125  
<211> 24  
<212> DNA  
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<400> 125  
cagcagtatg gtagctcacc tacc 24

<210> 126  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 126

Gln Gln Tyr Gly Ser Ser Pro Thr  
1 5

<210> 127  
<211> 51  
<212> DNA  
<213> Homo sapiens

<400> 127  
agggtccagcc agagtgtgtt atacagctcc aacaataaga actacttagt t 51

<210> 128  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 128

Arg Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  
1 5 10 15

Val

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<210> 129  
 <211> 1350  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctccagt 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 900  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaaag ggagcccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag 1080  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140



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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200  
 ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320  
 cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 130  
 <211> 469  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 130

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys  
 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe  
 35 40 45

Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Ile Gly Glu Ile Asn His Ala Gly Ile Thr Asn Tyr Asn Pro  
 65 70 75 80

Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln  
 85 90 95

Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 100 105 110

Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr

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115

120

125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
 210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
 225 230 235 240

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

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser

305                      310                      315                      320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln  
370 375 380

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |

Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
435 440 445

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser |
| 450 |     |     |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |

Leu Ser Pro Gly Lys  
465

<210> 131

$\langle 211 \rangle$  642

<212> DNA

### <213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 131

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ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac      180
aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca      240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag      300
ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt                          642

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<210> 132

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 132

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1           5           10          15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
          20          25          30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
          35          40          45

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Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val  
65 70 75 80

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110

Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

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<210> 133  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 133  
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 ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacagggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 134  
 <211> 234  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 134

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser

## A-1937-W0-PCT\_ST25

20

25

30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
 35 40 45

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

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
 85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr  
 100 105 110

Gly Ser Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg  
 115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
 130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 180 185 190

Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 195 200 205

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

210

215

220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230

<210> 135  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

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 agattgtcct gtgctgcatc tggttacgtc ttacagact atggaatgaa ttgggttaga 180  
 caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
 atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca 300  
 gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
 ggatacagat cttatgccat ggactactgg ggccagggtg ccctagtcac cgtctctagt 420  
 gcctccacca agggccccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
 tacgtggacg gcgtggagggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 960



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agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
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aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260  
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320  
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
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<210> 136  
<211> 470  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 136

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Tyr Val Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly  
50 55 60

Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro  
65 70 75 80

Ile Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr

## A-1937-W0-PCT\_ST25

85

90

95

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

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp  
 115 120 125

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

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

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

## A-1937-W0-PCT\_ST25

275

280

285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 305 310 315 320

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 385 390 395 400

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 450 455 460

Ser Leu Ser Pro Gly Lys

465

470

<210> 137  
 <211> 1344  
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<220>  
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<400> 137  
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 acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
 ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240  
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaattggg 300  
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc cagtgcctcc 360  
 accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
 tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 660  
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780  
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg 900  
 taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
 aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 1080

A-1937-W0-PCT\_ST25

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag 1200  
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg taaa 1344

<210> 138

<211> 467

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 138

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile  
35 40 45

Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro  
65 70 75 80

Ser Leu Lys Ser Arg Val Thr Met Ser Ile Asp Thr Ser Lys Asn Gln  
85 90 95

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
100 105 110

A-1937-W0-PCT\_ST25

Tyr Cys Ala Arg Glu Ile Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly  
115 120 125

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

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

A-1937-W0-PCT\_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
305 310 315 320

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Pro Gly Lys  
465

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<212> DNA

<213> Homo sapiens

<400> 139

cgggcaagtc aggacatcag aaatgattta ggc

33

<210> 140

<211> 11

<212> PRT

<213> Homo sapiens

<400> 140

Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Gly

1

5

10

<210> 141

<211> 21

<212> DNA

<213> Homo sapiens

<400> 141

gctgcgtcca gtttgcaaag t

21

<210> 142

<211> 11

<212> PRT

<213> Homo sapiens

<400> 142

Ala Ala Trp Asp Asp Ser Leu Asn Gly Val Val

1

5

10

<210> 143

<211> 27

<212> DNA

<213> Homo sapiens

<400> 143

ctacaacata atagttatcc gctcact

27

<210> 144

<211> 9



A-1937-W0-PCT\_ST25

<212> PRT

<213> Homo sapiens

<400> 144

Leu Gln His Asn Ser Tyr Pro Leu Thr  
1 5

<210> 145

<211> 42

<212> DNA

<213> Homo sapiens

<400> 145

actgggagca gttccaacat cggggcaggt tatgatgtac ac 42

<210> 146

<211> 14

<212> PRT

<213> Homo sapiens

<400> 146

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His  
1 5 10

<210> 147

<211> 21

<212> DNA

<213> Homo sapiens

<400> 147

ggtaacagca atcgccctc a 21

<210> 148

<211> 7

<212> PRT

<213> Homo sapiens

<400> 148

Gly Asn Ser Asn Arg Pro Ser  
1 5

A-1937-W0-PCT\_ST25

<210> 149  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
 cagtcctatg acagcagcct gagtggttcg gtg 33

<210> 150  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
 Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val  
 1 5 10

<210> 151  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<400> 151  
 aaagccagtc agaacgtagg tactaacgta gcc 33

<210> 152  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
 Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala  
 1 5 10

<210> 153  
 <211> 21  
 <212> DNA  
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<400> 153  
 agtgcctctt tcctctatag t 21

<210> 154  
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 <212> PRT  
 <213> Homo sapiens

<400> 154

Ser Ala Ser Phe Leu Tyr Ser  
 1 5

<210> 155  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 155

caacagtata acatctaccc actcaca

27

<210> 156  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 156

Gln Gln Tyr Asn Ile Tyr Pro Leu Thr  
 1 5

<210> 157  
 <211> 15  
 <212> DNA  
 <213> Homo sapiens

<400> 157

gattatgcga tgcata

15

<210> 158  
 <211> 5  
 <212> PRT  
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<400> 158

A-1937-W0-PCT\_ST25

Asp Tyr Ala Met His  
1 5

<210> 159  
<211> 51  
<212> DNA  
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<400> 159  
gccattacgt ggaatagcgg acacatcgat tatgcagaca gtgtggaggg c 51

<210> 160  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 160  
Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
1 5 10 15

Gly

<210> 161  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 161  
gtctcctact tgtctacagc ttcgtcgctc gactat 36

<210> 162  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 162  
Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
1 5 10

A-1937-W0-PCT\_ST25

<210> 163  
 <211> 15  
 <212> DNA  
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<400> 163  
 agctatggca tgcac 15

<210> 164  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 164  
 Ser Tyr Gly Met His  
 1 5

<210> 165  
 <211> 51  
 <212> DNA  
 <213> Homo sapiens

<400> 165  
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<210> 166  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 166  
 Val Ile Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Thr Asp Ser Val Lys  
 1 5 10 15

Gly

<210> 167  
 <211> 39  
 <212> DNA

<213> Homo sapiens

<400> 167

ccaacagtaa ctctctacta ctactacggt atggacgtc

39

<210> 168

<211> 13

<212> PRT

<213> Homo sapiens

<400> 168

Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
1 5 10

<210> 169

<211> 15

<212> DNA

<213> Homo sapiens

<400> 169

agttacttct ggagc

15

<210> 170

<211> 5

<212> PRT

<213> Homo sapiens

<400> 170

Ser Tyr Phe Trp Ser  
1 5

<210> 171

<211> 48

<212> DNA

<213> Homo sapiens

<400> 171

tatatctatt acagtgggag caccaactac aaccctccc tcaagagt

48

<210> 172

<211> 16

A-1937-W0-PCT\_ST25

<212> PRT

<213> Homo sapiens

<400> 172

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Tyr | Tyr | Ser | Gly | Ser | Thr | Asn | Tyr | Asn | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 173

<211> 30

<212> DNA

<213> Homo sapiens

<400> 173

gaaattggga gctactacgg ctttgactac 30

<210> 174

<211> 10

<212> PRT

<213> Homo sapiens

<400> 174

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Gly | Ser | Tyr | Tyr | Gly | Phe | Asp | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |

<210> 175

<211> 15

<212> DNA

<213> Homo sapiens

<400> 175

agttacttct ggagc 15

<210> 176

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 176

A-1937-W0-PCT\_ST25

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr 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 Tyr Asn Ile Tyr Pro Leu  
85 90 95

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

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

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

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

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

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



A-1937-W0-PCT\_ST25

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

Phe Asn Arg Gly Glu Cys  
210

<210> 177  
<211> 48  
<212> DNA  
<213> Homo sapiens

<400> 177  
tatatctatt acagtgggaa caccaaatac aaccctccc tcaagagt 48

<210> 178  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 178

Tyr Ile Tyr Tyr Ser Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 179  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 179  
gaaactggga gctactacgg ctttgactac 30

<210> 180  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 180

Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr  
1 5 10

A-1937-W0-PCT\_ST25

<210> 181

<211> 21

<212> DNA

<213> Homo sapiens

<400> 181

accaacagtg ttgcttgga c

21

<210> 182

<211> 7

<212> PRT

<213> Homo sapiens

<400> 182

Thr Asn Ser Val Ala Trp Asn

1

5

<210> 183

<211> 54

<212> DNA

<213> Homo sapiens

<400> 183

aggacatact acaggtccaa gtggtataat gattatgcag tttctgtgaa aagt

54

<210> 184

<211> 18

<212> PRT

<213> Homo sapiens

<400> 184

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Val

1

5

10

15

Lys Ser

<210> 185

<211> 39

<212> DNA

<213> Homo sapiens

A-1937-W0-PCT\_ST25

<400> 185  
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<210> 186  
<211> 13  
<212> PRT  
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<400> 186  
Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
1 5 10

<210> 187  
<211> 15  
<212> DNA  
<213> Homo sapiens

<400> 187  
ggttactact ggaac 15

<210> 188  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 188  
Gly Tyr Tyr Trp Asn  
1 5

<210> 189  
<211> 48  
<212> DNA  
<213> Homo sapiens

<400> 189  
gaaatcaatc atgctggaaa caccaactac aaccggtccc tcaagagt 48

<210> 190  
<211> 16  
<212> PRT

<213> Homo sapiens

<400> 190

Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 191

<211> 36

<212> DNA

<213> Homo sapiens

<400> 191

ggatattgta gaagtaccac ctgctacttt gactac 36

<210> 192

<211> 12

<212> PRT

<213> Homo sapiens

<400> 192

Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr  
1 5 10

<210> 193

<211> 21

<212> DNA

<213> Homo sapiens

<400> 193

accaacagtg ttgcttgga c 21

<210> 194

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 194

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

## A-1937-W0-PCT\_ST25

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser | 20  | 25  | 30  |
| Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro Arg Leu Leu | 35  | 40  | 45  |
| Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser | 50  | 55  | 60  |
| Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu | 65  | 70  | 75  |
| Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro | 85  | 90  | 95  |
| Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala | 100 | 105 | 110 |
| Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly | 115 | 120 | 125 |
| Thr Ala Lys Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala | 130 | 135 | 140 |
| Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln | 145 | 150 | 155 |
| Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys | 165 | 170 | 175 |
| Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr | 180 | 185 | 190 |
| Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser |     |     |     |

195

200

205

Phe Asn Arg Gly Glu Cys  
210

&lt;210&gt; 195

&lt;211&gt; 54

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

aggacatact acaggtccaa gtggtataat gattatgcag tttctctgaa aagt

54

&lt;210&gt; 196

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu  
1 5 10 15

Lys Ser

&lt;210&gt; 197

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 197

gaggatgggg atagctacta ccgctacggt atggacgtc

39

&lt;210&gt; 198

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 198

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

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

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

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

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

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

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

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

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

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

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

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

A-1937-W0-PCT\_ST25

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

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

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

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

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

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

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

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

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

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

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

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



A-1937-W0-PCT\_ST25

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

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

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

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

Gly Lys  
450

<210> 199  
<211> 21  
<212> DNA  
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<400> 199  
accaacagtg ttgcttgga c

21

<210> 200  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 200

Thr Asn Ser Val Ala Trp Asn  
1 5

<210> 201  
<211> 54  
<212> DNA  
<213> Homo sapiens

<400> 201

aggacatact acaggtccaa gtggtataat gattatgcag tttctgtgaa aggt

54

<210> 202  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens  
 <400> 202

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Val  
 1 5 10 15

Lys Gly

<210> 203  
 <211> 39  
 <212> DNA  
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<400> 203  
 gaggatgggg atagctacta ccgctacggt atggacgtc

39

<210> 204  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <223> Each X is independently M, G, A, V, I, or L

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
 <221> misc\_feature  
 <222> (14)..(14)

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<223> Xaa can be any naturally occurring amino acid

<400> 204

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Ser | Tyr | Asp | Xaa | Asn | Asn | Lys | Leu | Tyr | Thr | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 205

<211> 15

<212> DNA

<213> Homo sapiens

<400> 205

agctatgaca tgcac 15

<210> 206

<211> 5

<212> PRT

<213> Homo sapiens

<400> 206

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Ser | Tyr | Asp | Met | His |
| 1   |     |     |     | 5   |

<210> 207

<211> 51

<212> DNA

<213> Homo sapiens

<400> 207

gttatatcat atgatggaag tattaaatac tatgcagact ccgtgaaggg c 51

<210> 208

<211> 17

<212> PRT

<213> Homo sapiens

<400> 208

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Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 209  
<211> 45  
<212> DNA  
<213> Homo sapiens

<400> 209  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtc 45

<210> 210  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 210

Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val  
1 5 10 15

<210> 211  
<211> 15  
<212> DNA  
<213> Homo sapiens

<400> 211  
agctactgga tcggc 15

<210> 212  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 212

Ser Tyr Trp Ile Gly  
1 5

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<210> 213  
 <211> 51  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 atcatctatc ttggtgactc agataccaga tacagcccg t cttccaagg c 51

<210> 214  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
 1 5 10 15

Gly

<210> 215  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 agtaactggg gtcttgacta c 21

<210> 216  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Ser Asn Trp Gly Leu Asp Tyr  
 1 5

<210> 217  
 <211> 15  
 <212> DNA  
 <213> Homo sapiens

<400> 217  
gactatggaa tgaat 15

<210> 218  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 218  
  
Asp Tyr Gly Met Asn  
1 5

<210> 219  
<211> 51  
<212> DNA  
<213> Homo sapiens

<400> 219  
tggattaata cttacattgg agagcctatt tatgctgaca gcgtcaaggg c 51

<210> 220  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 220  
  
Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 221  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 221  
ggatacagat cttatgccat ggactac 27

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<210> 222  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 222

Gly Tyr Arg Ser Tyr Ala Met Asp Tyr  
 1 5

<210> 223  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 223

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala  
 1 5 10

<210> 224  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 224

Ala Ala Ser Thr Leu Gln Ser  
 1 5

<210> 225  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 225

Gln Lys Tyr Asn Ser Ala Pro Trp Thr  
 1 5

<210> 226  
 <211> 11  
 <212> PRT

<213> Homo sapiens

<400> 226

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly  
1 5 10

<210> 227

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 227

Glu Ile Gln His Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 228

<211> 9

<212> PRT

<213> Homo sapiens

<400> 228

Leu Gln His Asn Ser Tyr Pro Trp Thr  
1 5

<210> 229

<211> 11

<212> PRT

<213> Homo sapiens

<400> 229

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn  
1 5 10

<210> 230

<211> 15

<212> PRT

<213> Artificial Sequence



<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (1)..(1)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (5)..(6)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (13)..(13)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 230

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Gln | His | Ser | Xaa | Xaa | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 231

<211> 9

<212> PRT

<213> Homo sapiens

<400> 231

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Ser | Tyr | Ser | Thr | Pro | Trp | Thr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 232

<211> 11

<212> PRT

<213> Homo sapiens

<400> 232

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Ser | Gln | Ser | Ile | Ser | Ser | Tyr | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

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<210> 233  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 233

Xaa Gln His Asn Ser Tyr Pro Pro Thr  
 1 5

<210> 234  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 234

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr  
 1 5

<210> 235  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 235

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  
 1 5 10 15

Ala

<210> 236  
 <211> 708

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<212> DNA

## <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 236

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120

gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180

aaaccaggga aagcccctaa gctcctgatc tatgctacat ccagtttgca aagtgggggtc 240

ccatcaaggt tcagtggcag tggatctggg acagatttct ctctcaccat cagcagtctg 300

caacctgaag attttgcaac ttacttctgt caacagagtt acagtacccc tcggacgttc 360

ggccaagggga ccaaggtgga gatcaaacga acggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgcccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 237

<211> 9

&lt;212&gt; PRT

<213> Homo sapiens

<400> 237

Gln Gln Tyr Tyr Ser Thr Pro Leu Thr

1 5

<210> 238

<211> 12

<212> PRT

<213> Homo sapiens

&lt;400&gt; 238

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

&lt;210&gt; 239

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 239

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45

Gln Ser Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr  
 85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln  
 100 105 110

Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 115 120 125

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 240  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 240

Gln Gln Tyr Gly Ser Ser Pro Ile Thr  
1 5

<210> 241  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 241

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala  
1 5 10

<210> 242  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 242

Ala Ala Ser Thr Leu Gln Ser  
1 5

<210> 243  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 243

Gln Lys Tyr Asn Ser Ala Pro Leu Thr  
1 5

<210> 244  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 244

Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly  
1 5 10

<210> 245  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 245

Ala Ala Ser Ser Leu Gln Ser  
1 5

<210> 246  
<211> 9

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<212> PRT

<213> Homo sapiens

<400> 246

Leu Gln His Asn Ser Tyr Pro Leu Thr  
1 5

<210> 247

<211> 14

<212> PRT

<213> Homo sapiens

<400> 247

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His  
1 5 10

<210> 248

<211> 7

<212> PRT

<213> Homo sapiens

<400> 248

Gly Asn Ser Asn Arg Pro Ser  
1 5

<210> 249

<211> 11

<212> PRT

<213> Homo sapiens

<400> 249

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Val Val  
1 5 10

<210> 250

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 250

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc  | 60   |
| acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg    | 120  |
| cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat     | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac   | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca   | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct ccagtgcctc caccaagggc ccatcggctt tccccctggc accctcctcc   | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa  | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct   | 540  |
| gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc   | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac   | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct   | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg     | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag    | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc   | 900  |
| gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac   | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     | 1020 |
| gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc | 1080 |
| ccatcccga aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc    | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgtgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg    | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa                   | 1365 |



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<210> 251  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 251

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ser | Trp | Asn | Ser | Gly | Ser | Ile | Gly | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 252  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (2)..(2)  
 <223> Xaa can be any naturally occurring amino acid

<400> 252

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | Gln | Leu | Val | Tyr | Phe | Asp |
| 1   |     |     |     | 5   |     |     |     |

<210> 253  
 <211> 455  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 253

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

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

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

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

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

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
180 185 190

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

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

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro Gly Lys  
 450 455

<210> 254  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 254

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
 1 5 10 15

Gly

<210> 255  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 255

Thr Thr Val Thr Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
 1 5 10

<210> 256  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 256

A-1937-WO-PCT\_ST25

Ser Tyr Tyr Trp Ser  
1 5

<210> 257  
<211> 726  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 257  
atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60  
agatgcgaca tccagatgac ccagtctcca agctccctgt ctgctgtgtg gggcgatagg 120  
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180  
ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240  
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360  
aagactcctc tcactttcgg cggaggggacc aagggtggaga tcaaacgaac ggtggctgca 420  
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggaac tgcctctgtt 480  
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540  
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600  
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660  
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720  
gagtgt 726

<210> 258  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 258

A-1937-W0-PCT\_ST25

Tyr Ser Gly Ser Tyr Tyr Tyr Phe Asp  
1 5

<210> 259  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 259

Ser Tyr Tyr Trp Ser  
1 5

<210> 260  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 260

Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 261  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 261

Leu Thr Gly Tyr Phe Asp  
1 5

<210> 262  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 262

Ser Asn Ser Ala Ala Trp Asn  
1 5

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<210> 263  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 263  
 cgggcaagtc agagcattaa caactattta aat

33

<210> 264  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 264

Arg Asp Gly Tyr Asn Tyr Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
 1 5 10

<210> 265  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 265

Gly Tyr Tyr Trp Ser  
 1 5

<210> 266  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 266

Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
 1 5 10 15

<210> 267  
 <211> 13  
 <212> PRT

A-1937-W0-PCT\_ST25

<213> Homo sapiens

<400> 267

Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Thr Tyr Phe Asp  
1 5 10

<210> 268

<211> 7

<212> PRT

<213> Homo sapiens

<400> 268

Ser Gly Ser Tyr Tyr Trp Ser  
1 5

<210> 269

<211> 16

<212> PRT

<213> Homo sapiens

<400> 269

Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 270

<211> 14

<212> PRT

<213> Homo sapiens

<400> 270

Arg Asp Gly Tyr Asn Tyr Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
1 5 10

<210> 271

<211> 5

<212> PRT

<213> Homo sapiens

<400> 271



A-1937-W0-PCT\_ST25

Ser Asn Tyr Met Ser  
1 5

<210> 272  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 272

Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly  
1 5 10 15

<210> 273  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 273

Arg Asp Gly Tyr Asn Tyr Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
1 5 10

<210> 274  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 274

Ser Tyr Ala Met His  
1 5

<210> 275  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 275

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys  
1 5 10 15

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Gly

<210> 276  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 276

Glu Tyr Ser Ser Ser Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp  
 1 5 10

<210> 277  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 277

Ser Tyr Trp Ile Gly  
 1 5

<210> 278  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 278

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
 1 5 10 15

Gly

<210> 279  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 279

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Tyr Asn Trp Asn Asp Asn Trp Phe Asp  
1 5

<210> 280  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 280

Ser Asn Tyr Met Ser  
1 5

<210> 281  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 281

Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly  
1 5 10 15

<210> 282  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 282

Gly Tyr Ser Ser Ser Trp Tyr Tyr Phe Asp  
1 5 10

<210> 283  
<211> 2205  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 283  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg

60

## A-1937-W0-PCT\_ST25

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|----------------------------------------------------------------------|------|
| cgctgtgagg tacaactggg ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc    | 120  |
| aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg    | 180  |
| caagcgcctg gaaaagggct cgagtgggtt tccgccatta cgtggaatag cggacacatc    | 240  |
| gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc    | 300  |
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa    | 360  |
| gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc    | 420  |
| gtctctagtg cctccacca gggcccatcg gtctttcccc tggcaccctc ctccaagagc     | 480  |
| acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccgggtg   | 540  |
| acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta   | 600  |
| cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc   | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa     | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc    | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc  | 840  |
| cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagacc tgagggtcaag  | 900  |
| ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag   | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcttcaccg tcctgcacca ggactggctg    | 1020 |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa    | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc     | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc     | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg    | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag    | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga   | 1440 |
| tcccagggtac agttgcagga gtcagggtcca ggactgggtga agccctcgga gaccctctca | 1500 |

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ctcacctgta ccatctccgg ggacagtgtc tctaccaaca gtgttgcttg gaactggatt 1560  
aggcagcccc cagggaaaagg ccttgagtgg ataggaagga catactacag gtccaagtgg 1620  
tataatgatt atgcagtttc tctgaaaagt cgagtaacca tcagcccaga cacatccaag 1680  
aaccagttct ccctgaagct gagctctgtg actgccgcgg acacggctgt gtattactgt 1740  
gcaagagagg atggggatag ctactaccgc tacggtatgg acgtctgggg ccaagggacc 1800  
acggtcaccg tctcctcagg aggcggagga tctggtggcg gtggttcttg cggcggaggc 1860  
tccgacatcc agatgacca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc 1920  
accatcactt gcagggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta 1980  
gtttggtacc agcagaaaacc aggaaagggt cctaaactgc tcatttactg ggcatctacc 2040  
cgggaatccg ggggtccctag tcgattcagt ggcagcgggt ctgggacaga tttcactctc 2100  
accatcagca gcctgcagcc tgaagatgtg gcaacttatt actgtcagca atattataag 2160  
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<210> 284  
<211> 713  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 284

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1 5 10 15

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

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

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val

## A-1937-W0-PCT\_ST25

50

55

60

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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

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

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

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

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

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

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

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

## A-1937-W0-PCT\_ST25

245

250

255

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

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

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

## A-1937-W0-PCT\_ST25

435

440

445

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

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
 485 490 495

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

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

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
 530 535 540

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

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
 565 570 575

Gly Thr Thr Val Thr Val Ser 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

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

Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Val Trp



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625                                      630                                      635                                      640

Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala  
645                                      650                                      655

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val  
675                                      680                                      685

Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly  
690                                      695                                      700

Gly Gly Thr Lys Val Glu Ile Lys Arg  
705                                      710

<210> 285  
<211> 2166  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 285  
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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atcgatgca ttgggtccgg 180  
caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300  
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa 360  
gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttgggtcacc 420  
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 480

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
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| acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc   | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa    | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc  | 840  |
| cggacccttg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag    | 900  |
| ttcaactggt acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag   | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa    | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc    | 1200 |
| agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccacg    | 1260 |
| cctcccgtgc tggactccga cggctcctt ttcctctata gcaagctcac cgtggacaag    | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga   | 1440 |
| tcccagggtgc agctgcagga gtcgggcccc ggactgggtga agccttcgga gaccctgtcc | 1500 |
| ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag   | 1560 |
| ccccaggta agtgtctgga gtggattggc tatacttatt acagtgggca gaccaaatac    | 1620 |
| aaccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc    | 1680 |
| ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact   | 1740 |
| gggagctact acggctttga ctactggggc cagggaaccc tggtcaccgt ctctcagga    | 1800 |
| ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag    | 1860 |
| tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt   | 1920 |

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cagagcatta acaactatTT aaattggtat cagcagagac cagggaaagc ccctaagctc 1980  
 ctgatctatg ctgcatccag ttTgcaaagt ggggtcccat caaggttcag tggcagtTga 2040  
 tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2100  
 tactgtcaac agagttacag taccctcTgg acgttcggct gtgggaccaa gctggaaatc 2160  
 aaacga 2166

<210> 286  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 286

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

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

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

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

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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

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

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

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

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

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

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

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

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

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

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

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

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

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

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

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

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

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

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

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
675 680 685

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Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg  
690 695 700

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acga 324

<210> 288  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 288

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 Arg Ser Ser  
20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 289  
<211> 360  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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ccagggaagg ggctagagtg gattgggggaa atcaatcatg ctggaatcac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
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<210> 290  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 290



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

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

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

Gly Glu Ile Asn His Ala Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 291

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 291

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gggaaagccc ctaagctcct gatctatgct acatccagtt tgcaaagtgg ggtcccatca 180

A-1937-W0-PCT\_ST25

aggttcagtg gcagtggatc tgggacagat ttctctctca ccatcagcag tctgcaacct 240  
gaagattttg caacttactt ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagg tggagatcaa acga 324

<210> 292  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 292

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 293  
<211> 354  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 293

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acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc      120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac      180
ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg      240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaattggg      300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc cagt          354

```

<210> 294

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 294

```

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

```

```

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
          20              25              30

```

```

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35              40              45

```

```

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50              55              60

```

```

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

```

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

Arg Glu Ile Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
115

<210> 295  
<211> 342  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 295  
gacatccaga tgacccagtc tccaagctcc ctgtctgctg ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga 342

<210> 296  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 296

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

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

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys

<210> 297  
<211> 375  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 297  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300

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agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct ccagt 375

<210> 298

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 298

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

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

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

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

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

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 299

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<211> 342  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 299  
 gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
 tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
 gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcagcctga agatttcgca acttattact gtcagcaata ttataagact 300  
 cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga 342

<210> 300  
 <211> 113  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 300

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

|       |                     |
|-------|---------------------|
| <210> | 301                 |
| <211> | 375                 |
| <212> | DNA                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polynucleotide

|            |             |            |
|------------|-------------|------------|
| <400>      | 301         |            |
| gaggtacagt | tgctggagtc  | aggtggagga |
| ctggtgcagc | ccgggggggag | cttccgactc |
|            |             | 60         |
| agctgtgcc  | tctccgggga  | cagtgtctct |
| accaacagt  | ttgcttggaa  | ctggatcagg |
|            |             | 120        |
| caggccccag | ggaaaggcct  | tgagtgggtg |
| agcaggacat | actacaggtc  | caagtggtat |
|            |             | 180        |
| aatgattatg | cagtttctgt  | gaaaggtcga |
| ttcaccatca | gcccagacac  | atccaagaac |
|            |             | 240        |
| acgttctacc | tgcagatgaa  | ctctctgaga |
| gccgaggaca | cggctgtgta  | ttactgtgca |
|            |             | 300        |
| agagaggatg | gggatagcta  | ctaccgctac |
| ggtatggacg | tctggggcca  | agggaccacg |
|            |             | 360        |
| gtcaccgtct | ccagt       |            |
|            |             | 375        |

|       |                     |
|-------|---------------------|
| <210> | 302                 |
| <211> | 125                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 302



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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 Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

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

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

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

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

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 303

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 303

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc ggacaagtca ggacattaga gatgatttag gctggatatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccagtt tgcaaagtgg ggtcccatca 180

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aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240  
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa 300  
gggaccaagg tggaaatcaa acga 324

<210> 304  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 304

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
20 25 30

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

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 305  
<211> 369  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 305

```

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc      60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct      120
ccaggcaagg ggctggagtg ggtggcagtc atatcatatg atggaaataa taaactctat      180
acagactccg tgaagggccg attcaccatc tccagagacg attccaagag cagcctgtat      240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcca      300
acagtaactc tctactacta ctacggtatg gacgtctggg gccaaaggac cacggtcacc      360
gtctccagt                                     369

```

<210> 306

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 306

```

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

```

```

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

```

```

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

```

```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr

```

65                      70                      75                      —                      80

Ala Arg Asp Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
100 105 110

|       |                     |
|-------|---------------------|
| <210> | 307                 |
| <211> | 324                 |
| <212> | DNA                 |
| <213> | Artificial Sequence |

|            |             |            |            |            |            |  |     |
|------------|-------------|------------|------------|------------|------------|--|-----|
| <400>      | 307         |            |            |            |            |  |     |
| gacatccaga | tgaccagtc   | tccatcctcc | ctgtctgcat | ctgtaggaga | cagagtcacc |  | 60  |
| atcacttgcc | ggacaagtca  | ggacattaga | gatgatttag | gctggtatca | gcagaaacca |  | 120 |
| gggaaagccc | ctaagcgcct  | gatctatgat | gcatccagtt | tgcaaagtgg | ggtcccatca |  | 180 |
| aggttcagcg | gcagtggatc  | tgggacagaa | ttcactctca | caatcagcag | cctgcagcct |  | 240 |
| gaagattttg | caacttatta  | ctgtctacag | cataatagtt | accctccgac | gttcggccaa |  | 300 |
| gggaccaagg | tggaatatcaa | acga       |            |            |            |  | 324 |

|                       |                     |
|-----------------------|---------------------|
| $\langle 210 \rangle$ | 308                 |
| $\langle 211 \rangle$ | 107                 |
| $\langle 212 \rangle$ | PRT                 |
| $\langle 213 \rangle$ | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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|                                                                 |     |     |    |
|-----------------------------------------------------------------|-----|-----|----|
| 1                                                               | 5   | 10  | 15 |
| Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Arg Asp Asp | 20  | 25  | 30 |
| Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile | 35  | 40  | 45 |
| Tyr Asp Ala Ser Ser Leu Gln 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 |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro | 85  | 90  | 95 |
| Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys                     | 100 | 105 |    |

<210> 309  
 <211> 369  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 309                                                          |     |
| caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 60  |
| tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct  | 120 |
| ccaggcaagg ggctggagtg ggtggcagtc atatcatatg atggaaataa taaactctat  | 180 |
| acagactccg tgaagggccg attcaccatc tccagagacg attccaagag cacgctgtat  | 240 |
| ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagatcca  | 300 |
| acagtaactc tctactacta ctacggtatg gacgtctggg gccaaaggac cacggtcacc  | 360 |

gtctccagt

369

<210> 310  
 <211> 123  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 310

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr  
 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 Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120

<210> 311  
 <211> 2205  
 <212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 311

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg | 60   |
| cgctgtgagg tacaactggt ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc  | 120  |
| aggcttagct gtgcggcatc ggggttttact ttcgatgatt atgcgatgca ttgggtccgg | 180  |
| caagcgcttg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc  | 240  |
| gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc  | 300  |
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa  | 360  |
| gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc  | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc   | 480  |
| acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg  | 540  |
| acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc  | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaagggt ggacaagaaa  | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc  | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc caaaaacca aggacaccct catgatctcc | 840  |
| cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag   | 900  |
| ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag  | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg  | 1020 |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa  | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc  | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg  | 1260 |

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cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1320  
 agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1380  
 cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga 1440  
 tcccaggtag agttgcagga gtcagggtcca ggactgggtga agccctcgga gaccctctca 1500  
 ctcacctgta ccatctccgg ggacagtgtc tctaccaaca gtgttgcttg gaactggatt 1560  
 aggcagcccc cagggaaatg ccttgagtgg ataggaagga catactacag gtccaagtgg 1620  
 tataatgatt atgcagtttc tctgaaaagt cgagtaacca tcagcccaga cacatccaag 1680  
 aaccagttct ccctgaagct gagctctgtg actgccgcgg acacggctgt gtattactgt 1740  
 gcaagagagg atggggatag ctactaccgc tacgggtatgg acgtctgggg ccaagggacc 1800  
 acggtcaccg tctcctcagg aggcggagga tctgggtggcg gtggttcttg cggcggaggc 1860  
 tccgacatcc agatgacca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc 1920  
 accatcactt gcagggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta 1980  
 gtttggtacc agcagaaacc aggaaagggt cctaaactgc tcatttactg ggcatctacc 2040  
 cgggaatccg ggggtccctag tcgattcagt ggcagcgggt ctgggacaga tttcactctc 2100  
 accatcagca gcctgcagcc tgaagatgtg gcaacttatt actgtcagca atattataag 2160  
 actcctctca ctttcggctg tgggaccaag gtggagatca aacga 2205

<210> 312

<211> 713

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 312

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr



## A-1937-W0-PCT\_ST25

20

25

30

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

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

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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

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

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

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

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

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

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210

215

220

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

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

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

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

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

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

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

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

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

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

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405

410

415

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

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

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

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
 485 490 495

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

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

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
 530 535 540

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

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
 565 570 575

Gly Thr Thr Val Thr Val Ser 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

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595

600

605

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

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

Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala  
645 650 655

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val  
675 680 685

Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly  
690 695 700

Cys Gly Thr Lys Val Glu Ile Lys Arg  
705 710

<210> 313  
<211> 2151  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 313  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtgagg tgcagctggg gcagctctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgctg 180  
cagatgccccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc  | 300  |
| gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga  | 360  |
| agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc  | 420  |
| accaagggcc catcggctctt ccccttgga cctcctcca agagcacctc tgggggcaca   | 480  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  | 540  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc  | 600  |
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaatct  | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 780  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 1020 |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1200 |
| gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac  | 1260 |
| tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1380 |
| agcctctccc tgtctccggg tgggtggcga tcgggagggtg gcggatccca ggtgcagctg | 1440 |
| caggagtccg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc  | 1500 |
| tctggtggct ccatcagtag ttacttctgg agctggatcc ggcagcccc aggtaaggga   | 1560 |
| ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag  | 1620 |
| agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct  | 1680 |

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gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc 1740  
 tttgactact ggggccaggg aaccctgggt accgtctcct caggaggcgg aggatctggt 1800  
 ggcgggtggtt ctggcggcgg aggctccgac atccagatga cccagtctcc atcctccctg 1860  
 tctgcatctg taggagacag agtcaccatc acttgccggg caagtcagag cattaacaac 1920  
 tatttaaaatt ggtatcagca gagaccaggg aaagccccta agctcctgat ctatgctgca 1980  
 tccagtttgc aaagtgggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2040  
 actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2100  
 tacagtaccc ctcggacgtt cggccaaggg accaagctgg aaatcaaacg a 2151

<210> 314  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 314

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

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

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys

## A-1937-W0-PCT\_ST25

85

90

95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

## A-1937-W0-PCT\_ST25

275

280

285

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly



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

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

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

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

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

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr

## A-1937-W0-PCT\_ST25

660

665

670

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly  
 675 680 685

Thr Lys Leu Glu Ile Lys Arg  
 690 695

<210> 315  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 315  
 atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
 agatgcgagg ttcagctggc cgagtcagga ggcggctctg tgcagcctgg cggatcactg 120  
 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
 caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
 atttatgctg acagcgtcaa gggcagattc acgatctctc tagacacatc caagtcaaca 300  
 gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
 ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac cgtctctagt 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840

A-1937-W0-PCT\_ST25

gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 900  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc 960  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260  
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg 1320  
 cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtaaa 1410

<210> 316

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 316

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
 35 40 45

Tyr Val Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly  
 50 55 60

Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Tyr | Ala | Asp | Ser | Val | Lys | Gly | Arg | Phe | Thr | Ile | Ser | Leu | Asp | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Lys | Ser | Thr | Ala | Tyr | Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Arg | Gly | Tyr | Arg | Ser | Tyr | Ala | Met | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Lys | Ser | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp |

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260

265

270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
305 310 315 320

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
385 390 395 400

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
435 440 445

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

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450

455

460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 317  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 317

Ser Tyr Ala Met His  
1 5

<210> 318  
<211> 215  
<212> PRT  
<213> Homo sapiens

<400> 318

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

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

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

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

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Arg Thr Phe Gly Gln Gly Thr Lys Leu 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  
210 215

<210> 319  
<211> 2190  
<212> DNA  
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<220>  
<223> Synthetic polynucleotide

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cgctgtgagg tgcagctggg gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctgagatacc   | 240  |
| agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc   | 300  |
| gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga   | 360  |
| agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc   | 420  |
| accaagggcc catcggctct ccccttgga cctcctcca agagcacctc tgggggcaca     | 480  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   | 540  |
| tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc    | 600  |
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagtga gccc aaatct | 720  |
| tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca    | 780  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga cctgaggtc      | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 1020 |
| aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc       | 1080 |
| aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccgga ggagatgacc   | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1260 |
| tccgacggct cttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag    | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1380 |
| agcctctccc tgtctccggg tgggtggcgga tcgggagggtg gcggatcca ggtacagttg  | 1440 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc   | 1500 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg    | 1560 |
| aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca     | 1620 |



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gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg 1680  
aagctgagct ctgtgactgc cgcggaacac gctgtgtatt actgtgcaag agaggatggg 1740  
gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 1800  
tcaggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctccga catccagatg 1860  
accagtcctc caagctccct gtctgcgtct gtgggcgata gggtcaccat cacttgacgg 1920  
tccagccaga gtgtgttata cagctccaac aataagaact acttagtttg gtaccagcag 1980  
aaaccaggaa aggttcctaa actgctcatt tactgggcat ctaccggga atccggggtc 2040  
cctagtcgat tcagtggcag cgggtctggg acagatttca ctctcaccat cagcagcctg 2100  
cagcctgaag atgtggcaac ttattactgt cagcaatatt ataagactcc tctcactttc 2160  
ggcggaggga ccaaggtgga gatcaaacga 2190

<210> 320

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 320

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

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

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

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |
| Leu | Gln | Trp | Ser | Ser | Leu | Lys |
|     |     |     | 85  |     |     | Ala |
|     |     |     |     | Ser | Asp | Thr |
|     |     |     |     | 90  |     | Ala |
|     |     |     |     |     | Met | Tyr |
|     |     |     |     |     |     | 95  |
|     |     |     |     |     |     | Tyr |
|     |     |     |     |     |     | Cys |
| Ala | Arg | Ser | Asn | Trp | Gly | Leu |
|     |     |     | 100 |     |     | Asp |
|     |     |     |     | Tyr | Trp | Gly |
|     |     |     |     | 105 |     | Gln |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | 110 |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Val |
| Thr | Val | Ser | Ser | Ala | Ser | Thr |
|     |     |     |     |     |     | 115 |
|     |     |     |     |     |     | Lys |
|     |     |     |     |     |     | 120 |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Phe |
|     |     |     |     |     |     | 125 |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Ala |
| Pro | Ser | Ser | Lys | Ser | Thr | Ser |
|     |     |     |     |     |     | 130 |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | 135 |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Ala |
|     |     |     |     |     |     | Ala |
|     |     |     |     |     |     | 140 |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | Cys |
|     |     |     |     |     |     | Leu |
| Val | Lys | Asp | Tyr | Phe | Pro | Glu |
|     |     |     |     |     |     | 145 |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | 150 |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | 155 |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Trp |
|     |     |     |     |     |     | Asn |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | 160 |
| Ala | Leu | Thr | Ser | Gly | Val | His |
|     |     |     |     |     |     | 165 |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Phe |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Ala |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Gln |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | 175 |
| Gly | Leu | Tyr | Ser | Leu | Ser | Ser |
|     |     |     |     |     |     | 180 |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | 185 |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Leu |
| Gly | Thr | Gln | Thr | Tyr | Ile | Cys |
|     |     |     |     |     |     | 195 |
|     |     |     |     |     |     | Asn |
|     |     |     |     |     |     | 200 |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Asn |
|     |     |     |     |     |     | His |
|     |     |     |     |     |     | Lys |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | 205 |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Asn |
|     |     |     |     |     |     | Thr |
| Lys | Val | Asp | Lys | Lys | Val | Glu |
|     |     |     |     |     |     | 210 |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Lys |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Cys |
|     |     |     |     |     |     | Asp |
|     |     |     |     |     |     | 215 |
|     |     |     |     |     |     | Lys |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | His |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | 220 |
| Cys | Pro | Pro | Cys | Pro | Ala | Pro |
|     |     |     |     |     |     | 225 |
|     |     |     |     |     |     | Glu |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | 230 |
|     |     |     |     |     |     | Gly |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Phe |
|     |     |     |     |     |     | 235 |
|     |     |     |     |     |     | 240 |
| Leu | Phe | Pro | Pro | Lys | Pro | Lys |
|     |     |     |     |     |     | 245 |
|     |     |     |     |     |     | Asp |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Leu |
|     |     |     |     |     |     | Met |
|     |     |     |     |     |     | Ile |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | Arg |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | 250 |
|     |     |     |     |     |     | 255 |
|     |     |     |     |     |     | Pro |
| Glu | Val | Thr | Cys | Val | Val | Val |
|     |     |     |     |     |     | Asp |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Ser |
|     |     |     |     |     |     | His |
|     |     |     |     |     |     | Glu |
|     |     |     |     |     |     | Asp |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Glu |
|     |     |     |     |     |     | Val |

## A-1937-W0-PCT\_ST25

260

265

270

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

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly

## A-1937-W0-PCT\_ST25

450

455

460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
 465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
 485 490 495

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

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

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
 530 535 540

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

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

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

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

Gly Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser

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645

650

655

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

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

Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val  
690 695 700

Glu Ile Lys Arg  
705

<210> 321  
<211> 2151  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 321  
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cgctgtgagg tgcagctggg gcagctctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180  
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttgggtga ctgagatacc 240  
agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc 300  
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
accaagggcc catcgggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaaagttga gcccaaactct | 720  |
| tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca    | 780  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccttgaggtc     | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 1020 |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaacat ctcaaagcc       | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1260 |
| tccgacggct ctttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag     | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1380 |
| agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtgcagctg   | 1440 |
| caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc   | 1500 |
| tctggtggct ccatcagtag ttacttctgg agctggatcc ggcagcccc aggtaagtgt    | 1560 |
| ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag   | 1620 |
| agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct   | 1680 |
| gtgaccgtg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc    | 1740 |
| tttgactact ggggccaggg aaccctggtc accgtctcct caggaggcgg aggatctggt   | 1800 |
| ggcgggtggt ctggcggcgg aggctccgac atccagatga cccagtctcc atcctccctg   | 1860 |
| tctgcatctg taggagacag agtcaccatc acttgccggg caagtcagag cattaacaac   | 1920 |
| tatttaaatt ggtatcagca gagaccaggg aaagccccta agctcctgat ctatgctgca   | 1980 |
| tccagtttgc aaagtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc   | 2040 |

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actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2100

tacagtaccc ctcggacggtt cggctgtggg accaagctgg aaatcaaacg a 2151

<210> 322

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 322

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

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

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

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

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

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

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

## A-1937-W0-PCT\_ST25

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser



## A-1937-W0-PCT\_ST25

325

330

335

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

Ser Arg Glu Glu Met 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

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
 465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
 485 490 495

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

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser

## A-1937-W0-PCT\_ST25

515

520

525

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

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Asp Ile Gln Met Thr  
 580 585 590

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

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

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

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

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

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Cys Gly  
 675 680 685

Thr Lys Leu Glu Ile Lys Arg  
 690 695

&lt;210&gt; 323

A-1937-W0-PCT\_ST25

<211> 242  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 323

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser  
 35 40 45

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr  
 50 55 60

Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser  
 65 70 75 80

Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
 85 90 95

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala  
 100 105 110

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly  
 115 120 125

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe  
 130 135 140

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 145 150 155 160

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Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
165 170 175

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
180 185 190

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
195 200 205

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
210 215 220

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
225 230 235 240

Glu Cys

<210> 324  
<211> 1431  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 324  
atggacatga gaggatgcctgc acagctgctg ggccctgctgc tgctgtggct gagaggcgcc 60  
agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120  
cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
atcaggcagg cccaggggaa aggccttgag tgggtgagca ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctgtgaaa ggctgattca ccatcagccc agacacatcc 300  
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| accacggtca ccgtctccag tgcctccacc aagggcccat cggtcttccc cctggcaccc  | 480  |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc | 540  |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc  | 600  |
| ccggctgtcc tacagtcttc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag  | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc   | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc   | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac  | 900  |
| cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag  | 960  |
| ccgtgcgagg agcagtacgg cagcacgtac cgttgctgca gcgtcctcac cgtcctgcac  | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc  | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc  | 1140 |
| ctgcccccat cccggaagga gatgaccaag aaccagggtc gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac  | 1260 |
| tacaagacca cgcctcccgt gctgaagtcc gacggctcct tcttcctcta tagcaagctc  | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a           | 1431 |

<210> 325  
 <211> 477  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 325

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Met | Arg | Val | Pro | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Leu | Leu | Trp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

A-1937-W0-PCT\_ST25

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

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

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Ala  
50 55 60

Pro Gly Lys Gly Leu Glu Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys  
65 70 75 80

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

Pro Asp Thr Ser Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg  
100 105 110

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
115 120 125

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
130 135 140

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

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

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

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

A-1937-W0-PCT\_ST25

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

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

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

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

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

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

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

Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu  
325 330 335

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

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

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

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

A-1937-W0-PCT\_ST25

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

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

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

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

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

<210> 326  
<211> 726  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 326  
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cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120  
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180  
ttagtttggt accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240  
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360  
aagactcctc tcactttcgg cggaggggacc aagggtggaga tcaaacgaac ggtggctgca 420  
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtag cgctctgttt 480  
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540



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gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600  
 tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660  
 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720  
 gagtgt 726

<210> 327  
 <211> 242  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 327

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser  
 35 40 45

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr  
 50 55 60

Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser  
 65 70 75 80

Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
 85 90 95

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala  
 100 105 110

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly

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115 120 125

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe  
130 135 140

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
145 150 155 160

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
165 170 175

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
180 185 190

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
195 200 205

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
210 215 220

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
225 230 235 240

Glu Cys

<210> 328

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 328

atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60

agatgccagg tgcagctggt ggagctctggg ggaggcgtgg tccagcctgg gaggtccctg 120

## A-1937-W0-PCT\_ST25

agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180  
 caggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa 240  
 ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg 300  
 ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg 420  
 gtcaccgtct ccagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540  
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600  
 gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc 660  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720  
 aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 780  
 gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 840  
 atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900  
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc 960  
 gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac 1020  
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc 1080  
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140  
 ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc 1200  
 tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260  
 accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320  
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380  
 cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

&lt;210&gt; 329

&lt;211&gt; 475

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 329

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

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

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
 35 40 45

Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly  
 50 55 60

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro Thr Val Thr Leu Tyr Tyr  
 115 120 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser  
 130 135 140

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

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

## A-1937-W0-PCT\_ST25

165

170

175

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

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

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
 210 215 220

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

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
 290 295 300

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

Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val  
 325 330 335

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

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

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355

360

365

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

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

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

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

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

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

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
465 470 475

<210> 330

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 330

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120

gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180

aaaccaggga aagcccctaa gctcctgatc tatgatgcat ccagtttgca aagtggggtc 240

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ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360  
ggccaagggga ccaaggtgga aatcaaacga acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 331  
<211> 236  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 331

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser  
35 40 45

Gln Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

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

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr

## A-1937-W0-PCT\_ST25

85

90

95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
 100 105 110

His Asn Ser Tyr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 180 185 190

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

&lt;210&gt; 332

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 332



## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc    | 60   |
| agatgccagg tgcagctggg ggagctctggg ggaggcgtgg tccagcctgg gaggtccctg | 120  |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc  | 180  |
| caggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa  | 240  |
| ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg  | 300  |
| ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga  | 360  |
| gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg  | 420  |
| gtcaccgtct ccagtgcctc caccaagggc ccatcggctt tccccctggc accctcctcc  | 480  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 540  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 600  |
| gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc  | 660  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 720  |
| aagaaagtgt agcccaaatac ttgtgacaaa actcacacat gcccaccgtg cccagcacct | 780  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg  | 840  |
| atctcccgga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag | 900  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc  | 960  |
| gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac  | 1020 |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc    | 1080 |
| gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc | 1140 |
| ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc  | 1200 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1260 |
| accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1320 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1380 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa                  | 1425 |

A-1937-WO-PCT\_ST25

<210> 333  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 333

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

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

Tyr Ser Ala Ser Phe Leu Tyr 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 Tyr Asn Ile Tyr Pro Leu  
 85 90 95

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

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

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145                      150                      155                      160

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

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

Phe Asn Arg Gly Glu Cys  
210

|       |                     |
|-------|---------------------|
| <210> | 334                 |
| <211> | 708                 |
| <212> | DNA                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polynucleotide

|            |            |             |            |            |             |  |     |
|------------|------------|-------------|------------|------------|-------------|--|-----|
| <400>      | 334        |             |            |            |             |  |     |
| atggacatga | gagtgcctgc | acagctgctg  | ggcctgctgc | tgctgtggct | gagaggcgcc  |  | 60  |
| agatgcgaca | tccagatgac | ccagtctcca  | tcctccctgt | ctgcatctgt | aggagacaga  |  | 120 |
| gtcaccatca | cttgccggac | aagtcaggac  | attagagatg | atttaggctg | gtatcagcag  |  | 180 |
| aaaccagggg | aagcccctaa | gcgccctgatc | tatgatgcat | ccagtttgca | aagtgggggtc |  | 240 |
| ccatcaaggt | tcagcggcag | tggatctggg  | acagaattca | ctctcacaat | cagcagcctg  |  | 300 |
| cagcctgaag | attttgcaac | ttattactgt  | ctacagcata | atagttaccc | tccgacgttc  |  | 360 |
| ggccaagggg | ccaaggtgga | aatcaaacga  | acggtggctg | caccatctgt | cttcattcttc |  | 420 |
| ccgccatctg | atgagcagtt | gaaatctgga  | actgcctctg | ttgtgtgcct | gctgaataac  |  | 480 |
| ttctatccca | gagaggccaa | agtacagtgg  | aaggtggata | acgccctcca | atcgggtaac  |  | 540 |
| tcccaggaga | gtgtcacaga | gcaggacagc  | aaggacagca | cctacagcct | caagagcacc  |  | 600 |

A-1937-W0-PCT\_ST25

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 335

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 335

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser  
35 40 45

Gln Asp Ile Arg Asp Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val  
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
100 105 110

His Asn Ser Tyr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

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130

135

140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 336  
<211> 717  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 336  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagt ctgtgctgac gcagccgccc tcagtgtctg gggccccagg gcagagggtc 120  
accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aacttggtac 180  
cagcagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240  
gggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300  
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360

A-1937-W0-PCT\_ST25

ggttcgggtgt tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420  
 tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactgggtg 480  
 tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540  
 cccgtcaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600  
 gccgagagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660  
 caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca 717

<210> 337

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 337

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

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

Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser  
 35 40 45

Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Phe Pro  
 50 55 60

Gly Thr Ala Pro Lys Leu Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser  
 65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
 85 90 95

Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys

A-1937-W0-PCT\_ST25

100

105

110

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val Phe Gly Gly Gly Thr  
115 120 125

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

Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val  
145 150 155 160

Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys  
165 170 175

Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser  
180 185 190

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr  
195 200 205

Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His  
210 215 220

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
225 230 235

<210> 338

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 338

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60

cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120

## A-1937-W0-PCT\_ST25

aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgcgc 180  
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctgagatacc 240  
agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc 300  
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
accaagggcc catcggctctt ccccttgga cccctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctgaggactc 600  
tactccctca agagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 720  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg 960  
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020  
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1080  
aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc 1140  
aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg 1200  
gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac 1260  
tccgacggct ctttcttct ctatagcgac ctaccgtgg acaagagcag gtggcagcag 1320  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380  
agcctctccc tgtctccggg taaa 1404

&lt;210&gt; 339

&lt;211&gt; 468

&lt;212&gt; PRT



&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 339

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

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

Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu  
 35 40 45

Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly  
 50 55 60

Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr  
 65 70 75 80

Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys  
 85 90 95

Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp  
 100 105 110

Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp  
 115 120 125

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

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

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr

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165

170

175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
 180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr  
 195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn  
 210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser  
 225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
 245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
 260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
 275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
 290 295 300

Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr  
 305 310 315 320

Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
 325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
 340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

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355

360

365

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro  
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp Leu Thr  
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
450 455 460

Ser Pro Gly Lys  
465

<210> 340  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 340  
atggacatga ggggtccccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag 180  
aaaccaggga aagcccctaa ggcctgatc tatgctgcgt ccagtttgca aagtggggtc 240

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ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360  
ggcggaggga ccaaggtgga gatcaaacgt acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aaggtaggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 341  
<211> 236  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 341

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
35 40 45

Gln Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val  
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr

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85

90

95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
 100 105 110

His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 180 185 190

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

&lt;210&gt; 342

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 342

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg | 60   |
| cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg  | 120  |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc  | 180  |
| caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa  | 240  |
| tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg  | 300  |
| ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga  | 360  |
| gagggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc | 420  |
| acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc  | 480  |
| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc   | 540  |
| gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc | 600  |
| gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc  | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg | 720  |
| gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca  | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc  | 840  |
| atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct  | 900  |
| gagggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg  | 960  |
| tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag  | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg  | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc  | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac  | 1260 |
| gacaccacgc ctcccgctgt ggactccgac ggctccttct tcctctatag cgacctcacc  | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa               | 1428 |

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<210> 343  
 <211> 476  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 343

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

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

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
 35 40 45

Phe Thr Phe Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Pro Gly  
 50 55 60

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

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

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

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

Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
 130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser

145                      150                      155                      160

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

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

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

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

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

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

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

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

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

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr  
325 330 335

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val



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340

345

350

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

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

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

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

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

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

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

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

<210> 344

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 344

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60

cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc   | 180  |
| cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc   | 240  |
| agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc   | 300  |
| gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga   | 360  |
| agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc   | 420  |
| accaagggcc catcggctctt ccccttgga cccctctcca agagcacctc tgggggcaca   | 480  |
| gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac   | 540  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc    | 600  |
| tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 780  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 1020 |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc     | 1080 |
| aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc  | 1140 |
| aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg   | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1260 |
| tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag    | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1380 |
| agcctctccc tgtctccggg tgggtggcga tcgggagggtg gcggatccca ggtacagttg  | 1440 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc   | 1500 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg    | 1560 |

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aaatgccttg agtggatagg aaggacatac tacagggtcca agtggataa tgattatgca 1620  
 gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg 1680  
 aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg 1740  
 gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggg caccgtctcc 1800  
 tcaggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggtccga catccagatg 1860  
 acccagtctc caagctccct gtctgcgtct gtgggcgata gggtcacat cacttgacgg 1920  
 tccagccaga gtgtgttata cagctccaac aataagaact acttagtttg gtaccagcag 1980  
 aaaccaggaa aggttcctaa actgctcatt tactgggcat ctaccggga atccggggtc 2040  
 cctagtcgat tcagtggcag cgggtctggg acagatttca ctctcaccat cagcagcctg 2100  
 cagcctgaag atgtggcaac ttattactgt cagcaatatt ataagactcc tctcactttc 2160  
 ggctgtggga ccaaggtgga gatcaaacga 2190

<210> 345

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 345

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Lys | Ile | Ser | Cys | Lys | Thr | Ser | Glu | Tyr | Ser | Phe | Thr | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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

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

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

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

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
485 490 495

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

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

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

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

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

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

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

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

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

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

Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val  
690 695 700

Glu Ile Lys Arg  
705

<210> 346  
<211> 2175  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 346  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttccccg | 600  |
| gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc   | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg  | 720  |
| gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca  | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc   | 840  |
| atgatctccc ggacccctga ggtcacatgc gtgggtgggtgg acgtgagcca cgaagaccct | 900  |
| gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcca gacaaagccg  | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag   | 1020 |
| gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac    | 1260 |
| aagaccacgc ctcccgctgt ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtgg cggatcggga  | 1440 |
| ggtggcggat cccagggtgca gctgcaggag tcgggcccag gactggtgaa gccttcggag  | 1500 |
| accctgtccc tcacctgcac tgtctctggt ggctccatca gtagttactt ctggagctgg   | 1560 |
| atccggcagc cccaggtaa gggactggag tggattggct atatctatta cagtgggcag    | 1620 |
| accaaataca acccctccct caagagtcga gtcaccatat caatagacac gtccaagaac   | 1680 |
| cagttctccc tgaagctgag ctctgtgacc gctgcggaca cggccgtgta ttactgtgcg   | 1740 |
| agagaaactg ggagctacta cggctttgac tactggggcc agggaaacct ggtcaccgtc   | 1800 |
| tcctcaggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag  | 1860 |
| atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc   | 1920 |
| cgggcaagtc agagcattaa caactattta aattggtatc agcagagacc agggaaagcc   | 1980 |



A-1937-W0-PCT\_ST25

cctaagctcc tgatctatgc tgcattccagt ttgcaaagtg ggggtcccatc aaggttcagt 2040  
 ggccagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 2100  
 gcaacttact actgtcaaca gagttacagt acccctcgga cgttcggcca agggaccaag 2160  
 ctggaaatca aacga 2175

<210> 347  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 347

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

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

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys

## A-1937-W0-PCT\_ST25

115

120

125

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 180 185 190

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

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

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

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

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp

305                      310                      315                      320

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

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

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

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

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

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

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

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

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr

## A-1937-W0-PCT\_ST25

500

505

510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
 515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
 530 535 540

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

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

Thr Val Ser 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 Ser Leu Ser Ala  
 595 600 605

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

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

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

Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

690

695

700

<210> 348  
 <211> 2214  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 348  
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 cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
 agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
 caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
 tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
 ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
 acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540  
 gaaccggtga cgggtgctgt gaactcaggc gccctgacca gcggcgtgca caccttcccc 600  
 gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660  
 agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720  
 gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
 cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840  
 atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900  
 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 960  
 tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag 1020  
 gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1080

A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac   | 1260 |
| aagaccacgc ctcccgctgt ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtctttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtgg cggatcggga  | 1440 |
| gggtggcggat cccaggtaca gttgcaggag tcaggtccag gactgggtgaa gccctcggag | 1500 |
| accctctcac tcacctgtac catctccggg gacagtgtct ctaccaacag tgttgcttgg   | 1560 |
| aactggatta ggcagcccc agggaaaaggc cttgagtgga taggaaggac atactacagg   | 1620 |
| tccaagtggg ataagtatta tgcagtttct ctgaaaagtc gagtaaccat cagcccagac   | 1680 |
| acatccaaga accagttctc cctgaagctg agctctgtga ctgccgcgga cacggctgtg   | 1740 |
| tattactgtg caagagagga tggggatagc tactaccgct acggtatgga cgtctggggc   | 1800 |
| caagggacca cggtcaccgt ctctcagga ggccggaggat ctggtggcgg tggttctggc   | 1860 |
| ggcggaggct ccgacatcca gatgaccag tctccaagct ccctgtctgc gtctgtgggc    | 1920 |
| gatagggtca ccatcacttg caggtccagc cagagtgtgt tatacagctc caacaataag   | 1980 |
| aactacttag tttggtacca gcagaaacca ggaaagggtc ctaaactgct catttactgg   | 2040 |
| gcatctaccc gggaatccgg ggtccctagt cgattcagtg gcagcgggtc tgggacagat   | 2100 |
| ttcactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta ctgtcagcaa   | 2160 |
| tattataaga ctctctcac tttcggcgga gggaccaagg tggagatcaa acga          | 2214 |

<210> 349

<211> 716

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 349

A-1937-W0-PCT\_ST25

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

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

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

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

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

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

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

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

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

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

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

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

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



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

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

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

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

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

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

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

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

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

A-1937-W0-PCT\_ST25

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
580 585 590

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

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

Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr  
625 630 635 640

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
645 650 655

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
660 665 670

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu  
690 695 700

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
705 710 715

<210> 350

<211> 2175

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 350

atggacatga ggggtgccccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg

60

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg  | 120  |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc  | 180  |
| caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa  | 240  |
| tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg  | 300  |
| ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga  | 360  |
| gagggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc | 420  |
| acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc  | 480  |
| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc   | 540  |
| gaaccggtga cgggtgctgt gaactcaggc gccctgacca gcggcgtgca caccttcccg  | 600  |
| gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc  | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg | 720  |
| gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc  | 840  |
| atgatctccc ggaccctga ggtcacatgc gtgggtggtgg acgtgagcca cgaagaccct  | 900  |
| gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcaa gacaaagccg | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag  | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggctctcca acaaagccct cccagcccc  | 1080 |
| atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc  | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac  | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc  | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggtgg cggatcggga  | 1440 |
| ggtggcggat cccagggtgca gctgcaggag tcgggcccag gactggtgaa gccttcggag | 1500 |

A-1937-W0-PCT\_ST25

accctgtccc tcacctgcac tgtctctggg ggctccatca gtagttactt ctggagctgg 1560  
atccggcagc ccccaggtaa gtgtctggag tggattggct atatctatta cagtgggcag 1620  
accaaataca acccctccct caagagtcga gtcaccatat caatagacac gtccaagaac 1680  
cagttctccc tgaagctgag ctctgtgacc gctgcggaca cggccgtgta ttactgtgcg 1740  
agagaaactg ggagctacta cggctttgac tactggggcc agggaaacct ggtcaccgtc 1800  
tcctcaggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag 1860  
atgaccagct ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 1920  
cgggcaagtc agagcattaa caactattta aattggtatc agcagagacc agggaaagcc 1980  
cctaagctcc tgatctatgc tgcattccagt ttgcaaagtg gggccccatc aaggttcagt 2040  
ggcagtggtat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 2100  
gcaacttact actgtcaaca gagttacagt acccctcgga cgttcggctg tgggaccaag 2160  
ctggaaatca aacga 2175

<210> 351  
<211> 703  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 351

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val

## A-1937-W0-PCT\_ST25

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 180 185 190

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

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

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

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

## A-1937-W0-PCT\_ST25

245

250

255

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

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

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

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

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

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

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

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

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

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

## A-1937-W0-PCT\_ST25

435

440

445

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

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
 465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
 485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Tyr  
 500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
 515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
 530 535 540

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

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

Thr Val Ser 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 Ser Leu Ser Ala  
 595 600 605

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

Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys

625                      630                      635                      640

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

Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg  
690 695 700

<220>  
<223> Synthetic polynucleotide

[illegible]



## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc  | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg  | 720  |
| gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca  | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc  | 840  |
| atgatctccc ggaccctga ggtcacatgc gtgggtgggg acgtgagcca cgaagaccct   | 900  |
| gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg   | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag  | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc  | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac   | 1260 |
| aagaccacgc ctcccgctg gactccgac ggctccttct tcctctatag caagctcacc    | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtgg cggatcggga | 1440 |
| gggtggcgat cccaggtaca gttgcaggag tcaggtccag gactggtgaa gccctcggag  | 1500 |
| accctctcac tcacctgtac catctccggg gacagtgtct ctaccaacag tgttgcttgg  | 1560 |
| aactggatta ggagccccc agggaaatgc cttgagtgga taggaaggac atactacagg   | 1620 |
| tccaagtggg ataagtatta tgcagtttct ctgaaaagtc gagtaaccat cagcccagac  | 1680 |
| acatccaaga accagttctc cctgaagctg agctctgtga ctgccgga cacggctgtg    | 1740 |
| tattactgtg caagagagga tggggatagc tactaccgct acggtatgga cgtctggggc  | 1800 |
| caagggaaca cggtcaccgt ctctcagga ggaggaggat ctggtggcgg tggttctggc   | 1860 |
| ggcggaggct ccgacatcca gatgaccag tctccaagct ccctgtctgc gtctgtgggc   | 1920 |
| gatagggtca ccatcacttg caggtccagc cagagtgtgt tatacagctc caacaataag  | 1980 |
| aactacttag tttggtacca gcagaaacca ggaaagggtt ctaaactgct catttactgg  | 2040 |

A-1937-W0-PCT\_ST25

gcatctaccc gggaatccgg ggtccctagt cgattcagtg gcagcgggtc tgggacagat 2100  
 ttactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta ctgtcagcaa 2160  
 tattataaga ctctctcac tttcggctgt gggaccaagg tggagatcaa acga 2214

<210> 353  
 <211> 716  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 353

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

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

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

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

A-1937-W0-PCT\_ST25

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

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

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

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

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

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

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

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

A-1937-W0-PCT\_ST25

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

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

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

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

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

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

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

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

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

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

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

A-1937-W0-PCT\_ST25

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

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
580 585 590

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

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

Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr  
625 630 635 640

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
645 650 655

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
660 665 670

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu  
690 695 700

A-1937-W0-PCT\_ST25

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg  
705 710 715

<210> 354  
<211> 2166  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 354  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120  
tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
cagccccag gtaagggact ggagtggtatt ggctatatct attacagtgg gcagacaaaa 240  
tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc 300  
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360  
actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 420  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 540  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc 960  
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

## A-1937-WO-PCT\_ST25

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg 1260  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggta 1440  
 caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt 1500  
 gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga 1560  
 aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1620  
 agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1680  
 atgaactcac ttcgcgcgga agataccgcc gtatactact gcgcaaagt ctcctacttg 1740  
 tctacagctt cgtcgctcga ctattgggggt caaggaacgt tggtcaccgt ctctagtgga 1800  
 ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgatatcca aatgacacaa 1860  
 tcaccatcgt cgctttcagc gtctgttggc gaccgtgtga cgattacctg tcgcgcgtcc 1920  
 cagggaatcc ggaattacct cgcatggtat cagcaaaaac ccggaaaagc accgaagctc 1980  
 ctgatctatg ccgcctcgac tcttcagagt ggtgtgccgt cgaggtttag cgggtccggg 2040  
 tcaggtacgg actttactct cacaatttcc agcctgcagc ccgaagatgt agctacctat 2100  
 tactgccaga gatacaaccg agcgccttac acattcggac aagggacaaa agtcgagatc 2160  
 aagcgt 2166

&lt;210&gt; 355

&lt;211&gt; 700

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

A-1937-W0-PCT\_ST25

<400> 355

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Glu Thr Gly Ser Tyr Tyr Gly 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



## A-1937-W0-PCT\_ST25

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

## A-1937-W0-PCT\_ST25

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

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

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

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

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

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

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

Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

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565

570

575

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

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

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

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

Tyr Ala Ala Ser Thr Leu Gln 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 Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
675 680 685

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

<210> 356

<211> 2163

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 356

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60

cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg  | 180  |
| cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa    | 240  |
| tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc   | 300  |
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa   | 360  |
| actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca  | 420  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt   | 840  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 960  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aacctctcc    | 1080 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1140 |
| atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc  | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg   | 1440 |
| cagctgggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt  | 1500 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg  | 1560 |

A-1937-W0-PCT\_ST25

aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg 1620  
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag 1680  
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt 1740  
cttgactact ggggccaggg aaccctgggt accgtctcta gtggaggcgg aggatctggt 1800  
ggcgggtggt ctggcggcgg aggctcccag tctgtgctga cgcagccgcc ctcaagtgtct 1860  
ggggccccag ggcagagggt caccatctcc tgcactggga gcagttccaa catcggggca 1920  
ggttatgatg tacactggta ccagcagttt ccaggaacag cccccaaact cctcatccaa 1980  
ggtaacagca atcgccctc aggggtccct gaccgattct ctggctccaa gtctggcacc 2040  
tcagcctccc tggccatcac tgggctccag gctgaggatg aggctgatta ttactgccag 2100  
tcctatgaca gcagcctgag tggttcgggtg ttcggcggag ggaccaagct gaccgtccta 2160  
ggt 2163

<210> 357  
<211> 699  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 357

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

A-1937-W0-PCT\_ST25

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

A-1937-W0-PCT\_ST25

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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

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

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

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

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

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

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu 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 Gln Ser Val Leu Thr  
580 585 590

Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser  
595 600 605

Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp  
610 615 620

Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu Ile Gln Gly Asn  
625 630 635 640



A-1937-W0-PCT\_ST25

Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser  
645 650 655

Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu  
660 665 670

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695

<210> 358  
<211> 2175  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 358  
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cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120  
tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagaccaa 240  
tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtcaa gaaccagttc 300  
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360  
actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 420  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg acaaaaactca cacatgcccc cctgtgcccag cacctgaact cctgggggga | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    | 840  |
| gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 960  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaag ggagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag     | 1140 |
| atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc   | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atcccaggtg   | 1440 |
| cagttggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag actctcctgt   | 1500 |
| gcagcctctg gattcacctt cagtagctat gacatgcact gggtcgccca ggctccaggc   | 1560 |
| aaggggctgg agtgggtggc agttatatca tatgatggaa gtattaaata ctatgcagac   | 1620 |
| tccgtgaagg gccgattcac catctccaga gacaattcca agaacacgct gtatctgcaa   | 1680 |
| gtgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ggtccgtagt   | 1740 |
| gggagctact actattacta cagtatggac gtctggggcc aagggaccac ggtcaccgtc   | 1800 |
| tctagtggag gcggaggatc tgggtggcgg ggttctggcg gcggaggctc cgacatccag   | 1860 |
| atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc   | 1920 |
| cgggcaagtc aggacatcag aaatgattta ggctggtatc agcagaaacc agggaaagcc   | 1980 |
| cctaagcgcc tgatctatgc tgcgtccagt ttgcaaagtg gggtcctatc aaggttcagc   | 2040 |
| ggcagtggtat ctgggccaga attcactctc acaatcagca gcctgcagcc tgaagatttt  | 2100 |

A-1937-W0-PCT\_ST25

gcaacttatt actgtctaca acataatagt tatccgctca ctttcggcgg agggaccaag 2160

gtggagatca aacgt 2175

<210> 359

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 359

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

## A-1937-W0-PCT\_ST25

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

## A-1937-W0-PCT\_ST25

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

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

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

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

Ile Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg

## A-1937-W0-PCT\_ST25

515

520

525

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

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

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

Thr Val Ser 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 Ser Leu Ser Ala  
 595 600 605

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

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

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

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

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser  
 675 680 685

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg  
 690 695 700

&lt;210&gt; 360

## A-1937-WO-PCT\_ST25

<211> 2166  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 360  
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcg 60  
 cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120  
 tccctcacct gcaactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
 cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240  
 tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc 300  
 tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360  
 actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggacacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840  
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 900  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc 960  
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
 gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg  | 1260 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg  | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg  | 1380 |
| cagaagagcc tctccctgtc tccgggtggt ggcggtatcgg gaggtggcgg atccgaggta | 1440 |
| caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt  | 1500 |
| gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga  | 1560 |
| aaatgtctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac  | 1620 |
| agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag  | 1680 |
| atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg  | 1740 |
| tctacagctt cgtcgcctga ctattgggggt caaggaacgt tggtcaccgt ctctagtgga | 1800 |
| ggcggaggat ctggtggcgg tggttctggc ggcgagggt ccgatatcca aatgacacaa   | 1860 |
| tcaccatcgt cgctttcagc gtctgttggc gaccgtgtga cgattacctg tcgcgcgtcc  | 1920 |
| cagggaatcc ggaattacct cgcatggtat cagcaaaaac ccggaaaagc accgaagctc  | 1980 |
| ctgatctatg ccgcctcgac tcttcagagt ggtgtgccgt cgaggtttag cgggtccggg  | 2040 |
| tcaggtagcg actttactct cacaatttcc agcctgcagc ccgaagatgt agctacctat  | 2100 |
| tactgccaga gatacaaccg agcgccttac acattcggat gtgggacaaa agtcgagatc  | 2160 |
| aagcgt                                                             | 2166 |

<210> 361  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 361

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



A-1937-W0-PCT\_ST25

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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

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

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

A-1937-W0-PCT\_ST25

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

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

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

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

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

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

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

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

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

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

A-1937-W0-PCT\_ST25

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

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

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

Tyr Ala Ala Ser Thr Leu Gln 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 Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
675 680 685

Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg  
690 695 700

<210> 362  
<211> 2163  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 362  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120  
tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
cagccccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240  
tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc 300

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa   | 360  |
| actgggagct actacggcctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca | 420  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct   | 840  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 960  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1140 |
| atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg   | 1440 |
| cagctgggtgc agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatctcctgt | 1500 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg  | 1560 |
| aaatgcctgg agtggatggg gatcatctat cttgggtgact cagataccag atacagcccg  | 1620 |
| tccttccaag gccagggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag  | 1680 |
| tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt  | 1740 |

A-1937-W0-PCT\_ST25

cttgactact ggggccaggg aaccctggtc accgtctcta gtggaggcgg aggatctggt 1800  
 ggcggtggtt ctggcggcgg aggctcccag tctgtgctga cgcagccgcc ctcaagtgtct 1860  
 ggggccccag ggcagagggt caccatctcc tgcactggga gcagttccaa catcggggca 1920  
 ggttatgatg tacactggta ccagcagttt ccaggaacag cccccaact cctcatccaa 1980  
 ggtaacagca atcggccctc aggggtccct gaccgattct ctggctccaa gtctggcacc 2040  
 tcagcctccc tggccatcac tgggctccag gctgaggatg aggctgatta ttactgccag 2100  
 tcctatgaca gcagcctgag tggttcgggtg ttcggctgtg ggaccaagct gaccgtccta 2160  
 ggt 2163

<210> 363  
 <211> 699  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 363

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

## A-1937-W0-PCT\_ST25

85

90

95

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

## A-1937-W0-PCT\_ST25

275

280

285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
 450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr



## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 465 |     | 470 |     | 475 |     | 480 |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Tyr | Ser | Phe | Thr | Ser | Tyr | Trp | Ile | Gly | Trp | Val | Arg | Gln | Met |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Pro | Gly | Lys | Cys | Leu | Glu | Trp | Met | Gly | Ile | Ile | Tyr | Leu | Gly | Asp | Ser |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Asp | Thr | Arg | Tyr | Ser | Pro | Ser | Phe | Gln | Gly | Gln | Val | Thr | Ile | Ser | Ala |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Asp | Lys | Ser | Ile | Ser | Thr | Ala | Tyr | Leu | Gln | Trp | Ser | Ser | Leu | Lys | Ala |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ser | Asp | Thr | Ala | Met | Tyr | Tyr | Cys | Ala | Arg | Ser | Asn | Trp | Gly | Leu | 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 | Gln | Ser | Val | Leu | Thr |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Gln | Pro | Pro | Ser | Val | Ser | Gly | Ala | Pro | Gly | Gln | Arg | Val | Thr | Ile | Ser |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Cys | Thr | Gly | Ser | Ser | Ser | Asn | Ile | Gly | Ala | Gly | Tyr | Asp | Val | His | Trp |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Tyr | Gln | Gln | Phe | Pro | Gly | Thr | Ala | Pro | Lys | Leu | Leu | Ile | Gln | Gly | Asn |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Ser | Asn | Arg | Pro | Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Gly | Ser | Lys | Ser |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Gly | Thr | Ser | Ala | Ser | Leu | Ala | Ile | Thr | Gly | Leu | Gln | Ala | Glu | Asp | Glu |

660

665

670

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

Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly  
 690 695

<210> 364  
 <211> 2175  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 364  
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 cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120  
 tccctcacct gcaactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
 cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240  
 tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc 300  
 tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360  
 actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840

## A-1937-W0-PCT\_ST25

gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
 tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc 960  
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
 gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1260  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtggg gccggatcgg gaggtggcgg atcccagggtg 1440  
 cagttgggtg agtctggggg aggcgtgggt cagcctggga ggtccctgag actctcctgt 1500  
 gcagcctctg gattcacctt cagtagctat gacatgcact ggggccgcca ggctccaggc 1560  
 aagtgtctgg agtgggtggc agttatatca tatgatggaa gtattaaata ctatgcagac 1620  
 tccgtgaagg gccgattcac catctccaga gacaattcca agaacacgct gtatctgcaa 1680  
 gtgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ggtccgtagt 1740  
 gggagctact actattacta cagtatggac gtctggggcc aagggaccac ggtcaccgtc 1800  
 tctagtggag gcggaggatc tgggtggcgg ggttctggcg gcggaggctc cgacatccag 1860  
 atgaccaggt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 1920  
 cgggcaagtc aggacatcag aaatgattta ggctggatatc agcagaaacc agggaaagcc 1980  
 cctaagcgcc tgatctatgc tgcgtccagt ttgcaaagtg ggggcccatc aaggttcagc 2040  
 ggagtggtat ctggggccaga attcactctc acaatcagca gcctgcagcc tgaagatttt 2100  
 gcaacttatt actgtctaca acataatagt tatccgctca ctttcggctg tgggaccaag 2160  
 gtggagatca aacgt 2175

A-1937-WO-PCT\_ST25

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

<220>  
 <223> Synthetic polynucleotide

<400> 365

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

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

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

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

A-1937-W0-PCT\_ST25

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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

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Pro Pro Ser Arg Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly  
450 455 460

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala  
485 490 495

Pro Gly Lys Cys Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser  
500 505 510

Ile Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala  
530 535 540

A-1937-W0-PCT\_ST25

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Val Arg Ser Gly Ser  
545 550 555 560

Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr Thr Val  
565 570 575

Thr Val Ser 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 Ser Leu Ser Ala  
595 600 605

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile  
610 615 620

Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
625 630 635 640

Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile Ser Ser  
660 665 670

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser  
675 680 685

Tyr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg  
690 695 700

<210> 366

<211> 2187

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 366

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| cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc  | 120  |
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg  | 180  |
| attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag  | 240  |
| tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc  | 300  |
| aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac  | 360  |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg  | 420  |
| accacggtca ccgtctcctc agcctccacc aaggggccat cggtcttccc cctggcaccc  | 480  |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc | 540  |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc  | 600  |
| ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag  | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca   | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc  | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac  | 900  |
| cctgaggtca agttcaactg gtacgtggac ggcggtggagg tgcataatgc caagacaaag | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac  | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc  | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc  | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac  | 1260 |
| tacaagacca cgctccccgt gctggactcc gacggctcct tcttcctcta tagcaagctc  | 1320 |
| accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag  | 1380 |



A-1937-W0-PCT\_ST25

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg 1440  
ggaggtggcg gatccgaggt acaactgggtg gaatcaggtg gaggtttggt gcagccgggg 1500  
agatcgctca ggcttagctg tgcggcatcg gggtttactt tcgatgatta tgcgatgcat 1560  
tgggtccggc aagcgcctgg aaaagggctc gagtgggttt ccgccattac gtggaatagc 1620  
ggacacatcg attatgcaga cagtgtggag ggcagattca caatctcacg agacaatgct 1680  
aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac 1740  
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ttggtcaccg tctctagtgg aggcggagga tctgggtggcg gtggttctgg cggcggaggc 1860  
tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttgg cgaccgtgtg 1920  
acgattacct gtcgcgcgtc ccagggaatc cggaattacc tcgcatggta tcagcaaaaa 1980  
cccggaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg 2040  
tcgaggttta gcgggtccgg gtcaggtacg gactttactc tcacaatttc cagcctgcag 2100  
cccgaagatg tagctaccta ttactgccag agatacaacc gagcgcctta cacattcgga 2160  
caagggacaa aagtcgagat caagcgt 2187

<210> 367

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 367

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu

## A-1937-W0-PCT\_ST25

35

40

45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
 180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
 195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro | Cys | Glu | Glu | Gln | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Ser | Thr | Tyr | Arg | Cys | Val | Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser |

## A-1937-W0-PCT\_ST25

420

425

430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
 450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
 465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
 485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
 500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
 515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
 565 570 575

Gly Thr Leu Val Thr Val Ser 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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

A-1937-W0-PCT\_ST25

610

615

620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser 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 Gln  
675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu  
690 695 700

Ile Lys Arg  
705

<210> 368  
<211> 2184  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 368  
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cgctgtcagg tacagttgca ggagtcaggc ccaggactgg tgaagccctc ggagaccctc 120  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
attaggcagc cccaggggaa aggccttgag tggataggaa ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360

## A-1937-W0-PCT\_ST25

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tgtgcaagag  | aggatgggga  | tagctactac  | cgctacggta  | tggacgtctg  | gggccaaggg  | 420  |
| accacgggtca | ccgtctcctc  | agcctccacc  | aaggggcccat | cggtcttccc  | cctggcaccc  | 480  |
| tcctccaaga  | gcacctctgg  | gggcacagcg  | gccctgggct  | gcctgggtcaa | ggactacttc  | 540  |
| cccgaaccgg  | tgacgggtgc  | gtggaactca  | ggcgccctga  | ccagcggcgt  | gcacaccttc  | 600  |
| ccggctgtcc  | tacagtccctc | aggactctac  | tccctcagca  | gcgtgggtgac | cgtgccctcc  | 660  |
| agcagcttgg  | gcacccagac  | ctacatctgc  | aacgtgaatc  | acaagcccag  | caacaccaag  | 720  |
| gtggacaaga  | aagttgagcc  | caaatcttgt  | gacaaaactc  | acacatgccc  | accgtgcccc  | 780  |
| gcacctgaac  | tcctgggggg  | accgtcagtc  | ttcctcttcc  | ccccaaaacc  | caaggacacc  | 840  |
| ctcatgatct  | cccggacccc  | tgaggtcaca  | tgctgggtgg  | tggacgtgag  | ccacgaagac  | 900  |
| cctgaggtca  | agttcaactg  | gtacgtggac  | ggcgtggagg  | tgcataatgc  | caagacaaag  | 960  |
| ccgtgtgagg  | agcagtacgg  | cagcacgtac  | cgttgtgtca  | gcgtcctcac  | cgtcctgcac  | 1020 |
| caggactggc  | tgaatggcaa  | ggagtacaag  | tgcaaggctc  | ccaacaaagc  | cctcccagcc  | 1080 |
| cccatcgaga  | aaaccatctc  | caaagccaaa  | gggcagcccc  | gagaaccaca  | ggtgtacacc  | 1140 |
| ctgcccccat  | cccgggagga  | gatgaccaag  | aaccagggtca | gcctgacctg  | cctgggtcaaa | 1200 |
| ggcttctatc  | ccagcgacat  | cgccgtggag  | tgggagagca  | atgggcagcc  | ggagaacaac  | 1260 |
| tacaagacca  | cgctccccgt  | gctggactcc  | gacggctcct  | tcttcctcta  | tagcaagctc  | 1320 |
| accgtggaca  | agagcagggtg | gcagcagggg  | aacgtcttct  | catgctccgt  | gatgcatgag  | 1380 |
| gctctgcaca  | accactacac  | gcagaagagc  | ctctccctgt  | ctccgggtgg  | tggcggatcg  | 1440 |
| ggaggtggcg  | gatccgaggt  | gcagctgggtg | cagtctggag  | cagaggtgaa  | aaagcccggg  | 1500 |
| gagtctctga  | agatctcctg  | taagacttct  | gaatacagct  | ttaccagcta  | ctggatcggc  | 1560 |
| tgggtgcgcc  | agatgcccgg  | gaaaggcctg  | gagtggatgg  | ggatcatcta  | tcttgggtgac | 1620 |
| tcagatacca  | gatacagccc  | gtccttccaa  | ggccagggtca | ccatctcagc  | cgacaagtcc  | 1680 |
| atcagtaccg  | cctacctgca  | gtggagcagc  | ctgaaggcct  | cggacaccgc  | catgtattac  | 1740 |
| tgtgcgagaa  | gtaactgggg  | tcttgactac  | tggggccagg  | gaaccctggg  | caccgtctct  | 1800 |

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agtggaggcg gaggatctgg tggcgggtgg tctggcggcg gaggctccca gtctgtgctg 1860  
acgcagccgc cctcagtgtc tggggcccca gggcagaggg tcaccatctc ctgcactggg 1920  
agcagttcca acatcggggc aggttatgat gtacactggg accagcagtt tccaggaaca 1980  
gccccaaac tcctcatcca aggtaacagc aatcggccct caggggtccc tgaccgattc 2040  
tctggctcca agtctggcac ctcagcctcc ctggccatca ctgggctcca ggctgaggat 2100  
gaggctgatt attactgcca gtcctatgac agcagcctga gtggttcggg gttcggcgga 2160  
gggaccaagc tgaccgtcct aggt 2184

<210> 369  
<211> 706  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 369

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

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Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285



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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

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Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

Arg Ser Asn Trp Gly Leu 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 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro  
595 600 605

Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly  
610 615 620

Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro  
625 630 635 640

Lys Leu Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp  
645 650 655

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr  
660 665 670

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Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp  
675 680 685

Ser Ser Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val  
690 695 700

Leu Gly  
705

<210> 370  
<211> 2196  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 370  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcg 60  
cgctgtcagg tacagttgca ggagtcaggc ccaggactgg tgaagccctc ggagaccctc 120  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
accacggtca ccgtctcctc agcctccacc aagggcccat cggctttccc cctggcaccc 480  
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600  
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660  
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720  
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc 780

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc  | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac  | 900  |
| cctgaggtca agttcaactg gtacgtggac ggctgtggagg tgcataatgc caagacaaag | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac  | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc  | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc  | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccaggctc gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac  | 1260 |
| tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc  | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg  | 1440 |
| ggaggtggcg gatcccaggt gcagttggtg gagtctgggg gaggcgtggt ccagcctggg  | 1500 |
| aggtccctga gactctcctg tgcagcctct ggattcacct tcagtagcta tgacatgcac  | 1560 |
| tgggtccgcc aggctccagg caaggggctg gagtgggtgg cagttatatc atatgatgga  | 1620 |
| agtattaaat actatgcaga ctccgtgaag ggccgattca ccatctccag agacaattcc  | 1680 |
| aagaacacgc tgtatctgca agtgaacagc ctgagagctg aggacacggc tgtgtattac  | 1740 |
| tgtgcgagag aggtccgtag tgggagctac tactattact acagtatgga cgtctggggc  | 1800 |
| caagggacca cggtcaccgt ctctagtgga ggccggaggat ctggtggcgg tggttctggc | 1860 |
| ggcggaggct ccgacatcca gatgaccag tctccatcct ccctgtctgc atctgtagga   | 1920 |
| gacagagtca ccatcacttg ccgggcaagt caggacatca gaaatgattt aggctggtat  | 1980 |
| cagcagaaac cagggaagc ccctaagcgc ctgatctatg ctgcgtccag tttgcaaagt   | 2040 |
| ggggtcccat caaggttcag cggcagtgga tctgggccag aattcactct cacaatcagc  | 2100 |
| agcctgcagc ctgaagattt tgcaacttat tactgtctac aacataatag ttatccgctc  | 2160 |
| actttcggcg gagggaccaa ggtggagatc aaacgt                            | 2196 |

<210> 371  
 <211> 710  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 371

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu

145                      150                      155                      160

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

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340

345

350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
 355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln  
 450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser  
 465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp  
 485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala  
 500 505 510

Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val Lys  
 515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

## A-1937-W0-PCT\_ST25

530

535

540

Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 545 550 555 560

Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val  
 565 570 575

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln  
 595 600 605

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
 610 615 620

Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln  
 625 630 635 640

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu  
 645 650 655

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu  
 660 665 670

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr  
 675 680 685

Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr  
 690 695 700

Lys Val Glu Ile Lys Arg  
 705 710

&lt;210&gt; 372



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&lt;211&gt; 2187

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 372

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg | 60   |
| cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc  | 120  |
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg  | 180  |
| attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag  | 240  |
| tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc  | 300  |
| aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac  | 360  |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg  | 420  |
| accacggtca ccgtctcctc agcctccacc aaggggcccat cggctttccc cctggcaccc | 480  |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc | 540  |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc  | 600  |
| ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag  | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca   | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc   | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac  | 900  |
| cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac  | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc  | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc  | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccagggtc gcctgacctg cctgggtcaaa | 1200 |

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac | 1260 |
| tacaagacca cgctcccggt gctggactcc gacggctcct tcttcctcta tagcaagctc | 1320 |
| accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg | 1440 |
| ggaggtggcg gatccgaggt acaactgggt gaatcaggtg gaggtttggt gcagccgggg | 1500 |
| agatcgctca ggcttagctg tgcggcatcg gggtttactt tcgatgatta tgcgatgcat | 1560 |
| tgggtccggc aagcgcctgg aaaatgtctc gagtgggttt ccgccattac gtggaatagc | 1620 |
| ggacacatcg attatgcaga cagtgtggag ggcagattca caatctcacg agacaatgct | 1680 |
| aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac | 1740 |
| tgcgcaaaag tctcctactt gtctacagct tcgtcgctcg actattgggg tcaaggaacg | 1800 |
| ttggtcaccg tctctagtgg aggcggagga tctggtggcg gtggttctgg cggcggaggc | 1860 |
| tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttgg cgaccgtgtg | 1920 |
| acgattacct gtcgcgcgtc ccagggaatc cggaattacc tcgcatggta tcagcaaaaa | 1980 |
| cccgaaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtccg | 2040 |
| tcgaggttta gcgggtccgg gtcaggtacg gactttactc tcacaatttc cagcctgcag | 2100 |
| cccgaagatg tagctaccta ttactgccag agatacaacc gagcgctta cacattcgga  | 2160 |
| tgtgggacaa aagtcgagat caagcgt                                     | 2187 |

<210> 373

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 373

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

A-1937-W0-PCT\_ST25

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

A-1937-W0-PCT\_ST25

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

A-1937-W0-PCT\_ST25

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
595 600 605

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
610 615 620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser 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 Gln  
675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Cys Gly Thr Lys Val Glu  
690 695 700

Ile Lys Arg  
705

<210> 374  
<211> 2184  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 374  
atggacatga ggggtcccg ctcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 120  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180

## A-1937-W0-PCT\_ST25

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| attaggcagc  | ccccagggaa  | aggccttgag  | tggataggaa  | ggacatacta  | caggtccaag  | 240  |
| tgggtataatg | attatgcagt  | ttctctgaaa  | agtcgagtaa  | ccatcagccc  | agacacatcc  | 300  |
| aagaaccagt  | tctccctgaa  | gctgagctct  | gtgactgccg  | cggacacggc  | tgtgtattac  | 360  |
| tgtgcaagag  | aggatgggga  | tagctactac  | cgctacggta  | tggacgtctg  | gggccaaggg  | 420  |
| accacggcca  | ccgtctcctc  | agcctccacc  | aaggggcccat | cggctcttccc | cctggcacccc | 480  |
| tcctccaaga  | gcacctctgg  | gggcacagcg  | gccctgggct  | gcctgggtcaa | ggactacttc  | 540  |
| cccgaaccgg  | tgacgggtgc  | gtggaactca  | ggcgccctga  | ccagcggcgt  | gcacaccttc  | 600  |
| ccggctgtcc  | tacagtccctc | aggactctac  | tccttcagca  | gcgtgggtgac | cgtgccctcc  | 660  |
| agcagcttgg  | gcacccagac  | ctacatctgc  | aacgtgaatc  | acaagcccag  | caacaccaag  | 720  |
| gtggacaaga  | aagttgagcc  | caaactctgt  | gacaaaactc  | acacatgccc  | accgtgcccc  | 780  |
| gcacctgaac  | tcctggggggg | accgtcagtc  | ttcctcttcc  | ccccaaaacc  | caaggacacc  | 840  |
| ctcatgatct  | cccggacccc  | tgaggtcaca  | tgcgtgggtg  | tggacgtgag  | ccacgaagac  | 900  |
| cctgagggtca | agttcaactg  | gtacgtggac  | ggcgtggagg  | tgcataatgc  | caagacaaag  | 960  |
| ccgtgtgagg  | agcagtacgg  | cagcacgtac  | cgttgtgtca  | gcgtcctcac  | cgtcctgcac  | 1020 |
| caggactggc  | tgaatggcaa  | ggagtacaag  | tgcaaggctc  | ccaacaaagc  | cctcccagcc  | 1080 |
| cccacgcaga  | aaaccatctc  | caaagccaaa  | gggcagcccc  | gagaaccaca  | ggtgtacacc  | 1140 |
| ctgcccccat  | cccgggagga  | gatgaccaag  | aaccagggtca | gcctgacctg  | cctgggtcaaa | 1200 |
| ggcttctatc  | ccagcgacat  | cgccgtggag  | tgggagagca  | atgggcagcc  | ggagaacaac  | 1260 |
| tacaagacca  | cgcctcccgt  | gctggactcc  | gacggctcct  | tcttcctcta  | tagcaagctc  | 1320 |
| accgtggaca  | agagcagggtg | gcagcagggg  | aacgtcttct  | catgctccgt  | gatgcatgag  | 1380 |
| gctctgcaca  | accactacac  | gcagaagagc  | ctctccctgt  | ctccgggtgg  | tggcggatcg  | 1440 |
| ggagggtggcg | gatccgaggt  | gcagctgggtg | cagtctggag  | cagaggtgaa  | aaagcccggg  | 1500 |
| gagtctctga  | agatctcctg  | taagacttct  | gaatacagct  | ttaccagcta  | ctggatcggc  | 1560 |
| tgggtgcgcc  | agatgcccgg  | gaaatgcctg  | gagtggatgg  | ggatcatcta  | tcttggtgac  | 1620 |

A-1937-W0-PCT\_ST25

tcagatacca gatacagccc gtccttccaa ggccagggtca ccatctcagc cgacaagtcc 1680  
atcagtaccg cctacctgca gtggagcagc ctgaaggcct cggacaccgc catgtattac 1740  
tgtgcgagaa gtaactgggg tcttgactac tggggccagg gaaccctggg caccgtctct 1800  
agtggaggcg gaggatctgg tggcgggtgg tctggcggcg gaggctccca gtctgtgctg 1860  
acgcagccgc cctcagtgtc tggggcccca gggcagaggg tcaccatctc ctgcactggg 1920  
agcagttcca acatcggggc aggttatgat gtacactggg accagcagtt tccaggaaca 1980  
gccccaaac tcctcatcca aggtaacagc aatcggccct caggggtccc tgaccgattc 2040  
tctggctcca agtctggcac ctcagcctcc ctggccatca ctgggctcca ggctgaggat 2100  
gaggctgatt attactgcca gtcctatgac agcagcctga gtgggttcggg gttcggctgt 2160  
gggaccaagc tgaccgtcct aggt 2184

<210> 375

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 375

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn



## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |
| Gln | Phe | Ser | Leu | Lys | Leu | Val |
|     |     |     | 85  |     |     | 90  |
|     |     |     |     |     |     | 95  |
| Tyr | Tyr | Cys | Ala | Arg | Glu | Asp |
|     |     |     | 100 |     |     | 105 |
|     |     |     |     |     |     | 110 |
| Asp | Val | Trp | Gly | Gln | Gly | Thr |
|     |     |     | 115 |     |     | 120 |
|     |     |     |     |     |     | 125 |
| Lys | Gly | Pro | Ser | Val | Phe | Pro |
|     |     |     |     |     |     | 135 |
|     |     |     |     |     |     | 140 |
| Gly | Gly | Thr | Ala | Ala | Leu | Gly |
|     |     |     |     |     |     | 150 |
|     |     |     |     |     |     | 155 |
|     |     |     |     |     |     | 160 |
| Pro | Val | Thr | Val | Ser | Trp | Asn |
|     |     |     |     |     |     | 165 |
|     |     |     |     |     |     | 170 |
|     |     |     |     |     |     | 175 |
| Thr | Phe | Pro | Ala | Val | Leu | Gln |
|     |     |     |     |     |     | 180 |
|     |     |     |     |     |     | 185 |
|     |     |     |     |     |     | 190 |
| Val | Val | Thr | Val | Pro | Ser | Ser |
|     |     |     |     |     |     | 195 |
|     |     |     |     |     |     | 200 |
|     |     |     |     |     |     | 205 |
| Asn | Val | Asn | His | Lys | Pro | Ser |
|     |     |     |     |     |     | 210 |
|     |     |     |     |     |     | 215 |
|     |     |     |     |     |     | 220 |
| Pro | Lys | Ser | Cys | Asp | Lys | Thr |
|     |     |     |     |     |     | 225 |
|     |     |     |     |     |     | 230 |
|     |     |     |     |     |     | 235 |
|     |     |     |     |     |     | 240 |
| Glu | Leu | Leu | Gly | Gly | Pro | Ser |
|     |     |     |     |     |     | 245 |
|     |     |     |     |     |     | 250 |
|     |     |     |     |     |     | 255 |
| Asp | Thr | Leu | Met | Ile | Ser | Arg |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Pro |
|     |     |     |     |     |     | Glu |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Thr |
|     |     |     |     |     |     | Cys |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Val |
|     |     |     |     |     |     | Val |

## A-1937-W0-PCT\_ST25

260

265

270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
 290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
 325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
 355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu

## A-1937-W0-PCT\_ST25

450

455

460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
 465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
 485 490 495

Ile Gly Trp Val Arg Gln Met Pro Gly Lys Cys Leu Glu Trp Met Gly  
 500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
 515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
 530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
 545 550 555 560

Arg Ser Asn Trp Gly Leu 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 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro  
 595 600 605

Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly  
 610 615 620

Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro  
 625 630 635 640

Lys Leu Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp

## A-1937-W0-PCT\_ST25

645

650

655

Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr  
 660 665 670

Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp  
 675 680 685

Ser Ser Leu Ser Gly Ser Val Phe Gly Cys Gly Thr Lys Leu Thr Val  
 690 695 700

Leu Gly  
 705

<210> 376  
 <211> 2196  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 376  
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 cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 120  
 tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
 attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240  
 tgggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
 aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360  
 tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
 accacggtca cgtctcctc agcctccacc aagggcccat cggctcttccc cctggcaccc 480  
 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
 cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ccggctgtcc tacagtccctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag   | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc    | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc   | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac   | 900  |
| cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag  | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac   | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc   | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   | 1260 |
| tacaagacca cgcctcccggt gctggactcc gacggctcct tcttcctcta tagcaagctc  | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag  | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg   | 1440 |
| ggagggtggcg gatcccaggt gcagttgggt gagtctgggg gaggcgtggt ccagcctggg  | 1500 |
| agggtccctga gactctctg tgcagcctct ggattcacct tcagtagcta tgacatgcac   | 1560 |
| tgggtccgcc aggtccagg caagtgtctg gagtgggtgg cagttatatc atatgatgga    | 1620 |
| agtattaaat actatgcaga ctccgtgaag ggccgattca ccatctccag agacaattcc   | 1680 |
| aagaacacgc tgtatctgca agtgaacagc ctgagagctg aggacacggc tgtgtattac   | 1740 |
| tgtgcgagag aggtccgtag tgggagctac tactattact acagtatgga cgtctggggc   | 1800 |
| caagggacca cggtcaccgt ctctagtgga ggcggaggat ctggtggcgg tggttctggc   | 1860 |
| ggcggagggt ccgacatcca gatgaccag tctccatcct ccctgtctgc atctgtagga    | 1920 |
| gacagagtca ccatcacttg ccgggcaagt caggacatca gaaatgattt aggctgggtat  | 1980 |
| cagcagaaac cagggaaagc ccctaagcgc ctgatctatg ctgcgtccag ttgcaaagt    | 2040 |

A-1937-W0-PCT\_ST25

ggggtcccat caaggttcag cggcagtgga tctgggccag aattcactct cacaatcagc 2100  
 agcctgcagc ctgaagattt tgcaacttat tactgtctac aacataatag ttatccgctc 2160  
 actttcggct gtgggaccaa ggtggagatc aaacgt 2196

<210> 377  
 <211> 710  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 377

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

A-1937-W0-PCT\_ST25

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

A-1937-W0-PCT\_ST25

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ala  
500 505 510



A-1937-W0-PCT\_ST25

Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val Lys  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
530 535 540

Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val  
565 570 575

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln  
595 600 605

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
610 615 620

Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln  
625 630 635 640

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu  
645 650 655

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu  
660 665 670

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr  
675 680 685

Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly Thr  
690 695 700

A-1937-W0-PCT\_ST25

Lys Val Glu Ile Lys Arg  
705 710

<210> 378  
<211> 2172  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 378  
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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180  
caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300  
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa 360  
gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc 420  
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcacccctc ctccaagagc 480  
acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccgggtg 540  
acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600  
cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc 660  
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720  
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 780  
ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840  
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgaggtcaag 900  
ttcaactggg acgtggacgg cgtggagggt cataatgcc aagacaaagcc gtgtgaggag 960  
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 1020

## A-1937-WO-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc   | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggatcaaagg cttctatccc  | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcaggtggc agcaggggaa cgtctttctca tgctccgtga tgcatgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1440 |
| tcccaggtgc agttacagca gtcgggcgca ggactgttga agccttcgga gaccctgtcc   | 1500 |
| ctcacctgcg ctgtccatgg tgggtccttc agtgggttact actggaactg gattcgccag  | 1560 |
| ccaccaggga aggggctaga gtggattggg gaaatcaatc atgctggaaa caccaactac   | 1620 |
| aaccctgtcc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc   | 1680 |
| ctgacgctga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat   | 1740 |
| tgtagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc   | 1800 |
| tcaggaggcg gaggatctgg tggcggtggc tctggcggcg gaggctccga aattgtgttg   | 1860 |
| acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccacctt ctctgcagg    | 1920 |
| gccagtcaga gtgttagaag cagttactta gcctgggtacc agcagaaaacc tggccaggct | 1980 |
| cccaggctcc tcacttatgg tgcatccagc agggccactg gcatcccaga caggttcagt   | 2040 |
| ggcagtggtt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt   | 2100 |
| gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggccaagg gacacgactg   | 2160 |
| gagattaaac ga                                                       | 2172 |

&lt;210&gt; 379

&lt;211&gt; 702

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

A-1937-W0-PCT\_ST25

<400> 379

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

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180

185

190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

## A-1937-WO-PCT\_ST25

370

375

380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
 450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
 485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
 500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
 515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
 530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
 545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

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565

570

575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser  
595 600 605

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg  
610 615 620

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg  
625 630 635 640

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg  
660 665 670

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser  
675 680 685

Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg  
690 695 700

<210> 380

<211> 2172

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 380

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cgctgtgagg tacaactggt ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc 120

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg   | 180  |
| caagcgcctg gaaaagggct cgagtgggtt tccgccatta cgtggaatag cggacacatc   | 240  |
| gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc   | 300  |
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa   | 360  |
| gtctcctact tgtctacagc ttcgtcgcgc gactattggg gtcaaggaac gttggtcacc   | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtctttcccc tggcaccctc ctccaagagc   | 480  |
| acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg   | 540  |
| acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta   | 600  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc   | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa    | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctggggggac cgtcagtctt cctcttcccc ccaaaacca aggacacct catgatctcc     | 840  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgagggtcaag  | 900  |
| ttcaactggg acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag   | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa    | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacacct gccccatcc     | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1200 |
| agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccacg    | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga   | 1440 |
| tcccagggtgc agttacagca gtcgggcgca ggactgttga agccttcgga gaccctgtcc  | 1500 |
| ctcacctgcg ctgtccatgg tgggtccttc agtgggttact actggaactg gattcgccag  | 1560 |



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```

ccaccaggga agtgtctaga gtggattggg gaaatcaatc atgctggaaa caccaactac      1620
aaccctgtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc      1680
ctgacgctga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat      1740
ttagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc      1800
tcaggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctccga aattgtgttg      1860
acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctcctgcagg      1920
gccagtcaga gtgttagaag cagttactta gcctggtacc agcagaaacc tggccaggct      1980
cccaggctcc tcatctatgg tgcattcagc agggccactg gcatcccaga caggttcagt      2040
ggcagtggtt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt      2100
gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggctgtgg gacacgactg      2160
gagattaaac ga                                                              2172

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<210> 381  
 <211> 702  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 381

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Asp | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Ile | Thr | Trp | Asn | Ser | Gly | His | Ile | Asp | Tyr | Ala | Asp | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

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Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

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Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser  
595 600 605

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg  
610 615 620

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg  
625 630 635 640

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Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg  
660 665 670

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser  
675 680 685

Ser Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys Arg  
690 695 700

<210> 382  
<211> 2157  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 382  
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cgctgtgagg tgcagctggg gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgctg 180  
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240  
agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc 300  
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
accaagggcc catcggctctt ccccctggca cctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 600  
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct   | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 780  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 1020 |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1260 |
| tccgacggct ctttcttcct ctatagcaag ctaccgtgg acaagagcag gtggcagcag    | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1380 |
| agcctctccc tgtctccggg tgggtggcgga tcgggagggtg gcggatccca ggtgcagtta | 1440 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc   | 1500 |
| catggtgggt ccttcagtgg ttactactgg aactggattc gccagccacc agggaagggg   | 1560 |
| ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag   | 1620 |
| agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct   | 1680 |
| gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc   | 1740 |
| tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcagg aggcggagga   | 1800 |
| tctggtggcg gtggttctgg cggcggaggc tccgaaattg tgttgacgca gtctccaggc   | 1860 |
| accctgtctt tgtctccagg ggaaagagcc accctctcct gcagggccag tcagagtgtt   | 1920 |
| agaagcagtt acttagcctg gtaccagcag aaacctggcc aggctcccag gctcctcatc   | 1980 |
| tatggtgcat ccagcagggc cactggcatc ccagacaggt tcagtggcag tgggtctggg   | 2040 |
| acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt   | 2100 |

cagcagtatg gtagctcacc taccttcggc caagggacac gactggagat taaacga

2157

&lt;210&gt; 383

&lt;211&gt; 697

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 383

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335



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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

A-1937-W0-PCT\_ST25

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val  
580 585 590

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala  
595 600 605

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala  
610 615 620

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly  
625 630 635 640

Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly  
645 650 655

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp  
660 665 670

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Thr Phe Gly  
675 680 685

Gln Gly Thr Arg Leu Glu Ile Lys Arg  
690 695

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<211> 2157  
<212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 384

|                                                                    |      |
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| cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg  | 120  |
| aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc  | 180  |
| cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc  | 240  |
| agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc  | 300  |
| gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga  | 360  |
| agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc  | 420  |
| accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca   | 480  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  | 540  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc   | 600  |
| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaatct  | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 780  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccctgaggtc    | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 1020 |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1260 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1380 |
| agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccca ggtgcagtta | 1440 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc  | 1500 |
| catggtgggt ccttcagtgg ttactactgg aactggattc gccagccacc aggggaagtgt | 1560 |
| ctagagtgga ttgggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag | 1620 |
| agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct  | 1680 |
| gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc  | 1740 |
| tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcagg aggcggagga  | 1800 |
| tctggtggcg gtggttctgg cggcggaggc tccgaaattg tgttgacgca gtctccaggc  | 1860 |
| accctgtctt tgtctccagg ggaaagagcc accctctcct gcagggccag tcagagtgtt  | 1920 |
| agaagcagtt acttagcctg gtaccagcag aaacctggcc aggctcccag gctcctcatc  | 1980 |
| tatggtgcat ccagcagggc cactggcatc ccagacaggt tcagtggcag tgggtctggg  | 2040 |
| acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt  | 2100 |
| cagcagtatg gtagctcacc taccttcggc tgtgggacac gactggagat taaacga     | 2157 |

<210> 385

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 385

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Lys | Ile | Ser | Cys | Lys | Thr | Ser | Glu | Tyr | Ser | Phe | Thr | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

A-1937-W0-PCT\_ST25

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

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Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Cys Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val  
580 585 590

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala  
595 600 605

A-1937-W0-PCT\_ST25

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala  
610 615 620

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly  
625 630 635 640

Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly  
645 650 655

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp  
660 665 670

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Thr Phe Gly  
675 680 685

Cys Gly Thr Arg Leu Glu Ile Lys Arg  
690 695

<210> 386  
<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 386  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctggggg ccaagggacc 420



## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc   | 480  |
| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc    | 540  |
| gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttccccg | 600  |
| gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc   | 660  |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg  | 720  |
| gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca   | 780  |
| cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc   | 840  |
| atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct    | 900  |
| gaggtaaggt tcaactggta cgtggacggc gtggagggtgc ataatgcaa gacaaagccg   | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag   | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc    | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac   | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggtgg cggatcggga   | 1440 |
| ggtaggcgat cccagggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag  | 1500 |
| accctgtccc tcacctgcgc tgtccatggt gggtccttca gtggttacta ctggaactgg   | 1560 |
| attcgccagc caccaggga ggggctagag tggattgggg aaatcaatca tgctggaaac    | 1620 |
| accaactaca acccgctcct caagagtcga gtcaccatat cattagacac gtccaagaac   | 1680 |
| cagttctccc tgacgtgac ctctgtgacc gccgcggaca cggctgtgta ttactgtgcg    | 1740 |
| agaggatatt gtagaagtac cacctgttac tttgactact ggggccaggg aaccctagtc   | 1800 |
| accgtctcct caggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgaa   | 1860 |

A-1937-W0-PCT\_ST25

attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc 1920  
tcctgcaggg ccagtcagag tgtagaagc agttacttag cctggtacca gcagaaacct 1980  
ggccaggctc ccaggctcct catctatggg gcatccagca gggccactgg catcccagac 2040  
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 2100  
gaagattttg cagtgtatta ctgtcagcag tatggtagct cacctacctt cggccaaggg 2160  
acacgactgg agattaaacg a 2181

<210> 387  
<211> 705  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 387

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp

## A-1937-W0-PCT\_ST25

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly

## A-1937-W0-PCT\_ST25

290

295

300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
 450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
 465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp

## A-1937-W0-PCT\_ST25

485

490

495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
 500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
 515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
 530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
 545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
 565 570 575

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 580 585 590

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu  
 595 600 605

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln  
 610 615 620

Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 625 630 635 640

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile  
 645 650 655

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 660 665 670

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln

A-1937-W0-PCT\_ST25

675

680

685

Tyr Gly Ser Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
690 695 700

Arg  
705

<210> 388  
<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 388  
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cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gagggtccgta gtgggagcta ctactattac tacagtatgg acgtctggggg ccaagggacc 420  
acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540  
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600  
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660  
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct  | 900  |
| gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg  | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag  | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg  | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc  | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac  | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc  | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggtgg cggatcggga  | 1440 |
| gggtggcggat cccaggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag | 1500 |
| accctgtccc tcacctgcgc tgtccatggt gggtccttca gtggttacta ctggaactgg  | 1560 |
| attcgccagc caccagggaa gtgtctagag tggattgggg aaatcaatca tgctggaaac  | 1620 |
| accaactaca acccgtccct caagagtcga gtcaccatat cattagacac gtccaagaac  | 1680 |
| cagttctccc tgacgtgac ctctgtgacc gccgcggaca cggctgtgta ttactgtgcg   | 1740 |
| agaggatatt gtagaagtac cacctgttac tttgactact ggggccaggg aaccctagtc  | 1800 |
| accgtctcct caggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgaa  | 1860 |
| attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc  | 1920 |
| tcctgcaggg ccagtcagag tgtagaagc agttacttag cctggtacca gcagaaacct   | 1980 |
| ggccaggctc ccaggctcct catctatggt gcatccagca gggccactgg catcccagac  | 2040 |
| aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct  | 2100 |
| gaagattttg cagtgtatta ctgtcagcag tatggtagct cacctacctt cggctgtggg  | 2160 |
| acacgactgg agattaaacg a                                            | 2181 |

A-1937-WO-PCT\_ST25

<211> 705  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 389

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 145 150 155 160



A-1937-W0-PCT\_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

A-1937-W0-PCT\_ST25

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

A-1937-W0-PCT\_ST25

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu  
595 600 605

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln  
610 615 620

Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
625 630 635 640

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile  
645 650 655

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
660 665 670

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln  
675 680 685

Tyr Gly Ser Ser Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys  
690 695 700

Arg  
705

<210> 390  
<211> 2172  
<212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 390

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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg    120
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc    180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac    240
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tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc    420
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tctgggggca cagcgccctt gggctgcctg gtcaaggact acttccccga accggtgacg    540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgccttacag    600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc    660
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt    720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg    780
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg    840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc    900
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tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   1020
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atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   1260

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A-1937-W0-PCT\_ST25

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cccggtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc 1320
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tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc 1440
gaggtacaac tgggtggaatc aggtggaggt ttgggtgcagc cggggagatc gctcaggctt 1500
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 1560
cctggaaaag ggctcgagtg gggtttccgcc attacgtgga atagcggaca catcgattat 1620
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gcgtcccagg gaatccggaa ttacctcgca tggatatcagc aaaaacccgg aaaagcacccg 1980
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gagatcaagc gt 2172

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<210> 391  
 <211> 702  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 391

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Gly | Leu | Leu | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Ser | Leu | Thr | Cys | Ala | Val | His | Gly | Gly | Ser | Phe | Ser | Gly | Tyr |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

## A-1937-W0-PCT\_ST25

20

25

30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

## A-1937-W0-PCT\_ST25

210

215

220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

## A-1937-W0-PCT\_ST25

405

410

415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
 450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
 465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
 485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
 500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
 515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
 530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
 545 550 555 560

Ser Thr Ala Ser Ser Leu 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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser



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595

600

605

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg  
610 615 620

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
625 630 635 640

Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe  
645 650 655

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
660 665 670

Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala  
675 680 685

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
690 695 700

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 392  
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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc  | 420  |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc  | 480  |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag   | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 660  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt | 720  |
| gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg | 780  |
| gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccgg   | 840  |
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc  | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| ccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac   | 1620 |
| agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga | 1800 |

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tctggtggcg gtggttctgg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |
| gtgtctgggg ccccagggca gagggtcacc atctcctgca ctgggagcag ttccaacatc  | 1920 |
| ggggcagggtt atgatgtaca ctggtaccag cagtttccag gaacagcccc caaactcctc | 1980 |
| atccaaggta acagcaatcg gccctcaggg gtccctgacc gattctctgg ctccaagtct  | 2040 |
| ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac  | 2100 |
| tgccagtcct atgacagcag cctgagtggg tcggtgttcg gcggagggac caagctgacc  | 2160 |
| gtcctaggt                                                          | 2169 |

<210> 393  
 <211> 701  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 393

|                                                                          |
|--------------------------------------------------------------------------|
| Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu          |
| 1                      5                      10                      15 |

|                                                                 |
|-----------------------------------------------------------------|
| Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr |
| 20                      25                      30              |

|                                                                 |
|-----------------------------------------------------------------|
| Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile |
| 35                      40                      45              |

|                                                                 |
|-----------------------------------------------------------------|
| Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys |
| 50                      55                      60              |

|                                                                            |
|----------------------------------------------------------------------------|
| Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu            |
| 65                      70                      75                      80 |

|                                                                 |
|-----------------------------------------------------------------|
| Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala |
| 85                      90                      95              |

A-1937-W0-PCT\_ST25

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

A-1937-W0-PCT\_ST25

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

A-1937-W0-PCT\_ST25

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
580 585 590

Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val  
610 615 620

His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu Ile Gln  
625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
660 665 670

A-1937-W0-PCT\_ST25

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly  
675 680 685

Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695 700

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<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 394  
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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
tattgtagaa gtaccacctg ctactttgac tactggggcc aggggaaccct agtcaccgtc 420  
tcctcagcct ccaccaaggg cccatcgggtc ttccccctgg caccctcctc caagagcacc 480  
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540  
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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660  
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720  
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780  
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 840  
acccctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc 900

## A-1937-W0-PCT\_ST25

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag 960  
tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020  
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080  
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatccccg 1140  
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200  
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260  
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aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380  
tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc 1440  
caggtgcagt tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 1500  
tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct 1560  
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 1620  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 1680  
ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc 1740  
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atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1920  
acttgccggg caagtcagga catcagaaat gatttaggct ggtatcagca gaaaccaggg 1980  
aaagccccta agcgcctgat ctatgctgcg tccagtttgc aaagtggggt cccatcaagg 2040  
ttcagcggca gtggatctgg gccagaattc actctcacia tcagcagcct gcagcctgaa 2100  
gattttgcaa cttattactg tctacaacat aatagttatc cgctcacttt cggcggaggg 2160  
accaaggtgg agatcaaacg t 2181

&lt;210&gt; 395

&lt;211&gt; 705

&lt;212&gt; PRT



&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 395

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
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Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val

## A-1937-W0-PCT\_ST25

165

170

175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

## A-1937-W0-PCT\_ST25

355

360

365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 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 Asp Met His Trp Val Arg  
 485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp  
 500 505 510

Gly Ser Ile 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 Val Asn Ser Leu  
 530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Val Arg Ser

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545 550 555 560

Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr  
565 570 575

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
595 600 605

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln  
610 615 620

Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
625 630 635 640

Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro  
645 650 655

Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile  
660 665 670

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His  
675 680 685

Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695 700

Arg  
705

<210> 396  
<211> 2172  
<212> DNA  
<213> Artificial Sequence

## A-1937-W0-PCT\_ST25

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 396

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| cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg   | 120  |
| tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc | 180  |
| cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac   | 240  |
| tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc   | 300  |
| tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga   | 360  |
| tattgtagaa gtaccacctg ctactttgac tactggggcc aggggaacctt agtcaccgtc  | 420  |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc   | 480  |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg   | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggcggtgcaca ctttcccggc tgtcctacag  | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc   | 660  |
| cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga caagaaagtt    | 720  |
| gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg  | 780  |
| gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg   | 840  |
| acccctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc  | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag   | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc   | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc   | 1320 |

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aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380  
 tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc 1440  
 gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 1500  
 agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 1560  
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 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 1680  
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 agtggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctccga tatccaaatg 1860  
 acacaatcac catcgtcgct ttcagcgtct gttggcgacc gtgtgacgat tacctgtcgc 1920  
 gcgtcccagg gaatccggaa ttacctcgca tggatatcagc aaaaacccgg aaaagcaccg 1980  
 aagctcctga tctatgccgc ctcgactctt cagagtgggt tgccgtcgag gtttagcggg 2040  
 tccgggtcag gtacggactt tactctcaca atttccagcc tgcagcccga agatgtagct 2100  
 acctattact gccagagata caaccgagcg ccttacacat tcggatgtgg gacaaaagtc 2160  
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<210> 397

<211> 702

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 397

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

A-1937-W0-PCT\_ST25

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

A-1937-W0-PCT\_ST25

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415



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Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu 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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
595 600 605

A-1937-W0-PCT\_ST25

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg  
610 615 620

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
625 630 635 640

Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe  
645 650 655

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
660 665 670

Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala  
675 680 685

Pro Tyr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg  
690 695 700

<210> 398  
<211> 2169  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 398  
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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaaccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
tattgtagaa gtaccacctg ctactttgac tactggggcc aggggaaccct agtcaccgtc 420

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc  | 480  |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag  | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 660  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt | 720  |
| gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg | 780  |
| gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg   | 840  |
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc  | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| ccggggaaat gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac  | 1620 |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggctctg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga  | 1800 |
| tctggtggcg gtggttctgg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |

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gtgtctgggg ccccagggca gagggtcacc atctcctgca ctgggagcag ttccaacatc 1920  
 ggggcagggtt atgatgtaca ctggtaccag cagtttccag gaacagcccc caaactcctc 1980  
 atccaaggta acagcaatcg gccctcaggg gtccctgacc gattctctgg ctccaagtct 2040  
 ggacacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac 2100  
 tgccagtcct atgacagcag cctgagtggg tcggtgttcg gctgtgggac caagctgacc 2160  
 gtcctaggt 2169

<210> 399  
 <211> 701  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 399

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln

## A-1937-W0-PCT\_ST25

100

105

110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg

## A-1937-W0-PCT\_ST25

290

295

300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
 450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
 465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg

## A-1937-W0-PCT\_ST25

485

490

495

Gln Met Pro Gly Lys Cys Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
 500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
 515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
 530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
 545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
 565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
 580 585 590

Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
 595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val  
 610 615 620

His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu Ile Gln  
 625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
 660 665 670

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly

675

680

685

Ser Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly  
 690 695 700

&lt;210&gt; 400

&lt;211&gt; 2181

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 400

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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg      120
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc      180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac      240
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc      300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga      360
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaccct agtcaccgtc      420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc      480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg      540
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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc      660
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gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg      780
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      900
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag      960

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## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc | 1440 |
| caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 1500 |
| tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct  | 1560 |
| ccaggcaagt gtctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat  | 1620 |
| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 1680 |
| ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc  | 1740 |
| cgtagtggga gctactacta ttactacagt atggacgtct ggggcccaagg gaccacggtc | 1800 |
| accgtctcta gtggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgac  | 1860 |
| atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc  | 1920 |
| acttgccggg caagtcagga catcagaaat gatttaggct ggtatcagca gaaaccaggg  | 1980 |
| aaagccccta agcgcctgat ctatgctgcg tccagtttgc aaagtgggggt cccatcaagg | 2040 |
| ttcagcggca gtggatctgg gccagaattc actctcacia tcagcagcct gcagcctgaa  | 2100 |
| gattttgcaa cttattactg tctacaacat aatagttatc cgctcacttt cggctgtggg  | 2160 |
| accaaggtgg agatcaaacg t                                            | 2181 |

&lt;210&gt; 401

&lt;211&gt; 705

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

A-1937-W0-PCT\_ST25

<220>

<223> Synthetic polynucleotide

<400> 401

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

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Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
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 Asp Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ala Val Ile Ser Tyr Asp  
500 505 510

Gly Ser Ile 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 Val Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Val Arg Ser  
545 550 555 560

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Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr  
565 570 575

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
595 600 605

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln  
610 615 620

Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
625 630 635 640

Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro  
645 650 655

Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile  
660 665 670

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His  
675 680 685

Asn Ser Tyr Pro Leu Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys  
690 695 700

Arg  
705

<210> 402  
<211> 2169  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 402

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg  | 60   |
| cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg   | 120  |
| tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc | 180  |
| cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac   | 240  |
| tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc   | 300  |
| tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga   | 360  |
| tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc   | 420  |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc   | 480  |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg   | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag    | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc   | 660  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt   | 720  |
| gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg  | 780  |
| gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg    | 840  |
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag   | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc   | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc   | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac   | 1380 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaagg cttctggata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| cccgggaaag gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac  | 1620 |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga  | 1800 |
| tctggtggcg gtggttctgg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |
| gtgtctgggg ccccagggca gagggtcacc atctcctgca ctgggagcag ttccaacatc  | 1920 |
| ggggcagggt atgatgtaca ctggtaccag cagcttccag gaacagcccc caaactcctc  | 1980 |
| atctatggta acagcaatcg gccctcaggg gtccctgacc gattctctgg ctccaagtct  | 2040 |
| ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac  | 2100 |
| tgccagtcct atgaaagcag cctgagtggg tcggtgttcg gcggaggggac caagctgacc | 2160 |
| gtcctaggt                                                          | 2169 |

<210> 403  
 <211> 701  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 403

|                                                                                                          |
|----------------------------------------------------------------------------------------------------------|
| Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu                                          |
| 1                      5                                      10                                      15 |

|                                                                                    |
|------------------------------------------------------------------------------------|
| Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr                    |
| 20                                      25                                      30 |

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

## A-1937-W0-PCT\_ST25

35

40

45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly



## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Ala | Lys | Thr | Lys | Pro | Cys | Glu | Glu | Gln | Tyr | Gly | Ser | Thr | Tyr | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Val | Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Tyr | Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Leu | Pro | Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys | Asn | Gln | Val | Ser | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Asp | Ser | Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Ser | Arg | Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His |

## A-1937-W0-PCT\_ST25

420

425

430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
 450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
 465 470 475 480

Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
 485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
 500 505 510

Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
 515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
 530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
 545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
 565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
 580 585 590

Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
 595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val

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610

615

620

His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr  
625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
660 665 670

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly  
675 680 685

Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695 700

<210> 404  
<211> 2169  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 404  
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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaaccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
tattgtagaa gtaccacctg ctactttgac tactggggcc aggggaaccct agtcaccgtc 420  
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag  | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 660  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt  | 720  |
| gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg | 780  |
| gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg  | 840  |
| accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaagg cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| ccggggaaag gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac  | 1620 |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga  | 1800 |
| tctggtggcg gtggttcttg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |
| gtgtctgggg ccccaggga gagggtcacc atctcctgca ctgggagcag ttccaacatc   | 1920 |

A-1937-W0-PCT\_ST25

ggggcagggtt atgatgtaca ctggtaccag cagcttccag gaacagcccc caaactcctc 1980  
atctatggta acagcaatcg gccctcaggg gtccctgacc gattctctgg ctccaagtct 2040  
ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac 2100  
tgccagtcct atgaaagcag cctgagtggg tcggtgttcg gcggagggac caagctgacc 2160  
gtcctaggt 2169

<210> 405

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 405

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Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

A-1937-W0-PCT\_ST25

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

A-1937-W0-PCT\_ST25

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Ala Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

A-1937-W0-PCT\_ST25

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
580 585 590

Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val  
610 615 620

His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr  
625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
660 665 670

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly  
675 680 685



A-1937-W0-PCT\_ST25

Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695 700

<210> 406  
<211> 2163  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 406  
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tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180  
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240  
tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc 300  
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360  
actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 420  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 540  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc 960  
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

## A-1937-W0-PCT\_ST25

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg 1260  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgagggtg 1440  
 cagctggtgc agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatctcctgt 1500  
 aaggcttctg gatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg 1560  
 aaaggcctgg agtggatggg gatcatctat cttggtgaat cagaaaccag atacagcccg 1620  
 tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag 1680  
 tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggt 1740  
 cttgactact ggggccaggg aaccctggtc accgtctcta gtggaggcgg aggatctggt 1800  
 ggcggtggtt ctggcggcgg aggctcccag tctgtgctga cgcagccgcc ctcagtgtct 1860  
 ggggccccag ggcagagggt caccatctcc tgcactggga gcagttccaa catcggggca 1920  
 ggttatgatg tacactggta ccagcagctt ccaggaacag cccccaaact cctcatctat 1980  
 ggtaacagca atcggccctc aggggtccct gaccgattct ctggctccaa gtctggcacc 2040  
 tcagcctccc tggccatcac tgggctccag gctgaggatg aggctgatta ttactgccag 2100  
 tcctatgaaa gcagcctgag tggttcgggtg ttcggcggag ggaccaagct gaccgtccta 2160  
 ggt 2163

&lt;210&gt; 407

&lt;211&gt; 699

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

A-1937-W0-PCT\_ST25

<400> 407

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

## A-1937-W0-PCT\_ST25

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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

## A-1937-W0-PCT\_ST25

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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
 450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Ala  
 465 470 475 480

Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
 485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Glu Ser  
 500 505 510

Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
 515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
 530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
 545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly

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565

570

575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr  
580 585 590

Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser  
595 600 605

Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp  
610 615 620

Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn  
625 630 635 640

Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser  
645 650 655

Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu  
660 665 670

Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly Ser Val  
675 680 685

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695

<210> 408

<211> 2163

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 408

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggcg 60

cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg  | 180  |
| cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa    | 240  |
| tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc   | 300  |
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa   | 360  |
| actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca  | 420  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt   | 840  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 960  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1140 |
| atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc  | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg   | 1440 |
| cagctgggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt  | 1500 |
| aaggcttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg  | 1560 |

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aaaggcctgg agtggatggg gatcatctat cttggtgaat cagaaaccag atacagcccg 1620  
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag 1680  
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt 1740  
cttgactact ggggccaggg aaccctggtc accgtctcta gtggaggcgg aggatctggt 1800  
ggcgggtggtt ctggcggcgg aggctcccag tctgtgctga cgcagccgcc ctcaagtgtct 1860  
ggggccccag ggcagagggt caccatctcc tgcactggga gcagttccaa catcggggca 1920  
ggttatgatg tacactggta ccagcagctt ccaggaacag cccccaaact cctcatctat 1980  
ggtaacagca atcgccctc aggggtccct gaccgattct ctggctcaa gtctggcacc 2040  
tcagcctccc tggccatcac tgggctccag gctgaggatg aggctgatta ttactgccag 2100  
tcctatgaaa gcagcctgag tggttcgggtg ttcggcggag ggaccaagct gaccgtccta 2160  
ggt 2163

<210> 409  
<211> 699  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 409

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60



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Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

A-1937-W0-PCT\_ST25

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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Ala  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Glu Ser  
500 505 510

Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu 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 Gln Ser Val Leu Thr  
580 585 590

Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser  
595 600 605

Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp  
610 615 620

Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn  
625 630 635 640

A-1937-W0-PCT\_ST25

Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser  
645 650 655

Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu  
660 665 670

Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly Ser Val  
675 680 685

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
690 695

<210> 410  
<211> 2169  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 410  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaaccgt ccctcaagag tcgagtcacc atatcattag acacgtcaa gaaccagttc 300  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc 420  
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480  
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540  
gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag 600  
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt  | 720  |
| gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg   | 780  |
| gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg  | 840  |
| accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaagg cttctggata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| cccgggaaat gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac  | 1620 |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga  | 1800 |
| tctggtggcg gtggttcttg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |
| gtgtctgggg ccccagggca gagggtcacc atctcctgca ctgggagcag ttccaacatc  | 1920 |
| ggggcagggt atgatgtaca ctggtaccag cagcttccag gaacagcccc caaactcctc  | 1980 |
| atctatggta acagcaatcg gccctcaggg gtccctgacc gatttcttgg ctccaagtct  | 2040 |
| ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac  | 2100 |

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tgccagtcct atgaaagcag cctgagtggt tcggtgttcg gctgtgggac caagctgacc 2160

gtcctaggt 2169

<210> 411

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 411

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

## A-1937-W0-PCT\_ST25

130

135

140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

## A-1937-W0-PCT\_ST25

325

330

335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
 450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
 465 470 475 480

Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
 485 490 495

Gln Met Pro Gly Lys Cys Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
 500 505 510

Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile



## A-1937-W0-PCT\_ST25

515

520

525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
 530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
 545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
 565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
 580 585 590

Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
 595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val  
 610 615 620

His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr  
 625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
 660 665 670

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly  
 675 680 685

Ser Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly  
 690 695 700

&lt;210&gt; 412

## A-1937-W0-PCT\_ST25

<211> 2169  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 412  
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 tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
 cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
 tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
 tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
 tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc 420  
 tcctcagcct ccaccaaggc cccatcggtc ttccccctgg caccctcctc caagagcacc 480  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540  
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 600  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660  
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720  
 gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780  
 gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg 840  
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900  
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag 960  
 tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020  
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080  
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140  
 gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttc ctctatagca agctcaccgt ggacaagagc   | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc | 1440 |
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 1500 |
| tcctgtaagg cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 1560 |
| ccggggaaat gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac  | 1620 |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 1680 |
| ctgcagtggg gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 1740 |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga | 1800 |
| tctggtggcg gtggttctgg cggcggaggc tcccagtctg tgctgacgca gccgccctca  | 1860 |
| gtgtctgggg ccccagggca gagggtcacc atctcctgca ctgggagcag ttccaacatc  | 1920 |
| ggggcaggtt atgatgtaca ctggtaccag cagcttcag gaacagcccc caaactcctc   | 1980 |
| atctatggta acagcaatcg gccctcaggg gtccctgacc gattctcttg ctccaagtct  | 2040 |
| ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac  | 2100 |
| tgccagtcct atgaaagcag cctgagtggg tcgggtgtcg gctgtgggac caagctgacc  | 2160 |
| gtcctaggt                                                          | 2169 |

<210> 413

<211> 701

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 413

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Gly | Leu | Leu | Lys | Pro | Ser | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

A-1937-W0-PCT\_ST25

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

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Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

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Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Ala Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Cys Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val  
580 585 590

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Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr  
595 600 605

Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val  
610 615 620

His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr  
625 630 635 640

Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
645 650 655

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu  
660 665 670

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser Leu Ser Gly  
675 680 685

Ser Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly  
690 695 700

<210> 414  
<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 414  
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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga  | 360  |
| tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc  | 420  |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc  | 480  |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 540  |
| gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca cttcccggc tgcctacag     | 600  |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 660  |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt | 720  |
| gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg   | 780  |
| gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg  | 840  |
| accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 1500 |
| tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct  | 1560 |
| ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat  | 1620 |
| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 1680 |
| ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc  | 1740 |



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cgtagtggga gctactacta ttactacagt atggacgtct ggggccaagg gaccttggtc 1800  
accgtctcta gtggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgac 1860  
atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1920  
acttgccggg caagtcagga catcagaaat gatttaggct ggtatcagca gaaaccaggg 1980  
aaagccccta agctcctgat ctatgctgcg tccagtttgc aaagtggggt cccatcaagg 2040  
ttcagcggca gtggatctgg gccagaattc actctcacia tcagcagcct gcagcctgaa 2100  
gattttgcaa cttattactg tctacaacat aatagttatc cgctcacttt cggcggaggg 2160  
accaaggtgg agatcaaacg t 2181

<210> 415  
<211> 705  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 415

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

## A-1937-W0-PCT\_ST25

85

90

95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

## A-1937-W0-PCT\_ST25

275

280

285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 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

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 465 |     | 470 |     | 475 |     | 480 |     |     |     |     |     |     |     |     |     |
| Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Ser | Tyr | Asp | Met | His | Trp | Val | Arg |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val | Ala | Val | Ile | Ser | Tyr | Asp |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Gly | Ser | Ile | 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 | Val | Asn | Ser | Leu |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Arg | Glu | Val | Arg | Ser |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Gly | Ser | Tyr | Tyr | Tyr | Tyr | Tyr | Ser | Met | Asp | Val | Trp | Gly | Gln | Gly | Thr |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Leu | Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Gly | Gly | Gly | Gly | Ser | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ser | Ala | Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Asp | Ile | Arg | Asn | Asp | Leu | Gly | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Pro | Lys | Leu | Leu | Ile | Tyr | Ala | Ala | Ser | Ser | Leu | Gln | Ser | Gly | Val | Pro |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Pro | Glu | Phe | Thr | Leu | Thr | Ile |

## A-1937-W0-PCT\_ST25

660

665

670

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His  
 675 680 685

Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 690 695 700

Arg  
 705

<210> 416  
 <211> 2181  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 416  
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 cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120  
 tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180  
 cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240  
 tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300  
 tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360  
 tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaccct agtcaccgtc 420  
 tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540  
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 600  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660  
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg   | 780  |
| gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg  | 840  |
| acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc  | 900  |
| aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag  | 960  |
| tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat  | 1020 |
| ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc  | 1080 |
| atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg  | 1140 |
| gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc  | 1200 |
| gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct  | 1260 |
| cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc  | 1320 |
| aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac  | 1380 |
| tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc  | 1440 |
| caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 1500 |
| tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct  | 1560 |
| ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atgcaagtat taaatactat  | 1620 |
| gcagaatccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 1680 |
| ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc  | 1740 |
| cgtagtggga gctactacta ttactacagt atggacgtct ggggccaagg gaccttggtc  | 1800 |
| accgtctcta gtggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgac  | 1860 |
| atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc  | 1920 |
| acttgccggg caagtcagga catcagaaat gatttaggct ggtatcagca gaaaccaggg  | 1980 |
| aaagccccta agctcctgat ctatgctgcg tccagtttgc aaagtggggt cccatcaagg  | 2040 |
| ttcagcggca gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa  | 2100 |
| gattttgcaa cttattactg tctacaacat aatagttatc cgctcacttt cggcggaggg  | 2160 |

accaaggtgg agatcaaacg t

2181

&lt;210&gt; 417

&lt;211&gt; 705

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 417

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

A-1937-W0-PCT\_ST25

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335



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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
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 Asp Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp  
500 505 510

Ala Ser Ile Lys Tyr Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile  
515 520 525

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Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Val Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Val Arg Ser  
545 550 555 560

Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
595 600 605

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln  
610 615 620

Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
625 630 635 640

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln 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 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His  
675 680 685

Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
690 695 700

Arg  
705

A-1937-WO-PCT\_ST25

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 <211> 2187  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 418  
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 tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
 attaggcagc ccccagggaa aggccctgag tggataggaa ggacatacta caggtccaag 240  
 tgggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
 aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360  
 tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
 accacgggtca ccgtctcctc agcctccacc aaggggcccat cggctcttccc cctggcaccc 480  
 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
 cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600  
 ccggctgtcc tacagtccctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660  
 agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720  
 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca 780  
 gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc 840  
 ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900  
 cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 960  
 ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac 1020  
 caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc 1080  
 cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140

## A-1937-W0-PCT\_ST25

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ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260
tacaagacca cgctccccgt gctggactcc gacggctcct tcttcctcta tagcaagctc 1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg 1440
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cccgaaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg 2040
tcgaggttta gcgggtccgg gtcagggtacg gactttactc tcacaatttc cagcctgcag 2100
cccgaagatt tcgctaccta ttactgccag agatacaacc gagcgcctta cacattcgga 2160
caagggacaa aagtcgagat caagcgt 2187

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&lt;210&gt; 419

&lt;211&gt; 707

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 419

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

## A-1937-W0-PCT\_ST25

|     |     |     |     |
|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Thr | Leu | Ser | Leu |
|     | 20  | Thr | Cys |
|     |     | Thr | Ile |
|     |     | 25  | Ser |
|     |     | Gly | Asp |
|     |     | Ser | Val |
|     |     | 30  | Ser |
|     |     | Thr | Asn |
| Ser | Val | Ala | Trp |
|     | 35  | Asn | Trp |
|     |     | Ile | Arg |
|     |     | 40  | Gln |
|     |     | Pro | Pro |
|     |     | Gly | Lys |
|     |     | 45  | Gly |
|     |     | Leu | Glu |
| Trp | Ile | Gly | Arg |
|     | 50  | Thr | Tyr |
|     |     | Tyr | Arg |
|     |     | 55  | Ser |
|     |     | Lys | Trp |
|     |     | Tyr | Asn |
|     |     | 60  | Asp |
|     |     | Tyr | Ala |
| Val | Ser | Leu | Lys |
|     | 65  | Ser | Arg |
|     |     | Val | Thr |
|     |     | Ile | Ser |
|     |     | 70  | Pro |
|     |     | 75  | Asp |
|     |     | Thr | Ser |
|     |     | Lys | Asn |
|     |     | 80  |     |
| Gln | Phe | Ser | Leu |
|     |     | Lys | Leu |
|     |     | 85  | Ser |
|     |     | Ser | Val |
|     |     | 90  | Thr |
|     |     | Ala | Ala |
|     |     | Asp | Thr |
|     |     | 95  | Ala |
|     |     | Val |     |
| Tyr | Tyr | Cys | Ala |
|     |     | 100 | Arg |
|     |     | Glu | Asp |
|     |     | Gly | Asp |
|     |     | 105 | Ser |
|     |     | Tyr | Tyr |
|     |     | Arg | Tyr |
|     |     | 110 | Gly |
|     |     | Met |     |
| Asp | Val | Trp | Gly |
|     | 115 | Gln | Gly |
|     |     | Thr | Thr |
|     |     | 120 | Val |
|     |     | Thr | Val |
|     |     | 125 | Ser |
|     |     | Ser | Ala |
|     |     | Ser | Thr |
| Lys | Gly | Pro | Ser |
|     | 130 | Val | Phe |
|     |     | Pro | Leu |
|     |     | 135 | Ala |
|     |     | Pro | Ser |
|     |     | 140 | Ser |
|     |     | Lys | Ser |
|     |     | Thr | Ser |
| Gly | Gly | Thr | Ala |
|     | 145 | Ala | Leu |
|     |     | Gly | Cys |
|     |     | 150 | Leu |
|     |     | Val | Lys |
|     |     | 155 | Asp |
|     |     | Tyr | Phe |
|     |     | Pro | Glu |
|     |     | 160 |     |
| Pro | Val | Thr | Val |
|     |     | Ser | Trp |
|     |     | 165 | Asn |
|     |     | Ser | Gly |
|     |     | 170 | Ala |
|     |     | Leu | Thr |
|     |     | Ser | Gly |
|     |     | 175 | Val |
|     |     | His |     |
| Thr | Phe | Pro | Ala |
|     |     | 180 | Val |
|     |     | Leu | Gln |
|     |     | Ser | Ser |
|     |     | 185 | Gly |
|     |     | Leu | Tyr |
|     |     | Ser | Leu |
|     |     | 190 | Ser |
|     |     | Ser |     |
| Val | Val | Thr | Val |
|     |     | Pro | Ser |
|     |     | Ser | Ser |
|     |     | Ser | Leu |
|     |     | Gly | Thr |
|     |     | Gln | Thr |
|     |     | Tyr | Ile |
|     |     | Cys |     |

## A-1937-W0-PCT\_ST25

195

200

205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
 290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
 325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
 355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

385                      390                      395                      400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg | Ser |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

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580

585

590

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
595 600 605

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
610 615 620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
660 665 670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu  
690 695 700

Ile Lys Arg  
705

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<211> 2187  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic polynucleotide

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cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 120



## A-1937-W0-PCT\_ST25

|                                                                      |      |
|----------------------------------------------------------------------|------|
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg    | 180  |
| attaggcagc ccccagggaa aggcccttgag tggataggaa ggacatacta caggtccaag   | 240  |
| tgggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc   | 300  |
| aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac    | 360  |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg    | 420  |
| accacgggtca ccgtctcctc agcctccacc aaggggcccat cggctcttccc cctggcaccc | 480  |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc   | 540  |
| cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    | 600  |
| ccggctgtcc tacagtctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc    | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca     | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttctcttccc ccccaaaacc caaggacacc    | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac    | 900  |
| cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag   | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac    | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc    | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa  | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    | 1260 |
| tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc    | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag   | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg    | 1440 |
| ggagggtggcg gatccgaggt acaactgggtg gaatcagggt gaggtttggt gcagccgggg  | 1500 |
| agatcgctca ggcttagctg tgcggcatcg gggtttactt tcagtgatta tgcgatgcat    | 1560 |

A-1937-W0-PCT\_ST25

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 ggacacatcg attatgcaga aagtgtggag ggcagattca caatctcacg agacaatgct 1680  
 aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac 1740  
 tgcgcaaaag tctcctactt gtctacagct tcgtcgctcg actattgggg tcaaggaacg 1800  
 ttggtcaccg tctctagtgg aggcggagga tctgggtggcg gtggttctgg cggcggaggc 1860  
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 tcgaggttta gcgggtccgg gtcaggtacg gactttactc tcacaatttc cagcctgcag 2100  
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<211> 707

<212> PRT

<213> Artificial Sequence

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<223> Synthetic polynucleotide

<400> 421

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
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 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

A-1937-W0-PCT\_ST25

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

A-1937-W0-PCT\_ST25

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

A-1937-W0-PCT\_ST25

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Glu Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser 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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
610 615 620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

A-1937-W0-PCT\_ST25

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
660 665 670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu  
690 695 700

Ile Lys Arg  
705

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tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
accacggtca ccgtctctc agcctccacc aagggcccat cggtcttccc cctggcaccc 480  
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540

## A-1937-W0-PCT\_ST25

|                                                                      |      |
|----------------------------------------------------------------------|------|
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc    | 600  |
| ccggctgtcc tacagtcttc aggactctac tccctcagca gcgtggtgac cgtgccctcc    | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag    | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca     | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc    | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac    | 900  |
| cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag   | 960  |
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac    | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc    | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc    | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccagggtc gcctgacctg cctggtcaaa    | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac    | 1260 |
| tacaagacca cgcctcccggt gctggactcc gacggctcct tcttcctcta tagcaagctc   | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag   | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg    | 1440 |
| ggagggtggcg gatccgaggt acaactgggtg gaatcagggtg gaggtttggt gcagccgggg | 1500 |
| agatcgctca ggcttagctg tgcggcatcg gggtttactt tcagtgatta tgcgatgcat    | 1560 |
| tgggtccggc aagcgcctgg aaaatgtctc gagtgggttt ccgccattac gtggaatagc    | 1620 |
| ggacacatcg attatgcaga cgctgtggag ggcagattca caatctcacg agacaatgct    | 1680 |
| aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac    | 1740 |
| tgcgcaaag tctcctactt gtctacagct tcgtcgctcg actattgggg tcaaggaacg     | 1800 |
| ttggtcaccg tctctagtgg aggcggagga tctgggtggcg gtggttctgg cggcggaggc   | 1860 |
| tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttgg cgaccgtgtg    | 1920 |
| acgattacct gtcgcgcgtc ccagggaatc cggaattacc tcgcatggta tcagcaaaaa    | 1980 |

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cccggaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg 2040  
 tcgagggttta gcgggtccgg gtcagggtacg gactttactc tcacaatttc cagcctgcag 2100  
 cccgaagatt tcgctaccta ttactgccag agatacaacc gagcgcctta cacattcgga 2160  
 tgtgggacaa aagtcgagat caagcgt 2187

<210> 423  
 <211> 707  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 423

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr



## A-1937-W0-PCT\_ST25

115

120

125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
 180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
 195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
 290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     | 310 |     | 315 |     | 320 |     |     |     |     |     |     |     |     |     |
| Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Pro | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg | Glu | Glu | Met | Thr | Lys |
|     |     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |
| Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ser | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu | Asn | Asn | Tyr | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Phe | Phe | Leu | Tyr | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln | Gly | Asn | Val | Phe | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser |
|     |     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |
| Leu | Ser | Leu | Ser | Pro | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Glu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg | Ser |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Asp | Tyr | Ala |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Cys | Leu | Glu | Trp | Val | Ser |

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500

505

510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val Glu  
 515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
 530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
 545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
 565 570 575

Gly Thr Leu Val Thr Val Ser 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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 610 615 620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
 625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
 645 650 655

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 660 665 670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
 675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Cys Gly Thr Lys Val Glu

690

695

700

Ile Lys Arg  
705

<210> 424  
<211> 2187  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 424  
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cgctgtcagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 120  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420  
accacggtca ccgtctcctc agcctccacc aaggggcccat cggctttccc cctggcaccc 480  
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600  
ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660  
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720  
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc 780  
gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc 840  
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900  
cctgagggtca agttcaactg gtacgtggac ggcggtggagg tgcataatgc caagacaaag 960

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac   | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc   | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   | 1140 |
| ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   | 1260 |
| tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc   | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag  | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg   | 1440 |
| ggaggtggcg gatccgaggt acaactgggtg gaatcagggtg gaggtttggt gcagccgggg | 1500 |
| agatcgctca ggcttagctg tgccggcatcg gggtttactt tcagtgatta tgcgatgcat  | 1560 |
| tgggtccggc aagcgcctgg aaaatgtctc gagtgggttt ccgccattac gtggaatagc   | 1620 |
| ggacacatcg attatgcaga aagtgtggag ggcagattca caatctcacg agacaatgct   | 1680 |
| aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac   | 1740 |
| tgccgcaaag tctcctactt gtctacagct tcgtcgctcg actattgggg tcaaggaacg   | 1800 |
| ttggtcaccg tctctagtgg aggcggagga tctgggtggcg gtggttctgg cggcggaggc  | 1860 |
| tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttgg cgaccgtgtg   | 1920 |
| acgattacct gtcgcgcgtc ccagggaatc cggaattacc tcgcatggta tcagcaaaaa   | 1980 |
| cccggaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg  | 2040 |
| tcgaggttta gcgggtccgg gtcagggtacg gactttactc tcacaatttc cagcctgcag  | 2100 |
| cccgaagatt tcgctaccta ttactgccag agatacaacc gagcgcctta cacattcgga   | 2160 |
| tgtgggacaa aagtcgagat caagcgt                                       | 2187 |

&lt;210&gt; 425

&lt;211&gt; 707

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 425

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

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Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

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Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Glu Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560



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Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser 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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
610 615 620

Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly  
625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly  
645 650 655

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
660 665 670

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
675 680 685

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Cys Gly Thr Lys Val Glu  
690 695 700

Ile Lys Arg  
705

<210> 426

<211> 2151

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

A-1937-W0-PCT\_ST25

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cgctgtgagg tgcagctggg gcagctctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaaggcttc tggatacagc tttaccagct actggatcgg ctgggtgctg 180  
cagatgcccc ggaaaaggcct ggagtggatg gggatcatct atcttgggtga atcagaaacc 240  
agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc 300  
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
accaagggcc catcgggtctt ccccttgga ccctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 600  
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gccc aaatct 720  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780  
gtcttctctt tcccccaaa acccaaggac accctcatga tctccggac ccctgaggtc 840  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 960  
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020  
aagtgaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1080  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1140  
aagaaccagg tcagcctgac ctgcctgggt aaaggcttct atcccagcga catcgccgtg 1200  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260  
tccgacggct ccttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1320  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380

A-1937-W0-PCT\_ST25

agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccca ggtgcagctg 1440  
caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc 1500  
tctggtggct ccatcagtag ttactttctgg agctggatcc ggcagcccc aggtaaggga 1560  
ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag 1620  
agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct 1680  
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc 1740  
tttgactact ggggccaggg aaccctggtc accgtctcct caggaggcgg aggatctggt 1800  
ggcgggtggt ctggcggcgg aggctccgac atccagatga cccagtctcc atcctccctg 1860  
tctgcatctg taggagacag agtcaccatc acttgccggg caagtcagag cattaacaac 1920  
tatttaaatt ggtatcagca gagaccaggg aaagccccta agctcctgat ctatgctgca 1980  
tccagtttgc aaagtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2040  
actctacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2100  
tacagtaccc ctcggacgtt cggccaaggg accaagctgg aaatcaaacg a 2151

<210> 427

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 427

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
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Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

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Gly Ile Ile Tyr Leu Gly Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly  
435 440 445

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Asp Ile Gln Met Thr  
580 585 590

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
595 600 605

Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr Leu Asn Trp Tyr Gln  
610 615 620

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Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser  
625 630 635 640

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
645 650 655

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
660 665 670

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly  
675 680 685

Thr Lys Leu Glu Ile Lys Arg  
690 695

<210> 428  
<211> 2151  
<212> DNA  
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<220>  
<223> Synthetic polynucleotide

<400> 428  
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aagatctcct gtaaggcttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180  
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga atcagaaacc 240  
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gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcttcc 420  
accaagggcc catcggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggt gtcgtggaac 540

## A-1937-W0-PCT\_ST25

|                                                                    |      |
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| tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gccc aaatct | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 780  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc  | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 960  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 1020 |
| aagtgc aagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc  | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1260 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1380 |
| agcctctccc tgtctccggg tgggtggcga tcgggagggtg gcggatccca ggtgcagctg | 1440 |
| caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc  | 1500 |
| tctggtggct ccatcagtag ttacttctgg agctggatcc ggcagcccc aggtaaggga   | 1560 |
| ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag  | 1620 |
| agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct  | 1680 |
| gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc  | 1740 |
| tttgactact ggggccaggg aaccctggtc accgtctcct caggaggcgg aggatctggt  | 1800 |
| ggcgggtggt ctggcggcgg aggctccgac atccagatga ccagtcctcc atcctccctg  | 1860 |
| tctgcatctg taggagacag agtcaccatc acttgccggg caagtcagag cattaacaac  | 1920 |
| tatttaaatt ggtatcagca gagaccaggg aaagccccta agctcctgat ctatgctgca  | 1980 |



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tccagtttgc aaagtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2040  
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 tacagtaccc ctcggacggt cggccaaggg accaagctgg aaatcaaacg a 2151

<210> 429  
 <211> 695  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 429

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 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Glu Ser Glu Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

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Lys 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 Glu Glu Met 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  
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Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
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Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

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Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Asp Ile Gln Met Thr  
580 585 590

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
595 600 605

Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr Leu Asn Trp Tyr Gln  
610 615 620

Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser  
625 630 635 640

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
645 650 655

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
660 665 670

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly  
675 680 685

Thr Lys Leu Glu Ile Lys Arg  
690 695

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 caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
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 ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
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 gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600  
 gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660  
 agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
 gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
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 tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag 1020  
 gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1080  
 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140

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gcaacttact actgtcaaca gagttacagt acccctcgga cgttcggcca agggaccaag 2160
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<210> 431

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 431

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| Ser | Leu | Arg | Leu |
|     | 20  |     |     |
| Ser | Cys | Ala | Ala |
|     |     | 25  |     |
| Ser | Gly | Phe | Thr |
|     |     |     | Phe |
| Ser | Ser | Tyr |     |
|     |     | 30  |     |
| Asp | Met | His | Trp |
|     | 35  |     |     |
| Val | Arg | Gln | Ala |
|     |     | 40  |     |
| Pro | Gly | Lys | Gly |
|     |     |     | Leu |
| Glu | Trp | Val |     |
|     |     | 45  |     |
| Ala | Val | Ile | Ser |
|     | 50  |     |     |
| Tyr | Asp | Gly | Ser |
|     |     | 55  |     |
| Ile | Lys | Tyr | Tyr |
|     |     |     | Ala |
| Asp | Ser | Val |     |
|     |     | 60  |     |
| Lys | Gly | Arg | Phe |
|     | 65  |     |     |
| Thr | Ile | Ser | Arg |
|     | 70  |     |     |
| Asp | Asn | Ser | Lys |
|     |     | 75  |     |
| Asn | Thr | Leu | Tyr |
|     |     | 80  |     |
| Leu | Gln | Val | Asn |
|     |     |     | 85  |
| Ser | Leu | Arg | Ala |
|     |     |     | Glu |
| Asp | Thr | Ala | Val |
|     |     | 90  |     |
| Tyr | Tyr | Cys |     |
|     |     | 95  |     |
| Ala | Arg | Glu | Val |
|     |     | 100 |     |
| Arg | Ser | Gly | Ser |
|     |     |     | Tyr |
| Tyr | Tyr | Tyr | Tyr |
|     |     |     | Tyr |
| Ser | Met | Asp |     |
|     |     | 110 |     |
| Val | Trp | Gly | Gln |
|     |     | 115 |     |
| Gly | Thr | Leu | Val |
|     |     |     | 120 |
| Thr | Val | Ser | Ser |
|     |     |     | Ala |
| Ser | Thr | Lys |     |
|     |     | 125 |     |
| Gly | Pro | Ser | Val |
|     | 130 |     |     |
| Phe | Pro | Leu | Ala |
|     |     | 135 |     |
| Pro | Ser | Ser | Lys |
|     |     |     | 140 |
| Ser | Thr | Ser | Gly |
|     |     |     |     |
| Gly | Thr | Ala | Ala |
|     | 145 |     |     |
| Leu | Gly | Cys | Leu |
|     |     | 150 |     |
| Val | Lys | Asp | Tyr |
|     |     | 155 |     |
| Phe | Pro | Glu | Pro |
|     |     |     | 160 |
| Val | Thr | Val | Ser |
|     |     |     | Trp |
| Asn | Ser | Gly | Ala |
|     |     |     | Leu |
| Thr | Ser | Gly | Val |
|     |     | 165 |     |
| His | Thr |     |     |
|     |     | 170 |     |
| Phe | Pro | Ala | Val |
|     |     | 180 |     |
| Leu | Gln | Ser | Ser |
|     |     |     | Gly |
| Leu | Tyr | Ser | Leu |
|     |     |     | 185 |
| Ser | Ser | Val |     |
|     |     | 190 |     |
| Val | Thr | Val | Pro |
|     |     |     | Ser |
| Ser | Ser | Ser | Leu |
|     |     |     | Gly |
| Thr | Gln | Thr | Tyr |
|     |     |     | Ile |
| Cys | Asn |     |     |

## A-1937-W0-PCT\_ST25

195

200

205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
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Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
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Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr



385                      390                      395                      400

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
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Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

## A-1937-WO-PCT\_ST25

580

585

590

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
 595 600 605

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile  
 610 615 620

Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys  
 625 630 635 640

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser  
 675 680 685

Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 690 695 700

&lt;210&gt; 432

&lt;211&gt; 2175

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 432

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agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180

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## A-1937-W0-PCT\_ST25

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| gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc   | 420  |
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| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc    | 540  |
| gaaccgggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc | 600  |
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| gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca  | 780  |
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| atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct   | 900  |
| gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg    | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag   | 1020 |
| gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagcccc   | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac   | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct   | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtg cggtatcgga   | 1440 |
| ggtggcggat cccaggtgca gctgcaggag tcgggcccag gactggtgaa gccttcggag   | 1500 |
| accctgtccc tcacctgcac tgtctctgggt ggctccatca gtagttactt ctggagctgg  | 1560 |
| atccggcagc ccccaggtaa gtgtctggag tggattggct atatctatta cagtgggcag   | 1620 |
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A-1937-W0-PCT\_ST25

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<210> 433  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 433

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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

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Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

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Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

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Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser 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 Ser Leu Ser Ala  
595 600 605

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile  
610 615 620

Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys  
625 630 635 640

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg  
645 650 655

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Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
660 665 670

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser  
675 680 685

Thr Pro Arg Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg  
690 695 700

<210> 434  
<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 434  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
ttggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540  
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600  
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660  
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780



## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cctgaactcc tggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc    | 840  |
| atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct    | 900  |
| gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgccaa gacaaagccg | 960  |
| tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag   | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc    | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg   | 1140 |
| cccccatccc gggaggagat gaccaagaac caggctcagc tgacctgcct ggtcaaaggc   | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac    | 1260 |
| aagaccacgc ctcccgctgt ggactccgac ggctccttct tcctctatag caagctcacc   | 1320 |
| gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggtgg cggatcggga   | 1440 |
| ggtggcggtat cccagggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag | 1500 |
| accctgtccc tcacctgcgc tgtccatggt gggtccttca gtggttacta ctggaactgg   | 1560 |
| attcgccagc caccagggaa ggggctagag tggattgggg aaatcaatca tgctggaaac   | 1620 |
| accaactaca acccgctcct caagagtcga gtcaccatat cattagacac gtccaagaac   | 1680 |
| cagttctccc tgacgctgac ctctgtgacc gccgcggaca cggctgtgta ttactgtgcg   | 1740 |
| agaggatatt gtagaagtac cacctgctac tttgactact ggggccaggg aaccctagtc   | 1800 |
| accgtctcct caggaggcgg aggatctggt ggcgggtggt ctggcggcgg aggctccgaa   | 1860 |
| attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc   | 1920 |
| tcctgcaggg ccagtcagag tgtagaagc agttacttag cctggtacca gcagaaacct    | 1980 |
| ggccaggctc ccaggctcct catctatggt gcatccagca gggccactgg catcccagac   | 2040 |
| aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct   | 2100 |
| gaagattttg cagtgtatta ctgtcagcag tatggtagct cacctacctt cggccaaggg   | 2160 |
| acacgactgg agattaaacg a                                             | 2181 |

<210> 435  
 <211> 705  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 435

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro

145                      150                      155                      160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu

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340

345

350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
 450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
 465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
 485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
 500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
 515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu

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530

535

540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu  
595 600 605

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln  
610 615 620

Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
625 630 635 640

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile  
645 650 655

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
660 665 670

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln  
675 680 685

Tyr Gly Ser Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
690 695 700

Arg  
705

<210> 436

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<211> 2181  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 436  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
ttggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540  
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600  
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660  
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720  
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840  
atgatctccc ggaccctga ggtcacatgc gtgggtgggg acgtgagcca cgaagaccct 900  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcca gacaaagccg 960  
tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag 1020  
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc 1080  
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140  
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac  | 1260 |
| aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc  | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtgg cggatcggga | 1440 |
| ggtaggcggat cccaggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag | 1500 |
| accctgtccc tcacctgcgc tgtccatggg gggtccttca gtggttacta ctggaactgg  | 1560 |
| attcgccagc caccagggaa gtgtctagag tggattgggg aaatcaatca tgctggaaac  | 1620 |
| accaactaca acccgtccct caagagtcga gtcaccatat cattagacac gtccaagaac  | 1680 |
| cagttctccc tgacgtgac ctctgtgacc gccgcggaca cggctgtgta ttactgtgcg   | 1740 |
| agaggatatt gtagaagtac cacctgctac tttgactact ggggccaggg aaccctagtc  | 1800 |
| accgtctcct caggaggcgg aggatctggg gccgggtggt ctggcggcgg aggctccgaa  | 1860 |
| attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc  | 1920 |
| tcctgcaggg ccagtcagag tgtagaagc agttacttag cctggtacca gcagaaacct   | 1980 |
| ggccaggctc ccaggctcct catctatggg gcatccagca gggccactgg catcccagac  | 2040 |
| aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct  | 2100 |
| gaagattttg cagtgtatta ctgtcagcag tatggtagct cacctacctt cggctgtggg  | 2160 |
| acacgactgg agattaaacg a                                            | 2181 |

<210> 437

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 437

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205



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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

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Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

A-1937-W0-PCT\_ST25

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu  
595 600 605

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln  
610 615 620

Ser Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
625 630 635 640

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile  
645 650 655

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
660 665 670

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln  
675 680 685

Tyr Gly Ser Ser Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys  
690 695 700

Arg  
705

<210> 438  
<211> 2166  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 438  
atggacatga ggggtcccg ctcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtgagg tacaactggg ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc 120  
aggcttagct gtgcggcatc ggggtttact ttcaagtatt atgcgatgca ttgggtccgg 180

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc   | 240  |
| gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc   | 300  |
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa   | 360  |
| gtctcctact tgtctacagc ttcgtcgtc gactattggg gtcaaggaac gttggtcacc    | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcacccctc ctccaagagc   | 480  |
| acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccgggtg | 540  |
| acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc   | 660  |
| acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa   | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctgggggggac cgtcagtctt cctcttcccc caaaaacca aggacaccct catgatctcc   | 840  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgagggtcaag  | 900  |
| ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagtg caaggctctc aacaaagccc tcccagcccc catcgagaaa   | 1080 |
| accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1260 |
| cctcccgtgc tggactccga cggctcctt ttcctctata gcaagctcac cgtggacaag    | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1440 |
| tcccagggtc agctgcagga gtcgggcca ggactgggtga agccttcgga gaccctgtcc   | 1500 |
| ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag   | 1560 |
| ccccaggta agggactgga gtggattggc tatatctatt acagtgggca gaccaaatac    | 1620 |

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aacccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc 1680  
 ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact 1740  
 gggagctact acggctttga ctactggggc cagggaaacc tggtcaccgt ctctcagga 1800  
 ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag 1860  
 tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt 1920  
 cagagcatta acaactatth aaattgggtat cagcagagac cagggaaagc ccctaagctc 1980  
 ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga 2040  
 tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2100  
 tactgtcaac agagttacag taccctcgg acgttcggcc aagggaacaa gctggaaatc 2160  
 aaacga 2166

<210> 439  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 439

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Val | Ser | Tyr | Leu | Ser | Thr | Ala | Ser | Ser | Leu | Asp | Tyr | Trp | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His |

## A-1937-W0-PCT\_ST25

260

265

270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
           275                                  280                                  285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
           290                                  295                                  300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
   305                                  310                                  315                                  320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
                                   325                                  330                                  335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
                                   340                                  345                                  350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
           355                                  360                                  365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
           370                                  375                                  380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
   385                                  390                                  395                                  400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
                                   405                                  410                                  415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
           420                                  425                                  430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
           435                                  440                                  445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln

## A-1937-W0-PCT\_ST25

450

455

460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
 485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
 500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
 515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
 530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
 545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 580 585 590

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 595 600 605

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 610 615 620

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 625 630 635 640

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly



## A-1937-W0-PCT\_ST25

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 Ser Tyr Ser Thr Pro Arg  
 675 680 685

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 690 695 700

<210> 440  
 <211> 2166  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 440  
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
 cgctgtgagg tacaactggg ggaatcaggg ggaggtttgg tgcagccggg gagatcgctc 120  
 aggcttagct gtgcggcatc ggggtttact ttcagtgatt atgcgatgca ttgggtccgg 180  
 caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
 gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300  
 ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa 360  
 gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc 420  
 gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 480  
 acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccgggtg 540  
 acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600  
 cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660  
 acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 840  |
| cggaccccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgagggtcaag | 900  |
| ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagtg caaggctctcc aacaaagccc tcccagcccc catcgagaaa  | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc   | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc    | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1440 |
| tcccagggtgc agctgcagga gtcgggcccc ggactgggtga agccttcgga gaccctgtcc | 1500 |
| ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag   | 1560 |
| cccccaggta agtgtctgga gtggattggc tatactctatt acagtgggca gaccaaatac  | 1620 |
| aaccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc    | 1680 |
| ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact   | 1740 |
| gggagctact acggctttga ctactggggc cagggaaccc tggtcaccgt ctctcagga    | 1800 |
| ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag    | 1860 |
| tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt   | 1920 |
| cagagcatta acaactatit aaattggtat cagcagagac cagggaagc ccctaagctc    | 1980 |
| ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga   | 2040 |
| tctgggacag atttactct caccatcagc agtctgcaac ctgaagattt tgcaacttac    | 2100 |
| tactgtcaac agagttacag taccctcgg acgttcggct gtgggaccaa gctggaaatc    | 2160 |

aaacga

2166

<210> 441  
 <211> 700  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 441

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

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Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
595 600 605

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
610 615 620

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
625 630 635 640

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
675 680 685

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg  
690 695 700

<210> 442  
<211> 2172  
<212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 442

|                                                                    |      |
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| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg | 60   |
| cgctgtgagg tacaactggg ggaatcaggg ggagggttgg tgcagccggg gagatcgctc  | 120  |
| aggcttagct gtgcggcatc gggggtttact ttcagtgatt atgcgatgca ttgggtccgg | 180  |
| caagcgcttg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc  | 240  |
| gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc  | 300  |
| ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa  | 360  |
| gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttggtcacc  | 420  |
| gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc   | 480  |
| acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg  | 540  |
| acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc  | 660  |
| accagacct acatctgcaa cgtgaatcac aagcccagca acaccaagggt ggacaagaaa  | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc  | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaacca aggacaccct catgatctcc | 840  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgaggtcaag   | 900  |
| ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag  | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg  | 1020 |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa  | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1140 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc  | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg  | 1260 |

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1380 |
| cactacacgc agaagagcct ctccctgtct cccgggtgggtg gcggatcggg aggtggcgga | 1440 |
| tcccagggtgc agttacagca gtcgggagca ggactgttga agccttcgga gaccctgtcc  | 1500 |
| ctcacctgcg ctgtccatgg tgggtccttc agtggttact actggaactg gattcgccag   | 1560 |
| ccaccaggga aggggctaga gtggattggg gaaatcaatc atgctggaaa caccaactac   | 1620 |
| aaccggtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc   | 1680 |
| ctgacgtga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat    | 1740 |
| tgtagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc   | 1800 |
| tcaggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctccga aattgtgttg   | 1860 |
| acgcagtctc caggcacct gtctttgtct ccaggggaaa gagccacct ctcctgcagg     | 1920 |
| gccagtcaga gtgttagaag cagttactta gcctggtagc agcagaaacc tggccaggct   | 1980 |
| cccaggctcc tcattctatg tgcattcagc agggccactg gcatcccaga caggttcagt   | 2040 |
| ggcagtggtg ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt   | 2100 |
| gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggccaagg gacacgactg   | 2160 |
| gagattaaac ga                                                       | 2172 |

<210> 443  
 <211> 702  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 443

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Asp | Tyr |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



## A-1937-W0-PCT\_ST25

20

25

30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

## A-1937-W0-PCT\_ST25

210

215

220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

## A-1937-W0-PCT\_ST25

405

410

415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
 450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
 485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
 500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
 515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
 530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
 545 550 555 560

Ser Thr Thr Cys Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser

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595

600

605

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg  
610 615 620

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg  
625 630 635 640

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg  
660 665 670

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser  
675 680 685

Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg  
690 695 700

<210> 444  
<211> 2172  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 444  
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cgctgtgagg tacaactggg ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc 120  
aggcttagct gtgcggcatc ggggtttact ttcagtgatt atcgatgca ttgggtccgg 180  
caagcgcttg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240  
gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300  
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa 360

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttgggcacc   | 420  |
| gtctctagtg cctccacca gggcccatcg gtcttcccc tggcaccctc ctccaagagc     | 480  |
| acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccgggtg | 540  |
| acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta  | 600  |
| cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc  | 660  |
| acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa   | 720  |
| gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 780  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 840  |
| cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagaccc tgaggtcaag | 900  |
| ttcaactgggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag | 960  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 1020 |
| aatggcaagg agtacaagtg caaggctctcc aacaaagccc tcccagcccc catcgagaaa  | 1080 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1140 |
| cgggaggaga tgaccaagaa ccaggctcagc ctgacctgcc tgggtcaaagg cttctatccc | 1200 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1260 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1320 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1380 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1440 |
| tcccagggtgc agttacagca gtcgggcgca ggactgttga agccttcgga gacctgtcc   | 1500 |
| ctcacctgcg ctgtccatgg tgggtccttc agtggttact actggaactg gattcgccag   | 1560 |
| ccaccaggga agtgtctaga gtggattggg gaaatcaatc atgctggaaa caccaactac   | 1620 |
| aaccctgccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc   | 1680 |
| ctgacgtga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat    | 1740 |
| tgtagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc   | 1800 |

| A-1937-W0-PCT_ST25 |            |             |            |             |            |      |
|--------------------|------------|-------------|------------|-------------|------------|------|
| tcaggaggcg         | gaggatctgg | tggcgggtggt | tctggcggcg | gaggctccga  | aattgtgttg | 1860 |
| acgcagtctc         | caggcaccct | gtctttgtct  | ccaggggaaa | gagccaccct  | ctcctgcagg | 1920 |
| gccagtcaga         | gtgttagaag | cagttactta  | gcctggtacc | agcagaaaacc | tggccaggct | 1980 |
| cccaggctcc         | tcatctatgg | tgcattccagc | agggccactg | gcatcccaga  | caggttcagt | 2040 |
| ggcagtgggt         | ctgggacaga | cttcactctc  | accatcagca | gactggagcc  | tgaagatttt | 2100 |
| gcagtgtatt         | actgtcagca | gtatggtagc  | tcacctacct | tcggctgtgg  | gacacgactg | 2160 |
| gagattaaac         | ga         |             |            |             |            | 2172 |

|       |                     |
|-------|---------------------|
| <210> | 445                 |
| <211> | 702                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polynucleotide

<400> 445

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ala Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

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Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

A-1937-W0-PCT\_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480



A-1937-W0-PCT\_ST25

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr 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 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser  
595 600 605

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg  
610 615 620

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg  
625 630 635 640

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg  
645 650 655

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg  
660 665 670

A-1937-W0-PCT\_ST25

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser  
675 680 685

Ser Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys Arg  
690 695 700

<210> 446  
<211> 708  
<212> DNA  
<213> Homo sapiens

<400> 446  
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gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180  
agaccaggga aagcccctaa gtcctgatc tatgctgcat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 300  
caacctgaag attttgcaac ttactactgt caacagagtt acagtacccc tcggacgttc 360  
ggccaaggga ccaagctgga aatcaaacga acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctggt accgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 447  
<211> 236  
<212> PRT  
<213> Homo sapiens

<400> 447

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

## A-1937-W0-PCT\_ST25

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser | 20  | 25  | 30  |
| Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser | 35  | 40  | 45  |
| Gln Ser Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys | 50  | 55  | 60  |
| Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val | 65  | 70  | 75  |
| Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr | 85  | 90  | 95  |
| Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln | 100 | 105 | 110 |
| Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile | 115 | 120 | 125 |
| Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp | 130 | 135 | 140 |
| Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn | 145 | 150 | 155 |
| Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu | 165 | 170 | 175 |
| Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp | 180 | 185 | 190 |
| Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr |     |     |     |

195

200

205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

&lt;210&gt; 448

&lt;211&gt; 717

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 448

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accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt acactggtac      180
cagcagcttc caggaacagc ccccaaactc ctcatctatg gtaacagcaa tcggccctca      240
gggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact      300
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgaaag cagcctgagt      360
ggttcggtgt tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc      420
tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactggtg      480
tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc      540
cccgtaagg cgggagtgga gaccaccaca ccctcaaac aaagcaacaa caagtacgcg      600
gccagcagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc      660
caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca      717

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&lt;210&gt; 449

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 449

A-1937-W0-PCT\_ST25

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Glu Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

A-1937-W0-PCT\_ST25

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 450  
<211> 708  
<212> DNA  
<213> Homo sapiens

<400> 450  
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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag 180  
aaaccaggga aagcccctaa gtcctgatc tatgctgcgt ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360  
ggcggaggga ccaaggtgga gatcaaactg acgggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
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tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 451  
<211> 214  
<212> PRT  
<213> Homo sapiens

<400> 451

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

## A-1937-W0-PCT\_ST25

|     |     |     |     |
|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Asp | Arg | Val | Thr |
|     | 20  | Ile | Thr |
|     |     | Cys | Arg |
|     |     | Ala | Ser |
|     |     | 25  | Gln |
|     |     |     | Asp |
|     |     |     | Ile |
|     |     |     | 30  |
|     |     |     | Arg |
|     |     |     | Asn |
|     |     |     | Asp |
| Leu | Gly | Trp | Tyr |
|     | 35  | Gln | Gln |
|     |     | Lys | Pro |
|     |     | 40  | Gly |
|     |     |     | Lys |
|     |     |     | Ala |
|     |     |     | Pro |
|     |     |     | 45  |
|     |     |     | Lys |
|     |     |     | Leu |
|     |     |     | Leu |
|     |     |     | Ile |
| Tyr | Ala | Ala | Ser |
|     | 50  | Ser | Ser |
|     |     | Leu | Gln |
|     |     | 55  | Ser |
|     |     |     | Gly |
|     |     |     | Val |
|     |     |     | Pro |
|     |     |     | 60  |
|     |     |     | Ser |
|     |     |     | Arg |
|     |     |     | Phe |
|     |     |     | Ser |
|     |     |     | Gly |
| Ser | Gly | Ser | Gly |
|     | 65  | Pro | Glu |
|     |     | 70  | Phe |
|     |     |     | Thr |
|     |     |     | Leu |
|     |     |     | Thr |
|     |     |     | 75  |
|     |     |     | Ile |
|     |     |     | Ser |
|     |     |     | Ser |
|     |     |     | Leu |
|     |     |     | Gln |
|     |     |     | 80  |
|     |     |     | Pro |
| Glu | Asp | Phe | Ala |
|     |     |     | 85  |
|     |     |     | Thr |
|     |     |     | Tyr |
|     |     |     | Tyr |
|     |     |     | Cys |
|     |     |     | Leu |
|     |     |     | 90  |
|     |     |     | Gln |
|     |     |     | His |
|     |     |     | Asn |
|     |     |     | Ser |
|     |     |     | Tyr |
|     |     |     | 95  |
|     |     |     | Pro |
|     |     |     | Leu |
| Thr | Phe | Gly | Gly |
|     |     | 100 | Gly |
|     |     |     | Thr |
|     |     |     | Lys |
|     |     |     | Val |
|     |     |     | 105 |
|     |     |     | Glu |
|     |     |     | Ile |
|     |     |     | Lys |
|     |     |     | Arg |
|     |     |     | Thr |
|     |     |     | 110 |
|     |     |     | Val |
|     |     |     | Ala |
|     |     |     | Ala |
| Pro | Ser | Val | Phe |
|     |     | 115 | Ile |
|     |     |     | Phe |
|     |     |     | Pro |
|     |     |     | 120 |
|     |     |     | Pro |
|     |     |     | Ser |
|     |     |     | Asp |
|     |     |     | Glu |
|     |     |     | Gln |
|     |     |     | 125 |
|     |     |     | Leu |
|     |     |     | Lys |
|     |     |     | Ser |
|     |     |     | Gly |
| Thr | Ala | Ser | Val |
|     | 130 | Val | Val |
|     |     | Cys | Leu |
|     |     | 135 | Leu |
|     |     |     | Asn |
|     |     |     | Asn |
|     |     |     | Phe |
|     |     |     | 140 |
|     |     |     | Tyr |
|     |     |     | Pro |
|     |     |     | Arg |
|     |     |     | Glu |
|     |     |     | Ala |
| Lys | Val | Gln | Trp |
|     | 145 | Lys | Val |
|     |     | 150 | Asp |
|     |     |     | Asn |
|     |     |     | Ala |
|     |     |     | 155 |
|     |     |     | Leu |
|     |     |     | Gln |
|     |     |     | Ser |
|     |     |     | Gly |
|     |     |     | Asn |
|     |     |     | Ser |
|     |     |     | 160 |
|     |     |     | Gln |
| Glu | Ser | Val | Thr |
|     |     | 165 | Glu |
|     |     |     | Gln |
|     |     |     | Asp |
|     |     |     | Ser |
|     |     |     | Lys |
|     |     |     | 170 |
|     |     |     | Asp |
|     |     |     | Ser |
|     |     |     | Thr |
|     |     |     | Tyr |
|     |     |     | 175 |
|     |     |     | Ser |
|     |     |     | Leu |
|     |     |     | Ser |
| Ser | Thr | Leu | Thr |
|     |     | 180 | Leu |
|     |     |     | Ser |
|     |     |     | Lys |
|     |     |     | Ala |
|     |     |     | 185 |
|     |     |     | Asp |
|     |     |     | Tyr |
|     |     |     | Glu |
|     |     |     | Lys |
|     |     |     | His |
|     |     |     | 190 |
|     |     |     | Lys |
|     |     |     | Val |
|     |     |     | Tyr |
| Ala | Cys | Glu | Val |
|     |     | Thr | His |
|     |     |     | Gln |
|     |     |     | Gly |
|     |     |     | Leu |
|     |     |     | Ser |
|     |     |     | Ser |
|     |     |     | Pro |
|     |     |     | Val |
|     |     |     | Thr |
|     |     |     | Lys |
|     |     |     | Ser |

195

200

205

Phe Asn Arg Gly Glu Cys  
210

&lt;210&gt; 452

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

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cgctgtgata tccaaatgac acaatcacca tcgtcgcttt cagcgtctgt tggcgaccgt 120

gtgacgatta cctgtcgcgc gtcccaggga atccggaatt acctcgcatt gtatcagcaa 180

aaacccggaa aagcaccgaa gctcctgatt tatgccgcct cgactcttca gagggtgtg 240

ccgtcgaggt ttagcgggtc cgggtcaggt acggacttta ctctcacaat ttccagcctg 300

cagcccgaag atttcgctac ctattactgc cagagataca accgagcgcc ttacacattc 360

ggacaaggga caaaagtcga gatcaagcgt acgggtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

&lt;210&gt; 453

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15



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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

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Phe Asn Arg Gly Glu Cys  
210

<210> 454

<211> 642

<212> DNA

<213> Homo sapiens

<400> 454

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagtcacc  | 60  |
| ctctcctgca gggccagtca gagtgtaaga agcagctact tagcctggta ccagcagaga  | 120 |
| gctggccagg ctcccaggct cctcatctat ggtgcatcca gccggggccac tggcatccca | 180 |
| gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag  | 240 |
| cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctctcctac cttcggccaa  | 300 |
| gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt                    | 642 |

<210> 455

<211> 214

<212> PRT

<213> Homo sapiens

<400> 455

|                                                                                                          |
|----------------------------------------------------------------------------------------------------------|
| Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly                                          |
| 1                      5                                      10                                      15 |

|                                                                                    |
|------------------------------------------------------------------------------------|
| Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser                    |
| 20                                      25                                      30 |

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Tyr Leu Ala Trp Tyr Gln Gln Arg Ala Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

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<210> 456  
 <211> 1350  
 <212> DNA  
 <213> Homo sapiens

<400> 456  
 caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcatg tctatggtgg gtccttcagt ggttactact ggaactggat ccgccagccc 120  
 ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaattac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240  
 aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaaactca cacatgccc cagtgtcccag cacctgaact cctgggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 780  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggc 900  
 agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1080  
 atgaccaaga accagggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg 1200  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

A-1937-W0-PCT\_ST25

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 457

<211> 450

<212> PRT

<213> Homo sapiens

<400> 457

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Asp Val Tyr Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 458  
<211> 708  
<212> DNA  
<213> Homo sapiens

<400> 458  
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcttctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcagggc attagcaatg atttagcctg gtatcagcag 180  
aaaccaggga aagcccctaa ggcctgatc ttgtctgcat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300

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cagcctgaag attttgcaac ttattactgt ctccagcata atagttaccc tcccactttc 360  
ggcggaggga ccaaggtgga gatcaaacga acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 459  
<211> 214  
<212> PRT  
<213> Homo sapiens  
<400> 459

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 Arg Ala Ser Gln Gly Ile Ser Asn Asp  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Phe Ala Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala



## A-1937-W0-PCT\_ST25

100

105

110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

&lt;210&gt; 460

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 460

atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgccagg tgcagctggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120

agactctcct gtgcagcctc tggattcacc ctcatagct atggcatgca ctgggtccgc 180

caggctccag gcaaggggct ggagtgggtg gcagttatgt catatgatgg aaataataaa 240

ttatatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaaaacg 300

ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360

A-1937-W0-PCT\_ST25

gacgaaactg aaaccctcta ctactactac ggtattgacg tctggggcca agggaccacg 420  
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 480  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540  
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600  
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660  
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720  
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct 780  
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 840  
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900  
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 960  
gaggagcagt acggcagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1020  
tggtgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc 1080  
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140  
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc 1200  
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260  
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320  
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380  
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

<210> 461

<211> 453

<212> PRT

<213> Homo sapiens

<400> 461

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Met Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr  
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 Glu Thr Glu Thr Leu Tyr Tyr Tyr Tyr Gly Ile Asp Val  
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
195 200 205

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Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

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Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Lys  
450

<210> 462  
<211> 727  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 462  
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agatgcgaca tccagatgac ccagtctcca agctccctgt ctgctgtgtt gggcgatagg 120  
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180  
ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240  
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360  
aagactcctc tcactttcgg cggaggggacc aaagaaacca ggaaagggtt ctaaactgct 420  
catttactgg gcatctaccc gggaatccgg ggtccctagt cgattcagtg gcagcgggtc 480  
tgggacagat ttcactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta 540  
ctgtcagcaa tattataaga ctctctcac tttcggcgga gggaccaaca aggacagcac 600  
ctacagcctc aagagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta 660

## A-1937-W0-PCT\_ST25

cgctgcgaa gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg 720

agagtgt 727

<210> 463

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 463

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 Tyr Thr Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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

## A-1937-W0-PCT\_ST25

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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

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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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 464

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 464

gacattcaaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60

atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120

ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc 180

aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240



A-1937-W0-PCT\_ST25

gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300  
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 465  
 <211> 448  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 465

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 Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Ala Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

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Ala Arg Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 466

<211> 36

<212> DNA

<213> Homo sapiens

<400> 466

agggccagtc agagtgttaag aagcagctac ttagcc

<210> 467  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 467  
 ggtgcatcca gcagggccac t 21

<210> 468  
 <211> 33  
 <212> DNA  
 <213> Homo sapiens

<400> 468  
 cgggcaagtc agggcattag caatgattta gcc 33

<210> 469  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 469  
 Arg Ala Ser Gln Gly Ile Ser Asn Asp Leu Ala  
 1 5 10

<210> 470  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 470  
 ggtgcatcca gccgggccac t 21

<210> 471  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 471

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Lys | Ala | Ser | Gln | Asn | Val | Gly | Thr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Ala | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ser | Ala | Ser | Phe | Leu | Tyr | Ser | Gly | Val | Pro | Tyr | 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 | Tyr | Asn | Ile | Tyr | Pro | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Glu | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 472  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 472  
gctgcatcca gtttgcaaag t

21

<210> 473  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 473

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

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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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Lys Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 474

<211> 24

<212> DNA

<213> Homo sapiens

<400> 474

cagcagtatg gtagctctcc tacc

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<210> 475  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 475

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr 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 Tyr Asn Ile Tyr Pro Leu  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln



145                      150                      155                      160

Ser Thr Leu Glu Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

```
<210> 476
<211> 27
<212> DNA
<213> Homo sapiens
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<400> 476
ctccagcata atagttaccc tcccact
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27

|       |                     |
|-------|---------------------|
| <210> | 477                 |
| <211> | 448                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 477

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 Tyr Val Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

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Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ala Val  
50 55 60

Lys Gly Arg Phe Thr Phe Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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

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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

<210> 478  
 <211> 15  
 <212> DNA  
 <213> Homo sapiens

<400> 478  
 ggttactact ggaac

15

<210> 479  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 479

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr 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 Tyr Asn Ile Tyr Pro Leu  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Glu Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 480  
<211> 15  
<212> DNA  
<213> Homo sapiens

<400> 480  
agctatggca tgcac

15

<210> 481  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 481

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Lys | Ala | Ser | Gln | Asn | Val | Gly | Thr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Trp | Tyr | Gln | Glu | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Ala | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ser | Ala | Ser | Phe | Leu | Tyr | Ser | Gly | Val | Pro | Tyr | 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 | Tyr | Asn | Ile | Tyr | Pro | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Glu | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

<210> 482  
 <211> 48  
 <212> DNA  
 <213> Homo sapiens

<400> 482  
 gaaatcaatc atagtggaat taccaactac aacccgtccc tcaagagt 48

<210> 483  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 483

Glu Ile Asn His Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
 1 5 10 15

<210> 484  
 <211> 51  
 <212> DNA  
 <213> Homo sapiens

<400> 484  
 gttatgtcat atgatggaaa taataaatta tatgcagact ccgtgaaggg c 51

<210> 485  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 485

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Val Met Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Ala Asp Ser Val Lys  
1 5 10 15

Gly

<210> 486  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 486  
ggatattgta gaagtaccac ctgctacttt gactac

36

<210> 487  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 487

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 Tyr Thr Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys



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85

90

95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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275

280

285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
 435 440 445

&lt;210&gt; 488

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<400> 488  
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<210> 489  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 489  
Asp Glu Thr Glu Thr Leu Tyr Tyr Tyr Tyr Gly Ile Asp Val  
1 5 10

<210> 490  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 490  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagtcacc 60  
ctctcctgca gggccagtca gagtgtaaga agcagctact tagcctggta ccagcagaga 120  
gctggccagg ctcccaggct cctcatctat ggtgcatcca gccggggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctctcctac cttcggccaa 300  
gggacacgac tggagattaa acga 324

<210> 491  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 491  
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

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Tyr Leu Ala Trp Tyr Gln Gln Arg Ala Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 492  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 492  
gacatccaga tgaccagtc tccatcctcc ctgtctgctt ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gggcattagc aatgatttag cctggtatca gcagaaacca 120  
gggaaagccc ctaagcgcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240  
gaagattttg caacttatta ctgtctccag cataatagtt accctccac tttcggcgga 300  
gggaccaagg tggagatcaa acga 324

<210> 493  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 493

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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|                                                                 |     |     |    |
|-----------------------------------------------------------------|-----|-----|----|
| 1                                                               | 5   | 10  | 15 |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asp | 20  | 25  | 30 |
| Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile | 35  | 40  | 45 |
| Phe Ala Ala Ser Ser Leu Gln 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 |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro | 85  | 90  | 95 |
| Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys                     | 100 | 105 |    |

<210> 494  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

|                                                                   |     |
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| <400> 494                                                         |     |
| caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc | 60  |
| acctgcgatg tctatggtgg gtccttcagt gggtactact ggaactggat ccgccagccc | 120 |
| ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaattac caactacaac | 180 |
| ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg | 240 |
| aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt | 300 |
| agaagtacca cctgctactt tgactactgg ggccaggga ccttggtcac cgtctcctca  | 360 |

<210> 495  
 <211> 120

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<212> PRT

<213> Homo sapiens

<400> 495

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Asp Val Tyr Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 496

<211> 369

<212> DNA

<213> Homo sapiens

<400> 496

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ccaggcaagg ggctggagtg ggtggcagtt atgtcatatg atggaaataa taaattatat 180

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa aacgctgtat 240  
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagacgaa 300  
 actgaaaccc tctactacta ctacggtatt gacgtctggg gccaaggac cacggtcacc 360  
 gtctcctca 369

<210> 497  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 497

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 Leu Ser Ser Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Met Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr  
 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 Glu Thr Glu Thr Leu Tyr Tyr Tyr Tyr Gly Ile Asp Val  
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120

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<210> 498  
 <211> 57  
 <212> DNA  
 <213> Homo sapiens

<400> 498  
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<210> 499  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<400> 499  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser

<210> 500  
 <211> 60  
 <212> DNA  
 <213> Homo sapiens

<400> 500  
 atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

<210> 501  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 501  
 Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro  
 1 5 10 15

Asp Thr Thr Gly  
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<210> 502  
 <211> 66  
 <212> DNA  
 <213> Homo sapiens

<400> 502  
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 agatgt 66

<210> 503  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<400> 503  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

Leu Arg Gly Ala Arg Cys  
 20

<210> 504  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 504  
 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro  
 1 5 10 15

Asp Thr Thr Gly  
 20

<210> 505  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<400> 505

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Met Glu Trp Thr Trp Arg Val Leu Phe Leu Val Ala Ala Ala Thr Gly  
1 5 10 15

Ala His Ser

<210> 506  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 506

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly  
1 5 10 15

Val His Ser

<210> 507  
<211> 1407  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 507  
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gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc 120  
tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggatccg cgagccacca 180  
gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg 240  
tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg 300  
ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga 360  
agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctctagtgcc 420  
tccaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 480

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acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      540
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      600
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac      660
atctgcaacg tgaatcaciaa gcccagcaac accaagggtg acaagaaagt tgagcccaaa      720
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg      780
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccc gacccctgag      840
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac      900
gtggacggcg tggagggtgca taatgccaag acaaagccgt gcgaggagca gtacggcagc      960
acgtaccgtt gcgtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag     1020
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa     1080
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccc gaaggagatg     1140
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc     1200
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg     1260
aagtccgacg gctccttctt cctctatagc aagctcaccg tggacaagag cagggtggcag     1320
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag     1380
aagagcctct ccctgtctcc gggtaaaa                                     1407

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<210> 508  
 <211> 450  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 508

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Gly | Leu | Leu | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

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Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Glu Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

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Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

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Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 509  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 509  
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gtcaccatca cttgtaaagc cagtcagaac gtaggtacta acgtagcctg gtatcaggaa 180  
aaaccaggta aagccccaaa agccctcatc tacagtgcct ctttcctcta tagtggtgta 240  
ccatacaggt tcagcggatc cggtagtggg actgatttca ccctcacgat cagtagcctc 300  
cagccagaag atttcgccac ttattactgt caacagtata acatctaccc actcacattc 360  
ggtcagggta ctaaagtaga aatcaaacgt acggtagcgg ccccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aaggtaggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcaccagt aacaaaaagc tttaatagag gagagtgt 708

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<210> 510  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 510

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
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Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser  
 35 40 45

Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Glu Lys Pro Gly Lys  
 50 55 60

Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val  
 65 70 75 80

Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110

Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 130 135 140

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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 511  
<211> 702  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 511  
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ctctcctgca gggccagtca gagtggttaga agcagttact tagcctggta ccagaagaaa 180  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240  
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 300  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 360  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 420  
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 480



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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 540  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 600  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 702

<210> 512  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 512

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 513  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 513  
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agattgtcct gtgctgcacg ttggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
aaggccccgg gaaagggcct ggaatggatg gggttgatta atacttacat tggagagcct 240  
atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca 300  
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt  | 420  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 540  |
| tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 600  |
| ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg acaaaaactca cacatgcccc cctgtgcccag cacctgaact cctgggggga | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    | 840  |
| gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc   | 960  |
| agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1140 |
| atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtaaa                                    | 1410 |

<210> 514

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 514

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
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Leu Arg Gly Ala Arg Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Tyr Val Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Lys Ala Pro Gly  
50 55 60

Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro  
65 70 75 80

Ile Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr  
85 90 95

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
305 310 315 320

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
370 375 380

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Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
450 455 460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 515  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 515  
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
agatgcgagg ttcagctggc cgagtcagga ggcggctctg tgcagcctgg cggatcactg 120  
agattgtcct gtgctgcatc tggttacacc ttcacagact atggaatgaa ttggggttaga 180  
aaggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300  
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac cgtctctagt 420  
gcctccacca agggccccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

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ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg      540
tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      600
ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg      900
tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1140
atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                         1410

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<210> 516  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 516

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1           5           10          15

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Leu Arg Gly Ala Arg Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly  
20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly  
35 40 45

Tyr Thr Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Lys Ala Pro Gly  
50 55 60

Lys Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro  
65 70 75 80

Ile Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr  
85 90 95

Ser Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp  
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
195 200 205



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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
305 310 315 320

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
385 390 395 400

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Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
450 455 460

Ser Leu Ser Pro Gly Lys  
465 470

<210> 517  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 517  
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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag 180  
aaaccaggga aagcccctaa ggcctgatc tatgctgcgt ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360  
ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc 600

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ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 518

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 518

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
35 40 45

Gln Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Glu Lys Pro Gly Lys  
50 55 60

Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val  
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr  
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
100 105 110

His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
115 120 125

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
180 185 190

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 519  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 519  
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agattgtcct gtgctgcacg tggttacacc ttcacagact atggaatgaa ttgggttaga 180  
caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300  
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360

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ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt      420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg      540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      600
ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttggtg acaaaaactca cacatgcccc cctgtgcccag cacctgaact cctggggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1140
atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                     1410

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<210> 520  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 520

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Lys Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 521  
<211> 1428  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 521  
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cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
aaggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gagggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
acgggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540  
gaaccgggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600  
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660  
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840  
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900  
gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcaa gacaaagccg 960

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```

tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag      1020
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc      1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg      1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc      1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac      1260
gacaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag cgacctcacc      1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct      1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa                    1428

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<210> 522  
 <211> 476  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 522

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Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1           5           10           15

```

```

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly
          20           25           30

```

```

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
          35           40           45

```

```

Phe Thr Phe Ser Ser Tyr Asp Met His Trp Val Arg Lys Ala Pro Gly
          50           55           60

```

```

Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys
65           70           75           80

```



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Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn  
85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp  
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr  
115 120 125

Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
145 150 155 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
195 200 205

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
210 215 220

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
225 230 235 240

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
245 250 255

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
260 265 270

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Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
275 280 285

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
305 310 315 320

Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr  
325 330 335

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
340 345 350

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
355 360 365

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
370 375 380

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
385 390 395 400

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
405 410 415

Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
420 425 430

Phe Phe Leu Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
435 440 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
450 455 460

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Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
465 470 475

<210> 523  
<211> 234  
<212> PRT  
<213> Homo sapiens

<400> 523

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
35 40 45

Val Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro  
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
85 90 95

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr  
100 105 110

Gly Ser Ser Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg  
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

145                      150                      155                      —                      160

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230

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<210> 524
<211> 642
<212> DNA
<213> Homo sapiens
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|             |            |             |             |            |             |  |     |
|-------------|------------|-------------|-------------|------------|-------------|--|-----|
| <400>       | 524        |             |             |            |             |  |     |
| gaaatttgtgt | tgacgcagtc | tccaggcacc  | ctgtctttgt  | ctccagggga | aagagccacc  |  | 60  |
| ctctcctgca  | gggccagtca | gagtgttaga  | agcagttact  | tagcctggta | ccagcagaaa  |  | 120 |
| cctggccagg  | ctcccaggct | cctcatctat  | ggtgcatcca  | gcagggccac | tggcatccca  |  | 180 |
| gacaggttca  | gtggcagtgg | gtctgggaca  | gacttcactc  | tcaccatcag | cagactggag  |  | 240 |
| cctgaagatt  | ttgcagtgta | ttactgtcag  | cagtatggta  | gctcacctac | cttcggccaa  |  | 300 |
| gggacacgac  | tggagattaa | acgaacggtg  | gctgcaccat  | ctgtcttcat | cttcccgcca  |  | 360 |
| tctgatgagc  | agttgaaatc | tggtaccgcc  | tctgtttgtgt | gcctgctgaa | taactttctat |  | 420 |
| cccagagagg  | ccaaagtaca | gtggaagggtg | gataacgccc  | tccaatcggg | taactcccag  |  | 480 |
| gagagtgtca  | cagagcagga | cagcaaggac  | agcacctaca  | gcctcagcag | caccctgacg  |  | 540 |
| ctgagcaaag  | cagactacga | gaaacacaaa  | gtctacgcct  | gcgaagtcac | ccatcagggc  |  | 600 |

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ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 525

<211> 726

<212> DNA

<213> Homo sapiens

<400> 525

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cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120

gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcacaaca taagaactac 180

ttagtttggg accagcagaa accaggaaa gttcctaaac tgctcattta ctgggcatct 240

acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300

ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360

aagactcctc tcactttcgg cggagggacc aagggtggaga tcaaacgaac ggtggctgca 420

ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtac cgcctctgtt 480

gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540

gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600

tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaaca caaagtctac 660

gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720

gagtgt 726

<210> 526

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 526

gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60

A-1937-W0-PCT\_ST25

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca | 120 |
| ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac  | 180 |
| aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca | 240 |
| gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag  | 300 |
| ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca   | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctggag  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcac cagtaacaaa aagctttaat agaggagagt gt                     | 642 |

<210> 527

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 527

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaaatttgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc | 60  |
| ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa  | 120 |
| cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca  | 180 |
| gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag  | 240 |
| cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa  | 300 |
| gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca | 360 |
| tctgatgagc agttgaaatc tggtaaccgcc tctgttgtgt gcctgctgaa taacttctat | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgaag  | 540 |

## A-1937-W0-PCT\_ST25

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 528  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 528  
 atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60  
 agatgcgagg ttcagctggg cgagtcagga ggccgtctcg tgcagcctgg cggatcactg 120  
 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
 caggccccgg gaaagggcct ggaatggatg gcttggatta atacttacat tggagagcct 240  
 atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300  
 gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
 ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 900  
 tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgagagga gcagtacggc 960  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

## A-1937-W0-PCT\_ST25

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccggtg 1260  
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtaaa 1410

&lt;210&gt; 529

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 529

cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccaggga cctagtcac cgtctctagt 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctggtcgag gactacttcc ccgaaccggt gacggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720



## A-1937-W0-PCT\_ST25

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| ccgtcagtct | tcctcttccc | cccaaaaccc | aaggacaccc  | tcatgatctc | ccggacccct | 780  |
| gaggtcacat | gcgtgggtgt | ggacgtgagc | cacgaagacc  | ctgaggtcaa | gttcaactgg | 840  |
| tacgtggacg | gcgtggaggt | gcataatgcc | aagacaaagc  | cgtgcgagga | gcagtacggc | 900  |
| agcacgtacc | gttgcgtcag | cgtcctcacc | gtcctgcacc  | aggactggct | gaatggcaag | 960  |
| gagtacaagt | gcaaggtctc | caacaaagcc | ctcccagccc  | ccatcgagaa | aaccatctcc | 1020 |
| aaagccaaag | ggcagccccg | agaaccacag | gtgtacaccc  | tgcccccatc | ccggaaggag | 1080 |
| atgaccaaga | accaggtcag | cctgacctgc | ctgggtcaaag | gcttctatcc | cagcgacatc | 1140 |
| gccgtggagt | gggagagcaa | tgggcagccg | gagaacaact  | acaagaccac | gcctcccgtg | 1200 |
| ctgaagtccg | acggctcctt | cttcctctat | agcaagctca  | ccgtggacaa | gagcaggtgg | 1260 |
| cagcagggga | acgtcttctc | atgctccgtg | atgcatgagg  | ctctgcacaa | ccactacacg | 1320 |
| cagaagagcc | tctccctgtc | tccgggtaaa |             |            |            | 1350 |

&lt;210&gt; 530

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 530

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gaaatttgtt | tgacgcagtc | tccaggcacc  | ctgtctttgt | ctccagggga | aagagccacc | 60  |
| ctctcctgca | gggccagtc  | gagtgtaga   | agcagttact | tagcctggta | ccagcagaaa | 120 |
| cctggccagg | ctcccaggct | cctcatctat  | ggtgcatcca | gcagggccac | tggcatccca | 180 |
| gacaggttca | gtggcagtg  | gtctgggaca  | gacttcactc | tcaccatcag | cagactggag | 240 |
| cctgaagatt | ttgcagtgt  | ttactgtcag  | cagtatggta | gctcacctac | cttcggccaa | 300 |
| gggacacgac | tggagattaa | acgaacgggtg | gctgcaccat | ctgtcttcat | cttcccgcc  | 360 |
| tctgatgagc | agttgaaatc | tggaaactgcc | aaagtttgt  | gcctgctgaa | taacttctat | 420 |
| cccagagagg | ccaaagtaca | gtggaagggtg | gataacgccc | tccaatcggg | taactcccag | 480 |

## A-1937-W0-PCT\_ST25

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 531  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 531  
 gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60  
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120  
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180  
 aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca 240  
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtcag 300  
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc gaagttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 532  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 532

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atggacatga gagtgcctgc acagctgctg ggcttgctgc tgctgtggct gagaggcgcc   | 60   |
| agatgcgagg ttcagctggg cgagtcagga ggcggtctcg tgcagcctgg cggatcactg   | 120  |
| agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga   | 180  |
| caggccccgg gaaagggcct ggaatggatg gggttgatta atacttacat tggagagcct   | 240  |
| atttatgctg acgccgtcaa gggcagattc acgttctctc gagacacatc caagtcaaca   | 300  |
| gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga   | 360  |
| ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt  | 420  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    | 840  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgagagga gcagtacggc | 960  |
| agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag    | 1140 |
| atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg   | 1260 |
| ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |
| cagaagagcc tctccctgtc tccgggtaaa                                    | 1410 |

A-1937-WO-PCT\_ST25

<210> 533  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial polynucleotide

<400> 533  
 gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60  
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120  
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc 180  
 aggttcagcg gatccggtag tggtagtgat ttaccacctca cgatcagtag cctccagcca 240  
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtcag 300  
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc gaagttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 534  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 534  
 gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60  
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120  
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc 180

A-1937-W0-PCT\_ST25

aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca 240  
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300  
ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccacca 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctggag 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 535  
<211> 450  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 535

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Glu Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

## A-1937-W0-PCT\_ST25

85

90

95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

## A-1937-W0-PCT\_ST25

275

280

285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 340 345 350

Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu  
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 385 390 395 400

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 435 440 445

Gly Lys  
 450

<210> 536

A-1937-WO-PCT\_ST25

<211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 536

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

Val Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr 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 Tyr Asn Ile Tyr Pro Leu  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Glu Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160



A-1937-W0-PCT\_ST25

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 537

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 537

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 Arg Ala Ser Gln Asp Ile Arg Asn Asp  
20 25 30

Leu Gly Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu

## A-1937-W0-PCT\_ST25

85

90

95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

&lt;210&gt; 538

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 538

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

A-1937-W0-PCT\_ST25

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp  
20 25 30

Leu Gly Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

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Phe Asn Arg Gly Glu Cys  
210

<210> 539

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 539

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Lys Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

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130

135

140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 540

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 540

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30

Val Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

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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 Tyr Asn Ile Tyr Pro Leu  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 541

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

A-1937-W0-PCT\_ST25

<400> 541

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Lys Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

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180

185

190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 542

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 542

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110



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Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 543

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 543

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
20 25 30

Leu Gly Trp Tyr Gln Lys Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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35

40

45

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

&lt;210&gt; 544

A-1937-WO-PCT\_ST25

<211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 544

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
 20 25 30

Leu Gly Trp Tyr Gln Lys Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
 35 40 45

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 545

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 545

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 Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr 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 Tyr Asn Ile Tyr Pro Leu

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85

90

95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 546

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 546

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Lys Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

A-1937-W0-PCT\_ST25

Phe Asn Arg Gly Glu Cys  
210

<210> 547  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 547

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 Arg Ala Ser Gln Asp Ile Arg Asn Asp  
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

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130

135

140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 548

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 548

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60



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Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Lys Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 549

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<400> 549

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Lys Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

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180

185

190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 550

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 550

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Lys Gly Thr Lys Val Glu Ile  
100 105 110

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 551  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 551

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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35

40

45

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
 85 90 95

Thr Phe Gly Lys Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

&lt;210&gt; 552

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<211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 552

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 Arg Thr Ser Gln Asp Ile Arg Asp Asp  
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
 35 40 45

Tyr Asp Ala Ser Ser Leu Gln 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro  
 85 90 95

Thr Phe Gly Lys Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 553  
<211> 1404  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 553  
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cgctgtgagg tgcagctggg gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120  
aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgctg 180  
aagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctgagatacc 240  
agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc 300  
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360  
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420  
accaagggcc catcggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 480  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctgaggactc 600  
tactccctca agagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 660

## A-1937-W0-PCT\_ST25

|                                                                    |      |
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| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattct | 720  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 780  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc  | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg  | 960  |
| taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 1020 |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc    | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1140 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac  | 1260 |
| tccgacggct ctttcttcct ctatagcgac ctcaccgtgg acaagagcag gtggcagcag  | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1380 |
| agcctctccc tgtctccggg taaa                                         | 1404 |

&lt;210&gt; 554

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 554

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc  | 60  |
| acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgcgagcca  | 120 |
| ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac | 180 |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg  | 240 |
| aagctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgcgag aggatattgt   | 300 |
| agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt  | 360 |



## A-1937-W0-PCT\_ST25

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
 tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg cacccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgagagga gcagtacggc 900  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag 1080  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200  
 ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320  
 cagaagagcc tctccctgtc tccgggtaaa 1350

&lt;210&gt; 555

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 555

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

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Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Glu Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

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Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

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Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 556  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 556  
atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagaag 180  
aaaccaggga aagcccctaa gctcctgatc tatgctacat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagtggcag tggatctggg acagatttct ctctcaccat cagcagtctg 300  
caacctgaag attttgcaac ttacttctgt caacagagtt acagtacccc tcggacgttc 360  
ggccaaggga ccaaggtgga gatcaaacga acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctggg accgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 557

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 557

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccgggagccc 120  
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaattggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gccc aaatct 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgag aggagcagta cggcagcacg 900  
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 1080

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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag 1200  
tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg taaa 1344

<210> 558  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 558

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Glu Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Met Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Ile Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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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 Glu 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys 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 Lys Glu Met 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 Lys  
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 Lys  
435 440 445

<210> 559

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 559

atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtggtgcc

60



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|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgctgtgt gggcgatagg   | 120 |
| gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac  | 180 |
| ttagtttggg accagaagaa accaggaaag gttcctaaac tgctcattta ctgggcatct  | 240 |
| acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact | 300 |
| ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat  | 360 |
| aagactcctc tcactttcgg cggagggacc aagggtggaga tcaaacgaac ggtggctgca | 420 |
| ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtac cgcctctgtt  | 480 |
| gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac  | 540 |
| gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc  | 600 |
| tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac  | 660 |
| gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga  | 720 |
| gagtgt                                                             | 726 |

<210> 560

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 560

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacattcaaa tgaccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc   | 60  |
| atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca ggaaaaacca | 120 |
| ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc  | 180 |
| aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca  | 240 |
| gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag  | 300 |
| ggtagctaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca  | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |

## A-1937-W0-PCT\_ST25

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 561  
<211> 1422  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 561  
atgaaacatc tgtggttctt cctgctgttg gtggcagccc ccagatgggt gctgagccag 60  
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc 120  
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gatcagggag 180  
ccccagggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat 240  
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 300  
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 360  
gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc 420  
accgtctcta gtgcctccac caagggccca tcggctcttc ccctggcacc ctctccaag 480  
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt cccgaaccg 540  
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600  
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg 660  
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 720  
aaagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 780  
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc 840  
tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc 900

A-1937-W0-PCT\_ST25

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgagag 960  
gagcagtacg gcagcacgta ccgttgctgc agcgtcctca ccgtcctgca ccaggactgg 1020  
ctgaatggca aggagtacaa gtgcaaggct tccaacaaag ccctcccagc ccccatcgag 1080  
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1140  
tcccgggaagg agatgaccaa gaaccaggct agcctgacct gcctgggtcaa aggcttctat 1200  
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260  
acgcctcccg tgctgaagtc cgacggctcc ttcttctct atagcaagct caccgtggac 1320  
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380  
aaccactaca cgcagaagag cctctccctg tctccgggta aa 1422

<210> 562  
<211> 455  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 562

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Glu Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

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Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Lys  
450 455

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<210> 563  
 <211> 726  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 563  
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 cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120  
 gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcacaaca taagaactac 180  
 ttagtttggg accagaagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240  
 acccggggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300  
 ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360  
 aagactcctc tcactttcgg cggagggacc aagggtggaga tcaaacgaac ggtggctgca 420  
 ccatctgtct tcactttccc gccatctgat gagcagttga aatctgggtac cgcctctgtt 480  
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540  
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600  
 tacagcctca agagcaccct gacgtgagc aaagcagact acgagaaaca caaagtctac 660  
 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720  
 gagtgt 726

<210> 564  
 <211> 1431  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 564  
 atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc   | 120  |
| cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg   | 180  |
| atcagggagg ccccagggaa aggccttgag tgggtgagca ggacatacta caggtccaag   | 240  |
| tggataatg attatgcagt ttctgtgaaa ggctgattca ctatcagccc agacacatcc    | 300  |
| aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac   | 360  |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg   | 420  |
| accacggtca ccgtctctag tgcctccacc aaggggcccat cggctcttccc cctggcaccc | 480  |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc  | 540  |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc   | 600  |
| ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc  | 660  |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag   | 720  |
| gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca    | 780  |
| gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc    | 840  |
| ctcatgatct cccggacccc tgaggtcaca tgcgtgggtgg tggacgtgag ccacgaagac  | 900  |
| cctgagggtca agttcaactg gtacgtggac ggctgggagg tgcataatgc caagacaaag  | 960  |
| ccgtgcgagg agcagtacgg cagcacgtac cgttgcgtca gcgtcctcac cgtcctgcac   | 1020 |
| caggactggc tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc  | 1080 |
| cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc   | 1140 |
| ctgcccccat cccggaagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa | 1200 |
| ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac   | 1260 |
| tacaagacca cgcctcccgt gctgaagtcc gacggctcct tcttcctcta tagcaagctc   | 1320 |
| accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag  | 1380 |
| gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a            | 1431 |

&lt;210&gt; 565

A-1937-W0-PCT\_ST25

<211> 455  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 565

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 Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Glu Ala Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Val Lys Gly Arg Phe Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 145 150 155 160



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Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

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Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Lys  
450 455

<210> 566  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 566  
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gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagaag 180  
aaaccaggga aagcccctaa gctcctgatc tatgatgcat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300

## A-1937-W0-PCT\_ST25

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 ccgccatctg atgagcagtt gaaatctggt accgcctctg ttgtgtgcct gctgaataac 480  
 ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540  
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
 cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

&lt;210&gt; 567

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 567

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
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 agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180  
 gaggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa 240  
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 ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg 420  
 gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540  
 ccggtgacgg tgctgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600  
 gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc 660  
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tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260  
accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320  
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380  
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

<210> 568

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 568

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

Gly Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Thr Asp Ser Val

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50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr  
 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 Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
 130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
 195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
 210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
 225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

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245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
 290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
 325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln  
 355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 385 390 395 400

Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Lys  
450

<210> 569  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 569  
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agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagaag 180  
aaaccaggga aagcccctaa ggcctgatc tatgatgcat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360  
ggccaaggga ccaagggtga aatcaaacga acgggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctggg accgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 570  
<211> 717  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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<400> 570  
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cgctgtcagt ctgtgctgac gcagccgccc tcagtgtctg gggccccagg gcagagggtc 120  
accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aacttggtac 180  
caggagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240  
gggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300  
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360  
ggttcgggtg tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420  
tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactggtg 480  
tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540  
cccgtaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600  
gccgagagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660  
caggtcacgc atgaagggag caccgtggag aagacagtgg cccctacaga atgttca 717

<210> 571  
<211> 446  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 571

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Lys | Ile | Ser | Cys | Lys | Thr | Ser | Glu | Tyr | Ser | Phe | Thr | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Gly | Trp | Val | Arg | Lys | Met | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



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Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp Ser Asp  
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Asp 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

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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

<210> 572  
 <211> 1410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

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 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
 aaggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
 atttatgctg acagcgtcaa gggcagattc acgatctctc tagacacatc caagtcaaca 300  
 gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
 ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtc 540  
 tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
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 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 900  
 tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgagagga gcagtacggc 960  
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gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200  
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccggtg 1260  
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg 1320  
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
cagaagagcc tctccctgtc tccgggtaaa 1410

<210> 573  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 573

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 Tyr Val Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

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Ala Arg Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 574

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 574  
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcaaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcga 360  
tctgatgagc agttgaaatc tggtaaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 575  
<211> 1350  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 575  
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ccagggaagg agctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

## A-1937-WO-PCT\_ST25

ggacacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
 tggaactcag ggcacctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 900  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag 1080  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200  
 ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320  
 cagaagagcc tctccctgtc tccgggtaaa 1350

&lt;210&gt; 576

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 576

gacattcaaa tgaccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60  
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca 120  
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180



## A-1937-WO-PCT\_ST25

aggttcagcg gatccggtag tggactgat ttcaccctca cgatcagtag cctccagcca 240  
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtgag 300  
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

&lt;210&gt; 577

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 577

atggacatga gtagtcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60  
 agatgcgagg ttcagctggg cgagtcagga ggcgggtctg tgcagcctgg cggatcactg 120  
 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
 caggccccgg gaaagaagct ggaatggatg ggttggatta atacttacat tggagagcct 240  
 atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca 300  
 gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
 ggatacagat cttatgccat ggactactgg ggccagggtg ccctagtcac cgtctctagt 420  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
 ggacacgcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
 tggaactcag gcgcccgtgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
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## A-1937-W0-PCT\_ST25

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
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 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840  
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 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960  
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 aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260  
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtaaa 1410

&lt;210&gt; 578

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 578

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 Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

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Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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

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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

<210> 579  
 <211> 450  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 579

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Glu Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

## A-1937-W0-PCT\_ST25

130

135

140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
 290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

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325

330

335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Lys  
450

<210> 580

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 580

atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60

agatgcgaca tccagatgac ccagctctcca tcctccctat ctgcatctgt aggagacaga 120

## A-1937-W0-PCT\_ST25

gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180  
aaaccaggga aagcccctaa gtcctgatc tatgctacat ccagtttgca aagtggggtc 240  
ccatcaaggt tcagtggcag tggatctggg acagatttct ctctcaccat cagcagtctg 300  
caacctgaag attttgcaac ttacttctgt caacagagtt acagtacccc tcggacgttc 360  
ggcaaaggga ccaaggtgga gatcaaacga acggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctggg accgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 581  
<211> 1344  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 581  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctgggtg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccagggaagg aactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaattggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 360  
accaagggcc catcggcttt cccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaaagttga gcccaaactct | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga ccttgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg   | 900  |
| taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggaa ggagatgacc   | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag   | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1320 |
| agcctctccc tgtctccggg taaa                                          | 1344 |

<210> 582  
 <211> 448  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 582

|                                                                                                          |
|----------------------------------------------------------------------------------------------------------|
| Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu                                          |
| 1                      5                                      10                                      15 |

|                                                                                    |
|------------------------------------------------------------------------------------|
| Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr                    |
| 20                                      25                                      30 |

|                                                                 |
|-----------------------------------------------------------------|
| Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Glu Leu Glu Trp Ile |
|-----------------------------------------------------------------|

## A-1937-W0-PCT\_ST25

35

40

45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Met Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Ile Gly Ser Tyr Tyr Gly 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 Glu 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

## A-1937-W0-PCT\_ST25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Cys | Glu | Glu | Gln | Tyr | Gly | Ser | Thr | Tyr | Arg | Cys | 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 | Lys | 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 | Lys | Glu | Met | 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 | Lys |
| 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 Lys  
 435 440 445

&lt;210&gt; 583

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 583

```

atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtggtgcc      60
cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg      120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcccaacaa taagaactac      180
ttagtttggg accagcagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct      240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact      300
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat      360
aagactcctc tcactttcgg caaagggacc aagggtggaga tcaaacgaac ggtggctgca      420
ccatctgtct tcatcttccc gccatctgat gagcagttga aatctgggtac cgcctctggt      480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac      540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc      600
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac      660
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga      720
gagtgt                                           726

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&lt;210&gt; 584

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 584

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atgaaacatc tgtggttctt cctgctgttg gtggcagccc ccagatgggt gctgagccag   | 60   |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc    | 120  |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gatcaggcag   | 180  |
| cccccaggga aagagcttga gtggatagga aggacatact acagggtccaa gtggtataat  | 240  |
| gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag   | 300  |
| ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga   | 360  |
| gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc   | 420  |
| accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag    | 480  |
| agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt cccgaaccg   | 540  |
| gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc   | 600  |
| ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg  | 660  |
| ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag  | 720  |
| aaagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 780  |
| ctcctggggg gaccgtcagt cttctcttc ccccaaaaac ccaaggacac cctcatgatc    | 840  |
| tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc  | 900  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgcgag   | 960  |
| gagcagtacg gcagcacgta ccgttgctgc agcgtcctca ccgtcctgca ccaggactgg   | 1020 |
| ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag  | 1080 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1140 |
| tcccggaagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggtttctat | 1200 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1260 |
| acgcctcccg tgctgaagtc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1320 |

A-1937-W0-PCT\_ST25

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380

aaccactaca cgcagaagag cctctccctg tctccgggta aa 1422

<210> 585

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 585

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Glu Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser

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130

135

140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
 180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
 195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
 210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
 290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

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325

330

335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Lys  
450 455

<210> 586  
<211> 1431  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 586  
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agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120



## A-1937-W0-PCT\_ST25

cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
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 aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360  
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 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca 780  
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 ctgcccccat cccggaagga gatgaccaag aaccagggtc gcctgacctg cctgggtcaaa 1200  
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 tacaagacca cgcctcccgt gctgaagtcc gacggctcct tcttcctcta tagcaagctc 1320  
 accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380  
 gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1431

&lt;210&gt; 587

&lt;211&gt; 726

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 587

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gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac      180
ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct      240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact      300
ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat      360
aagactcctc tcacttttcgg caaagggacc aagggtggaga tcaaacgaac ggtggctgca      420
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtag cgctctgttt      480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac      540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc      600
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac      660
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gagtgt                                           726

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<210> 588

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 588

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ile Ser Gly Asp Ser Val Ser Thr Asn

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## A-1937-W0-PCT\_ST25

20

25

30

Ser Val Ala Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Glu Leu Glu  
           35                          40                          45

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
       50                          55                          60

Val Ser Val Lys Gly Arg Phe Thr Ile Ser Pro Asp Thr Ser Lys Asn  
   65                          70                          75                          80

Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
                           85                          90                          95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
           100                          105                          110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
       115                          120                          125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
       130                          135                          140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
   145                          150                          155                          160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
                           165                          170                          175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
           180                          185                          190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
       195                          200                          205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu

## A-1937-W0-PCT\_ST25

210

215

220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
 290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
 305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
 325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys  
 355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser

## A-1937-W0-PCT\_ST25

405

410

415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Lys  
 450 455

<210> 589  
 <211> 1425  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 589  
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 agatgccagg tgcagctggg ggagctctggg ggaggcgctgg tccagcctgg gaggtccctg 120  
 agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180  
 caggctccag gcaaggagct ggagtggggtg gcagtcatat catatgatgg aaataataaa 240  
 ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg 300  
 ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg 420  
 gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540  
 ccggtgacgg tgctgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600  
 gtcctacagt cctcaggact ctactccctc gagagcgctgg tgaccgtgcc ctccagcagc 660  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720

## A-1937-W0-PCT\_ST25

aagaaagttag agcccaaatac ttgtgacaaa actcacacat gccaccgtg cccagcacct 780  
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 840  
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900  
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc 960  
gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac 1020  
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gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140  
ccatcccga aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1200  
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260  
accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320  
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380  
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

&lt;210&gt; 590

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 590

atggacatga gaggcctgc acagctgctg ggccctgctg tgctgtggct gagaggcgcc 60  
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180  
aaaccaggga aagcccctaa gtcctgatc tatgatgcat ccagtttgca aagtggggtc 240  
ccatcaagggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360  
ggcaaaggga ccaagggtga aatcaaacga acggtggctg caccatctgt cttcatcttc 420

A-1937-W0-PCT\_ST25

ccgccatctg atgagcagtt gaaatctggt accgcctctg ttgtgtgcct gctgaataac 480  
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 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600  
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
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<210> 591

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 591

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

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Thr Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr  
 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 Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
 100 105 110

A-1937-W0-PCT\_ST25

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300



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Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Lys  
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<210> 592

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

# A-1937-W0-PCT\_ST25

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ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360  
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ccgccatctg atgagcagtt gaaatctggg accgcctctg ttgtgtgcct gctgaataac 480  
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ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 593  
<211> 708  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag 180  
aaaccaggga aagcccctaa ggcctgatc tatgctgcgt ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360

A-1937-W0-PCT\_ST25

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ggcgaaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc | 420 |
| ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac | 480 |
| ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac | 540 |
| tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc | 600 |
| ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat | 660 |
| cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt              | 708 |

<210> 594

<211> 1428

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 594

|                                                                    |     |
|--------------------------------------------------------------------|-----|
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| cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg  | 120 |
| agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc  | 180 |
| caggctccag gcaagaagct ggagtgggtg gcagttatat catatgatgg aagtattaaa  | 240 |
| tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg  | 300 |
| ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga  | 360 |
| gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc  | 420 |
| acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc  | 480 |
| tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc   | 540 |
| gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc | 600 |
| gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc  | 660 |
| agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg  | 720 |
| gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca | 780 |

A-1937-W0-PCT\_ST25

cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840  
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcca gacaaagccg 960  
tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020  
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cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200  
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gacaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag cgacctcacc 1320  
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380  
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa 1428

<210> 595

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 595

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

A-1937-W0-PCT\_ST25

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

A-1937-W0-PCT\_ST25

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys  
450

<210> 596  
<211> 1350  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 596  
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acctgcgctg tccatgggtgg gtccttcagt gggtactact ggaactggat ccgccagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
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gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
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ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 900  
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

## A-1937-W0-PCT\_ST25

|                                                                   |      |
|-------------------------------------------------------------------|------|
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccggaagaag | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg | 1200 |
| ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg | 1320 |
| cagaagagcc tctccctgtc tccgggtaaa                                  | 1350 |

&lt;210&gt; 597

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 597

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc   | 60  |
| agatgcgagg ttcagctggc cgagtcagga ggcggctctcg tgcagcctgg cggatcactg  | 120 |
| agattgtcct gtgctgcac tggttacgtc ttcacagact atggaatgaa ttgggttaga    | 180 |
| caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct   | 240 |
| atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca   | 300 |
| gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga   | 360 |
| ggatacagat cttatgccat ggactactgg ggccagggtg ccctagtcac cgtctctagt   | 420 |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 480 |
| ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg   | 540 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600 |
| ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc    | 660 |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720 |
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga | 780 |



## A-1937-W0-PCT\_ST25

```

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctggtcgatg gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                     1410

```

&lt;210&gt; 598

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 598

```

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1           5           10          15

```

```

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
          20          25          30

```

```

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35          40          45

```

```

Gly Glu Ile Asn His Ala Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys
          50          55          60

```

A-1937-W0-PCT\_ST25

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

A-1937-W0-PCT\_ST25

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Lys Lys Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

A-1937-W0-PCT\_ST25

Gly Lys  
450

<210> 599  
<211> 448  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 599

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 Tyr Val Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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

## A-1937-W0-PCT\_ST25

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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

## A-1937-W0-PCT\_ST25

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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
 355 360 365

Leu Val Asp Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp  
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
 435 440 445

&lt;210&gt; 600

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 600

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180

ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240

## A-1937-W0-PCT\_ST25

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaattggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 360  
accaagggcc catcgggtctt ccccttggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
tactccctcg agagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gccc aaatct 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttctct tcccccaaaa acccaaggac accctcatga tctcccgga ccttgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg 900  
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
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tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg taaa 1344

&lt;210&gt; 601

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 601

A-1937-W0-PCT\_ST25

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Met Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Ile Gly Ser Tyr Tyr Gly 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 Glu Ser Val Val Thr Val Pro Ser Ser  
180 185 190



A-1937-W0-PCT\_ST25

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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Lys Lys Met 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

A-1937-W0-PCT\_ST25

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Lys  
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 Lys  
435 440 445

<210> 602  
<211> 1422  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 602  
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ccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat 240  
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 300  
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 360  
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gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600  
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A-1937-W0-PCT\_ST25

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aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380  
aaccactaca cgcagaagag cctctccctg tctccgggta aa 1422

<210> 603  
<211> 455  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 603

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

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Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

A-1937-W0-PCT\_ST25

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Lys Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

A-1937-W0-PCT\_ST25

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Lys  
 450 455

<210> 604  
 <211> 1431  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 604  
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 agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120  
 cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180  
 atcaggcagg cccaggggaa aggccttgag tgggtgagca ggacatacta caggtccaag 240  
 tgggtataatg attatgcagt ttctgtgaaa ggtcgattca ctatcagccc agacacatcc 300  
 aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360  
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 accacggtca ccgtctctag tgcctccacc aagggcccat cggctcttccc cctggcaccc 480  
 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540  
 cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600  
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 agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720  
 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca 780  
 gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc 840  
 ctcatgatct cccggacccc tgaggtcaca tgcgtgggtgg tggacgtgag ccacgaagac 900

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cctgagggtca agttcaactg gtacgtggac ggctgtggagg tgcataatgc caagacaaag 960  
ccgtgcgagg agcagtagcg cagcacgtac cggtgctgca gcgtcctcac cgtcctgcac 1020  
caggactggc tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc 1080  
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140  
ctgcccccat cccggaagaa gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa 1200  
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260  
tacaagacca cgcctcccgt gctgaagtcc gacggctcct tcttcctcta tagcaagctc 1320  
accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380  
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1431

<210> 605  
<211> 455  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 605

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 Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Val Lys Gly Arg Phe Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

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Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270



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Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Lys Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Lys  
450 455

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<210> 606  
 <211> 1425  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 606  
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 agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180  
 caggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa 240  
 ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg 300  
 ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg 420  
 gtcaccgtct ctagtgcctc caccaagggc ccatcggtct tccccctggc accctcctcc 480  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540  
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600  
 gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc 660  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720  
 aagaaagttg agcccaaatac ttgtgacaaa actcacacat gcccaccgtg cccagcacct 780  
 gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aaccaagga caccctcatg 840  
 atctcccgga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag 900  
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc 960  
 gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac 1020  
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc 1080  
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140

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ccatcccgga agaagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1200  
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260  
accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320  
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380  
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

<210> 607

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 607

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

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Asn Asn Lys Leu Tyr Thr Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr  
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 Pro Thr Val Thr Leu Tyr Tyr Tyr Tyr Gly Met Asp Val  
100 105 110

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

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Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Lys Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Lys  
450

<210> 608

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

A-1937-W0-PCT\_ST25

<400> 608

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| cgctgtgagg tgcagctggg gcagctctgga gcagaggtga aaaagcccgg ggagtctctg  | 120  |
| aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgctg   | 180  |
| cagatgcccc ggaaaaggcct ggagtggatg gggatcatct atcttgggtga ctcagatacc | 240  |
| agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc   | 300  |
| gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga   | 360  |
| agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc   | 420  |
| accaagggcc catcgggtctt cccctggca cctcctcca agagcacctc tgggggcaca    | 480  |
| gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac   | 540  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc    | 600  |
| tactccctca agagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 660  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gccc aaatct  | 720  |
| tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca    | 780  |
| gtcttctctt tcccccaaa acccaaggac accctcatga tctccggac ccctgaggtc     | 840  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 900  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgag aggagcagta cggcagcacg   | 960  |
| taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 1020 |
| aagtgaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc     | 1080 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 1140 |
| aagaaccagg tcagcctgac ctgcctgggt gatggcttct atcccagcga catcgccgtg   | 1200 |
| gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac   | 1260 |
| tccgacggct ccttcttct ctatagcgac ctcaccgtgg acaagagcag gtggcagcag    | 1320 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1380 |

agcctctccc tgtctccggg taaa

1404

&lt;210&gt; 609

&lt;211&gt; 446

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 609

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335



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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
355 360 365

Asp Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
370 375 380

Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp  
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 610

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 610

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgagg ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120

agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180

caggccccgg gaaagggcct ggaatggatg gggttgatta atacttacat tggagagcct 240

atttatgctg acagcgtcaa gggcagattc acgatctctc tagacacatc caagtcaaca 300

## A-1937-W0-PCT\_ST25

gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac cgtctctagt 420  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagga gcagtacggc 960  
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
atgaccaaga accaggctcag cctgacctgc ctggctgatg gcttctatcc cagcgacatc 1200  
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260  
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320  
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
cagaagagcc tctccctgtc tccgggtaaa 1410

&lt;210&gt; 611

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 611

A-1937-W0-PCT\_ST25

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 Tyr Val Phe Thr Asp Tyr  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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 Lys Ser Val Val Thr Val Pro Ser Ser  
180 185 190

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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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
355 360 365

Leu Val Asp Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
370 375 380

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Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 612  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 612  
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agattgtcct gtgctgcatc tggttacacc ttcacagact atggaatgaa ttggggttaga 180  
caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240  
atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300  
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt 420  
gcctccacca agggcccatc ggtctttccc ctggcaccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 540  
tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg cacccagacc 660

## A-1937-W0-PCT\_ST25

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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
aaatcttgtg acaaaaactca cacatgcccc cctgtgcccag cacctgaact cctggggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
aaagccaaag ggagcccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctggtcgatg gcttctatcc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                     1410

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&lt;210&gt; 613

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 613

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20           25           30

```

```

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35           40           45

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Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
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 Gly Tyr Arg Ser Tyr Ala Met 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
355 360 365

Leu Val Asp Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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



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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

<210> 614  
 <211> 1428  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 614  
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 cgctgtcagg tgcagttggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
 agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
 caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
 tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
 ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
 acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540  
 gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600  
 gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660  
 agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
 gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
 cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840  
 atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900  
 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 960  
 tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020

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gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1080  
 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140  
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 gacaccacgc ctcccgctgct ggactccgac ggctccttct tcctctatag cgacctcacc 1320  
 gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380  
 ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa 1428

<210> 615  
 <211> 454  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 615

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

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

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Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

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Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Asp Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys  
450

<210> 616  
<211> 448  
<212> PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 616

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 Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ala Val  
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
 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 Gly Tyr Arg Ser Tyr Ala Met 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

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165

170

175

Ser Ser Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys

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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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 617  
<211> 1410  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 617  
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agatgcgagg ttcagctggt cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg 120  
agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180  
aaggccccgg gaaagggcct ggaatggatg gggttgatta atacttacat tggagagcct 240  
atttatgctg acgccgtcaa gggcagattc acgttctctc gagacacatc caagtcaaca 300  
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360  
ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac cgtctctagt 420  
gcctccacca agggccccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

## A-1937-WO-PCT\_ST25

ggacacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 540  
 tggaactcag ggcacctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600  
 ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720  
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840  
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080  
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260  
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380  
 cagaagagcc tctccctgtc tccgggtaaa 1410

&lt;210&gt; 618

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 618

caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcgagac cctgtccctc 60  
 acctgcgctg tccatgggtg gtccttcagt gggttactact ggaactggat ccgcgagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180



## A-1937-W0-PCT\_ST25

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ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg      240
acgctgacct ctgtgaccgc cgcggaacacg gctgtgtatt actgtgcgag aggatattgt      300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt      360
gcctccacca agggcccatc ggtcttcccc ctggcacccct cctccaagag cacctctggg      420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg      480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540
ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga      720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc      900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccac cgggaaggag     1080
atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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&lt;210&gt; 619

&lt;211&gt; 1410

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 619

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc   | 60   |
| agatgcgagg ttcagctggg cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg  | 120  |
| agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga   | 180  |
| aaggccccgg gaaagggcct ggaatggatg gcttggatta atacttacat tggagagcct   | 240  |
| atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca   | 300  |
| gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga   | 360  |
| ggatacagat cttatgccat ggactactgg ggccagggtg ccctagtcac cgtctctagt   | 420  |
| gcctccacca agggccccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg  | 480  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 540  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 600  |
| ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 660  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 720  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 780  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacacc tcattgatctc ccggaccct    | 840  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg   | 900  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagga gcagtacggc     | 960  |
| agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 1020 |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1080 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag    | 1140 |
| atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1200 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctccgtg    | 1260 |
| ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtg   | 1320 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1380 |

cagaagagcc tctccctgtc tccgggtaaa

1410

&lt;210&gt; 620

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 620

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 Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Ala Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Ala Tyr  
 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 Gly Tyr Arg Ser Tyr Ala Met 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Asp Thr Thr Pro Pro Val Leu Asp  
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp 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 Lys  
435 440 445

<210> 621  
<211> 1428  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 621  
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cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
aaggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240  
tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300

## A-1937-W0-PCT\_ST25

ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
 ttggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540  
 gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600  
 gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660  
 agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
 gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
 cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840  
 atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900  
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 tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020  
 gactggctga atggcaagga gtacaagtgc aaggctctcca acaaagccct cccagcccc 1080  
 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacagggt gtacaccctg 1140  
 ccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1200  
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 gacaccacgc ctcccgctgct ggactccgac ggctccttct tcctctatag cgacctcacc 1320  
 gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380  
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&lt;210&gt; 622

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 622

A-1937-W0-PCT\_ST25

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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120  
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag 180  
aaaccaggga aagcccctaa gctcctgatc tatgctgcgt ccagtttgca aagtggggtc 240  
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300  
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360  
ggcggaggga ccaagggtgga gatcaaactg acgggtggctg caccatctgt cttcatcttc 420  
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480  
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540  
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc 600  
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660  
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 623

<211> 454

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 623

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

Asp Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val

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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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp



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245

250

255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
 385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
 405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu

435

440

445

Ser Leu Ser Pro Gly Lys  
450

<210> 624  
<211> 1428  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 624  
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60  
cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120  
agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180  
aaggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgc aagtattaaa 240  
tactatgcag aatccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300  
ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360  
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420  
ttggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480  
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540  
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600  
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660  
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720  
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780  
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840  
atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagacct 900  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 960

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag  | 1020 |
| gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc  | 1080 |
| atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg  | 1140 |
| cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc  | 1200 |
| ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac  | 1260 |
| gacaccacgc ctcccgctgct ggactccgac ggctccttct tcctctatag cgacctcacc | 1320 |
| gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct  | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa               | 1428 |

&lt;210&gt; 625

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 625

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcg | 60  |
| cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga   | 120 |
| gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag   | 180 |
| aaaccaggga aagcccctaa gctcctgata tatgctgcgt ccagtttgca aagtggggtc   | 240 |
| ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg   | 300 |
| cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc   | 360 |
| ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc   | 420 |
| ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac   | 480 |
| ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac   | 540 |
| tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc   | 600 |
| ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat   | 660 |

cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt

708

&lt;210&gt; 626

&lt;211&gt; 454

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 626

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

Asp Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Ser Tyr Asp Ala Ser Ile Lys Tyr Tyr Ala Glu 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 Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp  
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

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Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Asp Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Asp  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys  
450

<210> 627  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 627  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagaagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

## A-1937-WO-PCT\_ST25

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggtagcgcc aaagtgtgtg gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

&lt;210&gt; 628

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 628

gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60  
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca ggaaaaacca 120  
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180  
 aggttcagcg gatccggtag tggtagctat ttaccctca cgatcagtag cctccagcca 240  
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300  
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaaactgcc gaagtgtgtg gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

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<210> 629  
 <211> 1350  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 629  
 cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat ccgcgagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctggtcgag gactacttcc ccgaaccggt gacgggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 900  
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag 1080  
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140



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|                                                                   |      |
|-------------------------------------------------------------------|------|
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg | 1200 |
| ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg | 1320 |
| cagaagagcc tctccctgtc tccgggtaaa                                  | 1350 |

<210> 630  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 630                                                          |     |
| gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc  | 60  |
| atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca ggaaaaacca | 120 |
| ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc  | 180 |
| aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca  | 240 |
| gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag  | 300 |
| ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca   | 360 |
| tctgatgagc agttgaaatc tggaactgcc gaagttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcac cagtaacaaa aagctttaat agaggagagt gt                     | 642 |

<210> 631  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 631

Leu Gln His Gln Ser Tyr Pro Pro Thr  
1 5

<210> 632

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 632

Thr Gln Ser Val Ala Trp Asn  
1 5

<210> 633

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 633

Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

<210> 634

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 634

Glu Ile Asn His Ala Gly Gln Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
1 5 10 15

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<210> 635  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 635

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Ser | Gln | Asp | Xaa | Arg | Asp | Asp | Leu | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 636  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 636

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Ser | Ser | Leu | Gln | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 637  
 <211> 9

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 637

Xaa Gln His Gln Ser Tyr Pro Pro Thr  
 1 5

<210> 638  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(5)  
 <223> Each Xaa is independently A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(5)  
 <223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<400> 638

Xaa Gln His Asn Xaa Tyr Pro Pro Thr  
 1 5

<210> 639  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(4)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 639

Ser Tyr Xaa Xaa His  
 1 5

<210> 640  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(2)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(15)

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<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 640

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Tyr | Asp | Xaa | Asn | Asn | Lys | Xaa | Tyr | Thr | Asp | Xaa | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 641

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (5)..(5)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (10)..(11)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 641

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Xaa | Thr | Xaa | Tyr | Tyr | Tyr | Tyr | Xaa | Xaa | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 642

<211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 642

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Xaa | Asn | Asn | Tyr | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 643  
 <211> 7  
 <212> PRT  
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<220>  
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<400> 643

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Thr | Ser | Ser | Xaa | Gln | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 644  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

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<220>  
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<400> 644

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Xaa | Tyr | Tyr | Ser | Xaa | Ser | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

<210> 645  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <222> (7)..(7)



<223> Each Xaa is independently M, G, A, V, I, or L

<400> 645

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Ser | Tyr | Tyr | Xaa | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 646

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (2)..(3)

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<220>

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<222> (6)..(6)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (10)..(10)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 646

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Xaa | Asn | Asn | Tyr | Xaa | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 647

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

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<220>

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<220>  
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 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 647

Xaa Xaa Ser Ser Xaa Gln Ser  
 1 5

<210> 648  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(14)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 648

Tyr Xaa Tyr Tyr Ser Xaa Gln Thr Lys Tyr Asn Pro Ser Xaa Lys Ser  
 1 5 10 15

<210> 649  
 <211> 16  
 <212> PRT

<213> Artificial Sequence

<220>

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<220>

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<222> (2)..(2)

<223> Xaa may independently be M, G, A, V, I, or L

<220>

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<222> (6)..(6)

<223> Xaa may independently be M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

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<222> (14)..(14)

<223> Xaa may independently be M, G, A, V, I, or L

<400> 649

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Xaa | Tyr | Tyr | Ser | Xaa | Asn | Xaa | Lys | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 650

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (3)..(3)

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<220>

<221> MISC\_FEATURE

A-1937-WO-PCT\_ST25

<222> (7)..(7)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 650

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Xaa | Ser | Tyr | Tyr | Xaa | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |

<210> 651

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (7)..(7)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

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<222> (16)..(17)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 651

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Ser | Gln | Ser | Val | Xaa | Tyr | Ser | Ser | Asn | Asn | Lys | Asn | Tyr | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Xaa

<210> 652

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE  
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<400> 652

Trp Xaa Ser Thr Arg Glu Ser  
 1 5

<210> 653  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (8)..(8)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 653

Gln Gln Tyr Tyr Lys Thr Pro Xaa Thr  
 1 5

<210> 654  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 V, W, or Y

<220>  
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 <222> (3)..(3)

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<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 654

Thr Asn Xaa Xaa Xaa Trp Asn

1 5

<210> 655

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 655

Thr Asn Xaa Xaa Xaa Trp Asn

1 5

<210> 656

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

A-1937-W0-PCT\_ST25

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<220>  
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 <222> (16)..(16)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 656

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Xaa Val Ser Xaa  
 1 5 10 15

Lys Ser

<210> 657  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 657

Glu Asp Xaa Asp Ser Tyr Tyr Arg Tyr Xaa Xaa Asp Val  
 1 5 10

<210> 658  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<400> 658

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Val | Xaa | Tyr | Ser | Ser | Asn | Asn | Lys | Asn | Tyr | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 659  
<211> 18  
<212> PRT  
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<220>  
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<400> 659

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Tyr | Tyr | Arg | Ser | Lys | Trp | Tyr | Asn | Asp | Tyr | Xaa | Xaa | Ser | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |



Lys Ser

<210> 660  
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 <212> PRT  
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<220>  
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<400> 660

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Tyr | Tyr | Arg | Ser | Lys | Trp | Tyr | Asn | Asp | Tyr | Xaa | Xaa | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Lys Xaa

<210> 661  
 <211> 12  
 <212> PRT  
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<220>  
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<400> 661

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Val | Arg | Ser | Ser | Tyr | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 662  
 <211> 7  
 <212> PRT  
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<400> 662

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Ser | Arg | Xaa | Thr |
| 1   |     |     |     | 5   |     |     |

<210> 663  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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<222> (4)..(4)  
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<400> 663

Gln Gln Tyr Xaa Ser Ser Pro Thr  
 1 5

<210> 664  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 664

Xaa Tyr Tyr Trp Asn  
 1 5

<210> 665  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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<220>  
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 <222> (14)..(14)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 665

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Gln | His | Xaa | Xaa | Gln | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 666  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
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 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 666

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Asn | His | Xaa | Xaa | Asn | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 667  
 <211> 12  
 <212> PRT  
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<220>  
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<220>  
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 <400> 667

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Tyr | Cys | Arg | Ser | Thr | Thr | Cys | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 668  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <222> (6)..(6)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>  
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 <222> (11)..(12)  
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 668  
  

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Xaa | Arg | Ser | Ser | Tyr | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 669  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (1)..(2)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (10)..(10)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (12)..(12)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (15)..(15)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 669

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Tyr | Asp | Xaa | Asn | Asn | Lys | Xaa | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 670

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (5)..(6)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (10)..(10)

<223> Each Xaa is independently M, G, A, V, I, or L

<400> 670

Arg Xaa Ser Gln Xaa Xaa Ser Asn Asp Xaa

1

5

10

<210> 671

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (11)..(12)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (14)..(14)

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<223> Each Xaa is independently M, G, A, V, I, or L

<400> 671

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Glu | Thr | Glu | Thr | Xaa | Tyr | Tyr | Tyr | Tyr | Xaa | Xaa | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

<210> 672

<211> 14

<212> PRT

<213> Homo sapiens

<400> 672

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Cys | Ser | Ser | Thr | Ser | Cys | Tyr | Thr | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

<210> 673

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 673

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |

<210> 674

<211> 9

<212> PRT

<213> Homo sapiens

<400> 674

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | His | Asn | Ser | Tyr | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 675

<211> 14

<212> PRT

<213> Homo sapiens



&lt;400&gt; 675

Gly Thr Thr Gly Thr Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val  
 1 5 10

&lt;210&gt; 676

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (5)..(5)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I or L

&lt;400&gt; 676

Glu Asp Gly Asp Xaa Tyr Tyr Arg Tyr Gly Met Asp Val  
 1 5 10

&lt;210&gt; 677

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 677

Glu Ile Gln His Ala Gly Gln Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
 1 5 10 15

&lt;210&gt; 678

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

<400> 678

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Ser | Tyr | Glu | Gly | Asn | Asn | Lys | Leu | Tyr | Thr | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 679

<211> 17

<212> PRT

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<400> 679

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Tyr | Glu | Xaa | Asn | Asn | Lys | Leu | Tyr | Thr | Glu | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

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<400> 680

Glu Glu Gly Glu Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
 1 5 10

<210> 681  
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<400> 681

Glu Glu Xaa Glu Ser Tyr Tyr Arg Tyr Xaa Xaa Asp Xaa  
 1 5 10

<210> 682  
 <211> 48

A-1937-W0-PCT\_ST25

<212> DNA

<213> Homo sapiens

<400> 682

agggtctagtc agagcctcct gtatagtaat ggatacaact atttggat

48

<210> 683

<211> 16

<212> PRT

<213> Homo sapiens

<400> 683

Arg Ser Ser Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr Leu Asp  
1 5 10 15

<210> 684

<211> 21

<212> DNA

<213> Homo sapiens

<400> 684

ttgggttcta gtcgggcctc c

21

<210> 685

<211> 7

<212> PRT

<213> Homo sapiens

<400> 685

Leu Gly Ser Ser Arg Ala Ser  
1 5

<210> 686

<211> 27

<212> DNA

<213> Homo sapiens

<400> 686

atgcaacctc tacaaactcc gctcact

27

<210> 687

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<211> 9  
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<400> 687

Met Gln Pro Leu Gln Thr Pro Leu Thr  
 1 5

<210> 688  
 <211> 51  
 <212> DNA  
 <213> Homo sapiens

<400> 688  
 aagtcagtc agaataatattt atacagctcc aacaataaaa actacttagc t 51

<210> 689  
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<400> 689

Lys Ser Ser Gln Asn Ile Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu  
 1 5 10 15

Ala

<210> 690  
 <211> 21  
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<400> 690  
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<210> 691  
 <211> 17  
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A-1937-W0-PCT\_ST25

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<400> 691

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ser | Tyr | Asp | Xaa | Asn | Asn | Lys | Leu | Tyr | Ala | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 692

<211> 27

<212> DNA

<213> Homo sapiens

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27

<210> 693

<211> 9

<212> PRT

<213> Homo sapiens

<400> 693

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Tyr | Tyr | Ser | Ile | Pro | Trp | Thr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 694

<211> 51

<212> DNA

<213> Homo sapiens

A-1937-W0-PCT\_ST25

<400> 694  
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<210> 695  
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<220>  
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<400> 695  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10

<210> 696  
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<212> DNA  
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<400> 696  
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<210> 697  
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<400> 697  
Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asn Val His  
1 5 10

<210> 698  
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<400> 698  
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A-1937-W0-PCT\_ST25

<210> 699  
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<400> 699

Gly Asn Asn Asn Arg Pro Ser  
 1 5

<210> 700  
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<400> 700  
 cagtcctatg acagcagcct gagtgggttg gtg

33

<210> 701  
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<400> 701

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val  
 1 5 10

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<400> 702  
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42

<210> 703  
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<400> 703

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10

<210> 704

<211> 21

<212> DNA

<213> Homo sapiens

<400> 704

ggtaacagcc atcgccctc a

21

<210> 705

<211> 7

<212> PRT

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<400> 705

Gly Asn Ser His Arg Pro Ser  
1 5

<210> 706

<211> 33

<212> DNA

<213> Homo sapiens

<400> 706

cagtcctatg acagcagcct gagggttat gtc

33

<210> 707

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<212> PRT

<213> Homo sapiens

<400> 707

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Tyr Val  
1 5 10

<210> 708

<211> 42

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<212> DNA  
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<400> 708  
actgggagcg gctccaacat cggggcaggt tatgatgtac ac 42

<210> 709  
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<400> 709  
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1 5 10

<210> 710  
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<400> 710  
ggtaatagtc atcgccctc a 21

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

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<222> (17)..(17)

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<400> 711

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Tyr | Glu | Xaa | Asn | Asn | Lys | Xaa | Tyr | Xaa | Glu | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

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<211> 33

<212> DNA

<213> Homo sapiens

<400> 712

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33

<210> 713

<211> 11

<212> PRT

<213> Homo sapiens

<400> 713

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Ser | Gln | Ser | Phe | Ser | Ser | Tyr | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

A-1937-W0-PCT\_ST25

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<400> 714  
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<210> 715  
 <211> 17  
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<220>  
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<400> 715  
 Val Met Ser Tyr Glu Gly Asn Asn Lys Leu Tyr Ala Glu Ser Val Lys  
 1 5 10 15

Gly

<210> 716  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 716  
 caacagagtt acagtacccc tcgcagt 27

<210> 717  
 <211> 9  
 <212> PRT  
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<400> 717  
 Gln Gln Ser Tyr Ser Thr Pro Arg Ser  
 1 5

<210> 718

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<211> 33  
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<400> 718  
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<210> 719  
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<400> 719  
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 1 5 10

<210> 720  
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<400> 720  
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<210> 721  
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 Thr Ala Ser Ser Leu Gln Ser  
 1 5

<210> 722  
 <211> 39  
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<400> 722  
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<210> 723  
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<400> 723

Ser Glu Ser Asn Ser Asp Ile Gly Thr Asn Ala Val Asn  
 1 5 10

<210> 724  
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<400> 724

agtaataata agcggccctc a

21

<210> 725  
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<400> 725

Ser Asn Asn Lys Arg Pro Ser  
 1 5

<210> 726  
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<400> 726

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33

<210> 727  
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<400> 727

Ala Thr Trp Asp Asp Asn Leu Asn Gly Pro Leu

1

5

10

<210> 728  
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33

<210> 729  
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<400> 729

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 1 5 10 15

<210> 730  
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 <212> DNA  
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 gttgcatcca gtttgcaaag t

21

<210> 731  
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<400> 731

Val Ala Ser Ser Leu Gln Ser  
 1 5

<210> 732  
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<210> 733  
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<400> 733  
Gln Gln Ser Tyr Ser Asn Pro Gln Glu Cys Ser  
1 5 10

<210> 734  
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<400> 734  
cgggcaagtc agggcattag aaatgactta ggc 33

<210> 735  
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<220>  
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1 5 10 15

<210> 736  
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<210> 737  
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 <212> PRT  
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<400> 737

Ala Ala Ser Gly Leu Gln Gly  
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<210> 738  
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30

<210> 739  
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<400> 739

Leu Gln His Asn Ser Tyr Pro Thr Trp Thr  
 1 5 10

<210> 740  
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<400> 740  
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33

<210> 741  
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<400> 741

A-1937-W0-PCT\_ST25

Arg Ala Ser Gln Ser Ile Ser Tyr Tyr Leu Asn  
1 5 10

<210> 742  
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<400> 742  
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<210> 743  
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<220>  
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<400> 743

Arg Ser Ser Gln Ser Leu Leu Tyr Ser Gln Gly Tyr Asn Tyr Leu Asp  
1 5 10 15

<210> 744  
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<212> DNA  
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<400> 744  
caacagagtt acagttccat cacc 24

<210> 745  
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<212> PRT  
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<400> 745

Gln Gln Ser Tyr Ser Ser Ile Thr  
1 5

A-1937-W0-PCT\_ST25

<210> 746  
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<400> 746  
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33

<210> 747  
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<400> 747

Arg Ala Ser Gln Asn Ile Ser Ser Tyr Leu Asn  
 1 5 10

<210> 748  
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 <212> DNA  
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 actgcatcca gtttgcaaag t

21

<210> 749  
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 <212> PRT  
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<400> 749

Thr Ala Ser Ser Leu Gln Ser  
 1 5

<210> 750  
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 <212> DNA  
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 caacagagtt acagtaaccc tcctgagagc agt

33

A-1937-W0-PCT\_ST25

<210> 751  
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<400> 751

Gln Gln Ser Tyr Ser Asn Pro Pro Glu Ser Ser  
 1 5 10

<210> 752  
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 <212> DNA  
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<400> 752

aggcttagtc aaagcctcgt atacagtgac ggaaacacct acttgaat 48

<210> 753  
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<400> 753

Arg Ser Ser Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr Leu Asn  
 1 5 10 15

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<400> 754

aaggtttcta actgggactc t 21

<210> 755  
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Lys Val Ser Asn Trp Asp Ser  
1 5

<210> 756  
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<400> 756  
atgcaaggta cacactggcc t

21

<210> 757  
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<400> 757

Met Gln Gly Thr His Trp Pro  
1 5

<210> 758  
<211> 33  
<212> DNA  
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<400> 758  
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33

<210> 759  
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<220>  
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<400> 759

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| Arg | Ser | Ser | Gln | Ser | Xaa | Xaa | Tyr | Ser | Asn | Xaa | Tyr | Asn | Tyr | Xaa | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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<400> 760  
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21

<210> 761  
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<400> 761

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Ser | Arg | Leu | Gln | Ser |
| 1   |     |     |     | 5   |     |     |

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<400> 762  
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27

<210> 763  
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 <212> PRT  
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<400> 763

Gln Gln Ser Asp Ser Thr Pro Ile Thr  
1 5

<210> 764

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<212> DNA

<213> Homo sapiens

<400> 764

gctgcatcca gtttacaaag t

21

<210> 765

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1 5 10 15

<210> 766

<211> 24

<212> DNA  
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<400> 766  
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24

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Gln Gln Ser Phe Ser Thr Ile Thr  
1 5

<210> 768  
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<400> 768  
ggtgcatccc gtttgcaaag t

21

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<400> 769

Gly Ala Ser Arg Leu Gln Ser  
1 5

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24

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Gly

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<212> DNA

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48

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<400> 781

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| Asp | Arg | Ile | Ala | Ala | Pro | Gly | Thr | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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15

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|-----|-----|-----|-----|-----|
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| 1   |     |     |     | 5   |

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51

<210> 785

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<211> 17  
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<400> 785

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Tyr | Asp | Gly | Ser | Asn | Lys | Asp | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

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<400> 786

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<210> 787  
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 <213> Homo sapiens

<400> 787

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Arg | Asp | Ser | Tyr | Tyr | His | Tyr | Gly | Met | Asp | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |

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<400> 788

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<210> 789  
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&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(2)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (6)..(6)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;400&gt; 789

Xaa Xaa Ser Ser Arg Xaa Ser  
 1 5

&lt;210&gt; 790

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 790

gaggaaaggg attcctacta ccactacggt atggacgtc

39

&lt;210&gt; 791

&lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 791

agctatgtca tgagc

15

&lt;210&gt; 792

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 792

Ser Tyr Val Met Ser  
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Gly

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<210> 796  
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<400> 796  
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<210> 797  
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15

<210> 798

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51

<210> 800

<211> 17

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Val Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 801

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33

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<400> 802

Asp Gly Tyr Ser Ser Ala Trp Tyr Phe Asp Tyr  
 1 5 10

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Asn Tyr Ala Met Asn  
 1 5

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51

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21

<210> 809  
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Ser Ser Ser Ala Thr Trp Asn  
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Lys Ser

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<400> 813

Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro  
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<210> 814

<211> 21

<212> DNA

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<400> 814

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21

<210> 815

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Ser Asn Ser Ala Thr Trp Asn  
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Lys Ser

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<400> 818  
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 Gly Phe Tyr Met His  
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Trp Ile Asn Pro Asp Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln  
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Gly

<210> 822

<211> 27

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<213> Homo sapiens

<400> 822

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27

<210> 823

<211> 9

<212> PRT

<213> Homo sapiens

<400> 823

Glu Gly Ile Ala Val Ala Leu Thr Tyr  
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<210> 824

<211> 15

<212> DNA

<213> Homo sapiens

<400> 824

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15

&lt;210&gt; 825

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 825

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

&lt;210&gt; 826

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 826

gaaatcaatc atagtggaag aaccaactac aaccggtccc tcaagagt

48

&lt;210&gt; 827

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 827

Glu Ile Asn His Ser Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys Ser  
 1 5 10 15

&lt;210&gt; 828

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 828

gacagtggct ggcacttttc ttttgatatc

30

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<210> 829  
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 1 5 10

<210> 830  
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<400> 832

Val Ile Trp Phe Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val Lys  
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Gly

<210> 833  
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<213> Homo sapiens

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1 5 10

<210> 835  
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<210> 836  
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<400> 836  
  
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<210> 837  
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<210> 838

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<400> 838

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| Gly | Ile | Ser | Gly | Gly | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

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<400> 840

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| 1   |     |     |     | 5   |     |     |     |

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<400> 841  
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15

<210> 842  
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<400> 843

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<210> 844  
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<210> 847  
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Ala Tyr Tyr Met His  
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<210> 848

<211> 51

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Gly

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<212> PRT

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Gly Gly Ser Trp Glu Gly Phe Asp Tyr

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<210> 855  
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<210> 856

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 1 5

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51

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<400> 859

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Gly

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<210> 861  
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Gly Ser Ser Trp Glu Gly Phe Asp Tyr  
1 5

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Gly

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<211> 339

<212> DNA

<213> Homo sapiens

<400> 865

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tacctgcaga agccagggca gtctccacag ctctgatctt atttgggttc tagtcggggcc      180
tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc      240
agcagagtgg aggctgagga tgttgggggtt tattactgca tgcaacctct acaaactccg      300
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<211> 112

<212> PRT

<213> Homo sapiens

<400> 866

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
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Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
          35          40          45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Ser Arg Ala Ser Gly Val Pro
          50          55          60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65          70          75          80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Pro
          85          90          95

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Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
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 ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtagttt catatactac 180  
 gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240  
 ctgcaaataga acagcctgag agccgaggac acggctgtat attactgtgc gagagaccgt 300  
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 gtcaccgtct cctca 375

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 Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Ser Ile Ser Ser Ser Ser Ser Phe Ile Tyr Tyr Ala Asp Ser Val  
 50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
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 Arg Ile Ala Ala Pro Gly Thr Tyr Tyr Tyr Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
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tggtaccagc agaaaccagg acagcctcct agcctgctca tttactgggc atctaccgg 180  
gaatccggggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
ctcagcagcc tgcaggctga agatgtggca gtttatttct gtcaacaata ttatagtatt 300  
ccgtggacgt tcggccaagg gaccaagggtg gaaatcaaac ga 342

<210> 870  
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<212> PRT  
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<400> 870

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
1 5 10 15



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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Ile Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Ser Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Leu Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln  
85 90 95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys

<210> 871  
<211> 366  
<212> DNA  
<213> Homo sapiens

<400> 871  
cagggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60  
tcctgtgcag cgtctggatt caccttcagt acttatggca tgcactgggt ccgccaggct 120  
ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaagactat 180  
gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgttgtat 240  
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaggaa 300  
agggattcgt actaccatta cgggatggac gtctggggcc aagggaccac ggtcaccgtc 360  
tcttca 366

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<210> 872  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 872

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 Thr Tyr  
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asp Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Arg Asp Thr Leu Tyr  
 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 Glu Glu Arg Asp Ser Tyr Tyr His Tyr Gly Met Asp Val Trp  
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120

<210> 873  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<400> 873

gacatcgtga tgacccagtc tccagactcc ctgactgtgt ctctgggcga gggggccacc

60

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atcaactgca agtccagcca gagtgtttta tacagctcca acaataaaaa ctacttagct 120  
 tgggtaccagc agaaaccagg acagcctcct agcctgctca ttactgggc atctaccgg 180  
 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtatt 300  
 ccgtggacgt tcggccaagg gaccaagggtg gaaatcaaac ga 342

<210> 874  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens  
 <400> 874

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly  
 1 5 10 15

Glu Gly Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 35 40 45

Pro Pro Ser Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 100 105 110

Lys

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<210> 875  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

<400> 875  
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 tcctgtgcag cgtctggatt catcttcagt agttatggca tgcactgggt ccgccaggct 120  
 ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaagactat 180  
 gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgttgat 240  
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaggaa 300  
 agggattcct actaccacta cggtatggac gtctggggcc aaggggaccac ggtcaccgtc 360  
 tcttca 366

<210> 876  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 876  
 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 Ile Phe Ser Ser Tyr  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asp Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Arg Asp Thr Leu Tyr  
 65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Glu Arg Asp Ser Tyr Tyr His Tyr Gly Met Asp Val Trp  
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 877

<211> 336

<212> DNA

<213> Homo sapiens

<400> 877

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttata atgttcactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggactc 240

cagactgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttgg 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggt 336

<210> 878

<211> 111

<212> PRT

<213> Homo sapiens

<400> 878

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

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Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 879  
<211> 369  
<212> DNA  
<213> Homo sapiens

<400> 879  
gaaatacagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactt 60  
tcctgtgtag cctctggatt cacctttagc agctatgtca tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtggttag cacatactac 180  
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cacgctgtat 240  
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtggt 300  
accaactatt actactacta ctccggtatg gacgtctggg gccaaaggac cacggtcacc 360  
gtctcctca 369

<210> 880  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 880

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Glu Ile Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Thr Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Gly Gly Thr Asn Tyr Tyr Tyr Tyr Tyr Ser Gly Met Asp Val  
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 881

<211> 336

<212> DNA

<213> Homo sapiens

<400> 881

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggaa cagcccccaa actcctcatc tatggtaaca gccatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300

gtcttcggaa ctgggaccaa ggtcaccgtc ctaggt

336

<210> 882  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens  
 <400> 882

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Tyr Gly Asn Ser His Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu  
 100 105 110

<210> 883  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 883  
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctaagactc 60

tcctgtgcag cctctggatt cacctttagc aactatgccca tgagctgggt ccgccaggct 120



| A-1937-W0-PCT_ST25 |            |            |            |            |            |     |
|--------------------|------------|------------|------------|------------|------------|-----|
| ccaggaagg          | ggctgcagt  | ggtctcagtt | attagtggta | gaggtgtag  | cacatactac | 180 |
| gcagactccg         | tgaagggccg | gttcaccatc | tccagagaca | actccaagaa | cacgctgtat | 240 |
| ctgcaaatga         | acagcctgag | agccgaggac | acggccgtat | attactgtgc | gaaagacggg | 300 |
| tatagcagt          | cctggtactt | tgactactgg | ggccagggaa | ccctggtcac | cgtctcctca | 360 |

|       |              |
|-------|--------------|
| <210> | 884          |
| <211> | 120          |
| <212> | PRT          |
| <213> | Homo sapiens |

<400> 884

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 Asn Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gln Trp Val  
35 40 45

Ser Val Ile Ser Gly Arg Gly Gly Ser Thr 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 Val Tyr Tyr Cys  
85 90 95

Ala Lys Asp Gly Tyr Ser Ser Ala Trp Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

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<210> 885

<211> 336

<212> DNA

<213> Homo sapiens

<400> 885

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcggctc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
cttccaggaa cagcccccaa actcctcatc tatggtaata gtcacggcc ctcagggatc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat      300
gtcttcggaa ctgggaccaa ggtcaccgtc ctaggt                                336
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<210> 886

<211> 111

<212> PRT

<213> Homo sapiens

<400> 886

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1          5          10         15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Gly Ser Asn Ile Gly Ala Gly
20          25          30
```

```
Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35          40          45
```

```
Leu Ile Tyr Gly Asn Ser His Arg Pro Ser Gly Ile Pro Asp Arg Phe
50          55          60
```

```
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65          70          75          80
```

```
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85          90          95
```

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Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu  
 100 105 110

<210> 887  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 887  
 gaggtgcagc tgttgggaatc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt cacctttagc aactatgcca tgaactgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtctcagtc attagtggtc gtggtggtag tacatactat 180  
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaggaa cacgctgtat 240  
 ctgcaaataga acagcctgag agccgaggac acggccatat attactgtgc gaaagacggg 300  
 tatagcagtg cctggttctt tgactactgg ggccaggga cctgatcac cgtctcctca 360

<210> 888  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 888

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 Asn Tyr  
 20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Val Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Lys Asp Gly Tyr Ser Ser Ala Trp Phe Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Ile Thr Val Ser Ser  
115 120

<210> 889

<211> 324

<212> DNA

<213> Homo sapiens

<400> 889

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagctttagc agttatttaa attggtatca gcagaaacca 120

gggaaagccc ctgagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg caagttactt ctgtcaacag agttacagta cccctcgcag ttttggccag 300

gggaccaagc tggagatcaa acga 324

<210> 890

<211> 107

<212> PRT

<213> Homo sapiens

<400> 890

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 Arg Ala Ser Gln Ser Phe Ser Ser Tyr  
20 25 30

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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 891  
<211> 369  
<212> DNA  
<213> Homo sapiens

<400> 891  
caggtacaac tgcagcagtc aggtccagga ctggtgaagc cctcgagac cctctcactc 60  
acctgtgcca tctccgggga cagtgtctct agcagcagtg ctacttggaa ctggatcagg 120  
cagtcctccat cgagaggcct tgagtggctg ggaaggacat accagaggtc caagtggaat 180  
aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaggaac 240  
cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300  
agagaagtag tggctggccc gaggtggttc gaccctggg gccagggaac cctggtcacc 360  
gtctcctca 369

<210> 892  
<211> 123  
<212> PRT  
<213> Homo sapiens

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<400> 892

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Ser  
20 25 30

Ser Ala Thr Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
35 40 45

Trp Leu Gly Arg Thr Tyr Gln Arg Ser Lys Trp Asn Asn Asp Tyr Ala  
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Arg Asn  
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 893

<211> 324

<212> DNA

<213> Homo sapiens

<400> 893

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

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gggaaagccc ctaaactcct gatctatact gcatccagtt tgcaaagtgg gatcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

A-1937-W0-PCT\_ST25

gaagattttg caacttactt ctgtcaacag agttacagta cccctcgag ttttggccag 300

gggaccaagc tggagatcaa acga 324

<210> 894  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 894

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 Arg Ala Ser Gln Ser Val Thr 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 Thr Ala Ser Ser Leu Gln Ser Gly Ile 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 Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 895  
<211> 369  
<212> DNA  
<213> Homo sapiens

<400> 895  
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgagac cctctcactc 60

A-1937-W0-PCT\_ST25

acctgtgcc a tctccgggga cagtgtctct agcaacagtg ctacttggaa ctggatcagg 120  
cagtcctccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagttgtat 180  
aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240  
cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300  
agagaagtag tggctggccc gaggtgggtc gaccctggg gccagggaac cctggtcacc 360  
gtctcctca 369

<210> 896  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 896

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn  
20 25 30

Ser Ala Thr Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Leu Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro  
100 105 110



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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 897  
<211> 333  
<212> DNA  
<213> Homo sapiens

<400> 897  
cagtctgtgc tgactcaacc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60  
tcttgttctg aaagcaactc cgacatcgga actaatgctg taaactggta ccagcagttc 120  
ccaggaacgg cccccaaatt cctcatctat agtaataata agcggccctc aggagtcctt 180  
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240  
tctgaggatg aggctgatta ttactgtgca acatgggatg acaacctcaa tgggtccgcta 300  
ttcggcggag ggaccaagct gaccgtccta ggt 333

<210> 898  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 898

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Glu Ser Asn Ser Asp Ile Gly Thr Asn  
20 25 30

Ala Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Phe Leu  
35 40 45

Ile Tyr Ser Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln  
65 70 75 80

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Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Asn Leu  
85 90 95

Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 899  
<211> 354  
<212> DNA  
<213> Homo sapiens

<400> 899  
caggtgcaac tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgagggtc 60  
tcctgcaagg cttctggata caccttcacc ggcttctata tgcactgggt gcgacaggcc 120  
cctggacaag ggcttgagtg gatgggatgg atcaaccctg acagtgggtg cacaaactat 180  
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240  
atggagttga gtaggctgag atctgacgac acggccgtat attactgtgc gagagagggt 300  
atagcagtgg ctcttaccta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 900  
<211> 118  
<212> PRT  
<213> Homo sapiens

<400> 900

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Phe  
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

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Gly Trp Ile Asn Pro Asp Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Gly Ile Ala Val Ala Leu Thr Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser  
115

<210> 901  
<211> 330  
<212> DNA  
<213> Homo sapiens

<400> 901  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca 120  
gggaaagccc ctaagctcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
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ggccagggga ccaagctgga gatcaaacga 330

<210> 902  
<211> 109  
<212> PRT  
<213> Homo sapiens

<400> 902

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser 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 Val Ala Ser Ser Leu Gln 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 Ser Tyr Ser Asn Pro Gln  
85 90 95

Glu Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 903

<211> 354

<212> DNA

<213> Homo sapiens

<400> 903

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ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaagaac caactacaac 180

ccgtccctca agagtcgagt caccatatca gtggacacgt ccaagaacca gttctccctg 240

aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag ggacagtggc 300

tggcactttt cttttgatat ctgggaccaa gggacaatgg tcaccgtctc ttca 354

<210> 904

<211> 118

<212> PRT

A-1937-W0-PCT\_ST25

<213> Homo sapiens

<400> 904

Gln Glu Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ser Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Asp Ser Gly Trp His Phe Ser Phe Asp Ile Trp Asp Gln Gly Thr  
100 105 110

Met Val Thr Val Ser Ser  
115

<210> 905

<211> 327

<212> DNA

<213> Homo sapiens

<400> 905

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atcacttgcc gggcaagtca gggcattaga aatgacttag gctggtatca ggagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccggtt tacaaggtgg ggacccatca 180

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aggttcagcg gcagtggatc tgggacagaa ttactctca caatcagcag cctgcagcct 240  
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caagggacca aggtggaaat caaacga 327

<210> 906  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 906

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 Arg Ala Ser Gln Gly Ile Arg Asn Asp  
20 25 30

Leu Gly Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Tyr Ala Ala Ser Gly Leu Gln Gly Gly Asp 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Thr  
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 907  
<211> 357  
<212> DNA  
<213> Homo sapiens

<400> 907

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ccaggcatgg ggctggagtg ggtggcagtt atatggtttg atggaagtaa tgaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagagcga 300  
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<210> 908

<211> 119

<212> PRT

<213> Homo sapiens

<400> 908

Gln Val Gln Leu Val Glu Ser Gly Ala 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

Gly Met His Trp Val Arg Gln Ala Pro Gly Met Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Phe Asp Gly Ser Asn Glu 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 Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Trp Phe Gly Glu Leu Leu Asp Tyr Trp Gly Gln Gly  
100 105 110

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Thr Leu Val Thr Val Ser Ser  
115

<210> 909  
<211> 321  
<212> DNA  
<213> Homo sapiens

<400> 909  
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gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180  
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acacgactgg agattaaacg a 321

<210> 910  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 910

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Tyr Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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



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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 911  
<211> 351  
<212> DNA  
<213> Homo sapiens

<400> 911  
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ccagggaagg ggctggagtg ggtctcaggt attagtgggt gtggtggtag cacatactac 180  
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
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<210> 912  
<211> 117  
<212> PRT  
<213> Homo sapiens

<400> 912

Glu Val His 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 Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

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Ser Gly Ile Ser Gly Gly Gly Gly Ser Thr 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 Asn Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Glu Met Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met  
100 105 110

Val Thr Val Ser Ser  
115

<210> 913  
<211> 330  
<212> DNA  
<213> Homo sapiens

<400> 913  
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atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagagacca 120  
gggaaagccc ctaacctcct gctctttact gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcaacag tctgcaacct 240  
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ggccagggga ccaagctgga gatcaaacga 330

<210> 914  
<211> 109  
<212> PRT  
<213> Homo sapiens

<400> 914

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Asn Leu Leu Leu  
35 40 45

Phe Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Pro  
85 90 95

Glu Ser Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 915  
<211> 354  
<212> DNA  
<213> Homo sapiens

<400> 915  
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acctgcgctg tctatggtgg gtccttcagt ggggtactact ggagctggat ccgccagcct 120  
ccagggaagg ggctggagtg gattggggaa atcaatcctg ttggaagaac caactacaaa 180  
ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240  
aagctgagtt ctgtgaccgc cgcggacacg gctctgtatt actgtgagag ggacaatggg 300  
tggcactatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> 916  
<211> 118  
<212> PRT

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<213> Homo sapiens

<400> 916

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn Pro Val Gly Arg Thr Asn Tyr Lys Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Tyr Cys Ala  
85 90 95

Arg Asp Asn Gly Trp His Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr  
100 105 110

Met Val Thr Val Ser Ser  
115

<210> 917

<211> 333

<212> DNA

<213> Homo sapiens

<400> 917

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca ggtctagtca aagcctcgta tacagtgacg gaaacaccta cttgaattgg 120

tttcagcaga ggccaggccg atctccaagg cgcttaattt ataaggtttc taactgggac 180

A-1937-W0-PCT\_ST25

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgattccac actgataatc 240  
 agcaggggtgg aggctgagga tggtgggggtt tattactaca tgcaaggtag acactggcct 300  
 ctcggcggag ggaccaaggt ggagatcaaa cga 333

<210> 918  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 918

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly  
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser  
 20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Arg Ser  
 35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Ser Thr Leu Ile Ile  
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Tyr Met Gln Gly  
 85 90 95

Thr His Trp Pro Leu Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105 110

<210> 919  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 919

A-1937-W0-PCT\_ST25

cagggacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60  
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cctggacaag ggcttgagtg gatgggttgg atcaacccta acagtgggtg cacaaactat 180  
gcacagaagt ttcggggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240  
atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gactggcggc 300  
agctgggagg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 920

<211> 118

<212> PRT

<213> Homo sapiens

<400> 920

Gln Gly Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Ala Tyr  
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Thr Gly Gly Ser Trp Glu Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

A-1937-W0-PCT\_ST25

Leu Val Thr Val Ser Ser  
115

<210> 921  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 921  
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gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagtag tctgcaacct 240  
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gggacacgac tggagattaa acga 324

<210> 922  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 922

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 Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Arg Leu Gln 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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Thr Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 923  
<211> 321  
<212> DNA  
<213> Homo sapiens

<400> 923  
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca acagaaacca 120  
gggaaagccc ctaaattcct gatctatgct gcatccagtt tacaaagtgg ggtcccttca 180  
aggttttagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agtttcagta ccatcacctt cggccaaggg 300  
acacgactgg agattaaacg a 321

<210> 924  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 924

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45



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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Phe Ser Thr Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 925

<211> 351

<212> DNA

<213> Homo sapiens

<400> 925

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gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gatagaagtg 300

gctggggcctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc a 351

<210> 926

<211> 117

<212> PRT

<213> Homo sapiens

<400> 926

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 Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

A-1937-W0-PCT\_ST25

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Arg 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 Val Tyr Tyr Cys  
85 90 95

Ala Ile Glu Val Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met  
100 105 110

Val Thr Val Ser Ser  
115

<210> 927  
<211> 324  
<212> DNA  
<213> Homo sapiens

<400> 927  
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120  
gggacagccc ctaagttcct gatctatggg gcatcccggt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcacttca ccatcagcag tctgcaacct 240  
gaagactttg caacttacta ctgtcaacag agtgacacta ccccgatcac cttcggccaa 300  
gggacacgac tggagattaa acga 324

<210> 928  
<211> 107  
<212> PRT

A-1937-W0-PCT\_ST25

<213> Homo sapiens

<400> 928

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 Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Gly Ala Ser Arg Leu Gln 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 Ser Asp Thr Thr Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

<210> 929

<211> 354

<212> DNA

<213> Homo sapiens

<400> 929

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| tcctgcaagg cttctggata caccttcacc ggctactata tgcactggat tcgacaggcc  | 120 |
| cctgggcaag ggcttgagtg gctgggatgg atcatcccta acagtgggtgg cacaaattat | 180 |
| gcccagaagt ttcagggcag ggtcaccatg accaggggaca cgtccatcag cacagcctac | 240 |
| atggaactga gcaggctgag atctgacgac acggccgttt attactgtgc gactggcagc  | 300 |

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agctgggagg gatttgacta ctggggccag ggaaccctgg tcaccgtctc ctca

354

<210> 930  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens  
 <400> 930

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15

Ser Val Gln Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr  
 20 25 30

Tyr Met His Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu  
 35 40 45

Gly Trp Ile Ile Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Thr Gly Ser Ser Trp Glu Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser  
 115

<210> 931  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens  
 <400> 931

A-1937-W0-PCT\_ST25

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gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180  
aggttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agtttcagta gcatcacctt cggccaaggg 300  
acacgactgg agattaaacg a 321

<210> 932  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 932

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser His Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Phe Ser Ser Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
100 105

A-1937-W0-PCT\_ST25

<210> 933

<211> 351

<212> DNA

<213> Homo sapiens

<400> 933

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ccagggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatgg acagcctgag agccgaggac acggccgtat ataactgtgc gatagaagtg      300
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<400> 934

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Glu Val His Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
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Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45

Ser Gly Ile Ser Gly Arg Gly Gly Ser Thr 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 Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Asn Cys
          85          90          95

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Val Thr Val Ser Ser  
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Met Gln Pro Leu Gln Thr Pro Leu Thr  
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Gly Gly Gly Ser  
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1 5

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Lys Val Ser Asn Arg Asp Ser  
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| Ser | Ile | Ser | Ser | Ser | Ser | Ser | Tyr | Ile | Tyr | Tyr | Ala | Asp | Ser | Val | Lys |
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Gly

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| Gly | Ile | Ala | Ala | Ala | Gly | Tyr | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
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<400> 953

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| Val | Ile | Trp | Tyr | Asp | Gly | Ser | Asn | Lys | Tyr | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

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<400> 954

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Tyr | Ser | Ser | Ser | Ser | Tyr | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

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Thr Tyr Tyr Xaa Ser  
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Gly

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42

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Thr | Asn | Tyr | Ala | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Ala | Ala | Arg | Ala | Glu | Tyr | Phe | Gln | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

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| Ser | Ile | Ser | Ser | Ser | Ser | Ser | Phe | Ile | Tyr | Tyr | Ala | Asp | Xaa | Val | Lys |
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| Ser | Ile | Ser | Ser | Ser | Ser | Ser | Phe | Ile | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Xaa | Ser | Ser | Ser | Ser | Ser | Phe | Xaa | Tyr | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

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| Ser | Xaa | Ser | Ser | Ser | Ser | Ser | Phe | Xaa | Tyr | Tyr | Xaa | Glu | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Xaa | Ser | Ser | Ser | Ser | Ser | Phe | Xaa | Tyr | Tyr | Xaa | Asp | Xaa | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

Xaa

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Xaa | Xaa | Xaa | Pro | Xaa | Thr | Tyr | Tyr | Tyr | Tyr | Xaa | Xaa | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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| Lys | Ser | Ser | Gln | Asn | Xaa | Leu | Tyr | Ser | Ser | Asn | Asn | Lys | Asn | Tyr | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

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| Val | Ile | Trp | Tyr | Asp | Xaa | Ser | Asn | Lys | Asp | Tyr | Ala | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

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<400> 981

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Tyr | Glu | Gly | Ser | Asn | Lys | Asp | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

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<400> 982

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Trp | Tyr | Asp | Xaa | Ser | Asn | Lys | Asp | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

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<400> 983

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Trp | Tyr | Asp | Xaa | Ser | Asn | Lys | Asp | Tyr | Xaa | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

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<400> 984

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Trp | Tyr | Glu | Xaa | Ser | Asn | Lys | Asp | Tyr | Xaa | Glu | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Gly

<210> 985  
 <211> 13  
 <212> PRT  
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<220>  
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<220>  
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<400> 985

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Arg | Asp | Ser | Tyr | Tyr | His | Tyr | Xaa | Xaa | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |

<210> 986  
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 <212> PRT  
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<400> 986

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Ser | Gln | Ser | Xaa | Xaa | Tyr | Ser | Ser | Asn | Asn | Lys | Asn | Tyr | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 987  
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<220>  
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<400> 987

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Xaa | Ser | Ser | Ser | Asn | Xaa | Xaa | Xaa | Xaa | Tyr | Asn | Xaa | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

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<210> 988  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

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<220>  
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<400> 988

Xaa Asn Asn Asn Arg Pro Ser  
 1 5

<210> 989  
 <211> 11  
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<220>  
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<400> 989

Gln Ser Tyr Asp Xaa Ser Leu Ser Gly Trp Val  
 1 5 10

<210> 990  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 990

Gln Ser Tyr Glu Ser Ser Leu Ser Gly Trp Val  
1 5 10

<210> 991

<211> 11

<212> PRT

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<220>

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<400> 991

Gln Ser Tyr Asp Ser Ser Xaa Ser Xaa Trp Xaa  
1 5 10

<210> 992

<211> 11

<212> PRT

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<400> 992

Gln Ser Tyr Asp Xaa Ser Xaa Ser Xaa Trp Val  
 1 5 10

<210> 993  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

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<400> 993

Gln Ser Tyr Glu Ser Ser Xaa Ser Xaa Trp Val  
 1 5 10

<210> 994  
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<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<222> (3)..(4)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 994

Ser Tyr Xaa Xaa Ser  
1 5

<210> 995

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<221> MISC\_FEATURE

<222> (14)..(14)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 995

Val Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Xaa Val Lys  
1 5 10 15

Gly

<210> 996

<211> 17

<212> PRT

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<220>

<223> Synthetic polypeptide

<400> 996

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Ser | Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 997

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<220>

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<222> (17)..(17)



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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 997

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Ser | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 998

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<220>

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<220>

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 998

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Ser | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Xaa | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

Xaa

<210> 999

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<220>

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<221> MISC\_FEATURE  
 <222> (17)..(17)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 999

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Ser | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Glu | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1000  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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 <222> (14)..(14)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1000

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Thr | Asn | Tyr | Tyr | Tyr | Tyr | Tyr | Ser | Xaa | Xaa | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

<210> 1001  
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 <212> PRT  
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<220>  
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<220>  
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<222> (13)..(13)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1001

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Xaa | Ser | Ser | Ser | Asn | Xaa | Xaa | Xaa | Xaa | Tyr | Asp | Xaa | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

<210> 1002  
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<212> PRT  
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<220>  
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<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> Xaa may be M, G, A, V, I, or L

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<400> 1002

Xaa Asn Xaa His Arg Pro Ser

1 5

<210> 1003  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1003

Gly Gln Ser His Arg Pro Ser  
1 5

<210> 1004  
<211> 7  
<212> PRT  
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<220>  
<223> Synthetic polypeptide

<220>  
<221> MISC\_FEATURE  
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<400> 1004

Xaa Gln Ser His Arg Pro Ser  
1 5

<210> 1005  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<220>  
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<222> (5)..(5)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1005

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Tyr | Asp | Xaa | Ser | Leu | Ser | Gly | Tyr | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1006

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1006

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Glu | Ser | Ser | Leu | Ser | Gly | Tyr | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 1007

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<220>

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<222> (9)..(9)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (11)..(11)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1007

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Gln Ser Tyr Asp Ser Ser Xaa Ser Xaa Tyr Xaa  
1 5 10

<210> 1008  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<400> 1008

Gln Ser Tyr Asp Xaa Ser Xaa Ser Xaa Tyr Xaa  
1 5 10

<210> 1009  
<211> 11  
<212> PRT  
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<220>  
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 <222> (11)..(11)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1009

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Tyr | Glu | Ser | Ser | Xaa | Ser | Xaa | Tyr | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1010  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (3)..(4)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1010

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Asn | Tyr | Xaa | Xaa | Ser |
| 1   |     |     |     | 5   |

<210> 1011  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>



<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (1)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (4)..(4)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (6)..(7)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (12)..(12)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (15)..(15)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1011

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Arg | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1012

<211> 11

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1012

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Tyr | Ser | Ser | Ala | Trp | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1013

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1013

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Tyr | Ser | Ser | Ala | Trp | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1014

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

&lt;400&gt; 1014

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Tyr | Ser | Ser | Xaa | Trp | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

&lt;210&gt; 1015

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (2)..(2)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (6)..(6)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;400&gt; 1015

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Tyr | Ser | Ser | Xaa | Trp | Tyr | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

&lt;210&gt; 1016

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (2)..(2)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(4)

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<222> (7)..(10)

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<222> (13)..(13)

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<400> 1016

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Xaa | Ser | Xaa | Ser | Asn | Xaa | Xaa | Xaa | Xaa | Tyr | Asp | Xaa | His |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |

<210> 1017

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

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<400> 1017

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|-----|-----|-----|-----|-----|
| Asn | Tyr | Xaa | Xaa | Asn |
| 1   |     |     |     | 5   |

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<212> PRT

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<220>

A-1937-WO-PCT\_ST25

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<400> 1018

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Tyr | Ser | Ser | Ala | Trp | Phe | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1019  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1019

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Tyr | Ser | Ser | Ala | Trp | Phe | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

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<220>  
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<220>  
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<400> 1020

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Tyr | Ser | Ser | Xaa | Trp | Phe | Phe | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

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<210> 1021  
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<400> 1021

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Phe | Ser | Ser | Tyr | Xaa | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1022  
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<400> 1022

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ser | Xaa | Thr | Trp | Asn |
| 1   |     |     |     | 5   |     |     |

<210> 1023  
 <211> 18

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<212> PRT  
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<220>  
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<220>  
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<222> (16)..(16)  
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<400> 1023

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Tyr | Gln | Arg | Ser | Lys | Trp | Asn | Asn | Asp | Tyr | Xaa | Xaa | Ser | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Lys Ser

<210> 1024  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (2)..(5)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1024

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Xaa | Pro | Arg | Trp | Phe | Asp | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |

<210> 1025

A-1937-WO-PCT\_ST25

<211> 11  
 <212> PRT  
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<220>  
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 <222> (5)..(5)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
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 <222> (9)..(9)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> Xaa can be any naturally occurring amino acid

<400> 1025

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Ser | Xaa | Thr | Ser | Tyr | Xaa | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1026  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (5)..(5)  
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<400> 1026

Thr Xaa Ser Ser Xaa Gln Ser  
 1 5

<210> 1027  
 <211> 7  
 <212> PRT  
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<220>  
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<400> 1027

Ser Asn Ser Xaa Thr Trp Asn  
 1 5

<210> 1028  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 1028

Ser Gln Ser Ala Thr Trp Asn  
 1 5

<210> 1029  
 <211> 7  
 <212> PRT  
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<220>  
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<220>  
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<400> 1029

Ser Gln Ser Xaa Thr Trp Asn  
 1 5

<210> 1030  
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<220>  
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<220>  
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<400> 1030

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Arg Thr Tyr Tyr Arg Ser Lys Xaa Tyr Asn Asp Tyr Xaa Xaa Ser Xaa  
1 5 10 15

Lys Ser

<210> 1031  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<220>  
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<222> (5)..(5)  
<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>  
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<222> (7)..(8)  
<223> Xaa may independently be M, G, A, V, I, or L

<220>  
<221> MISC\_FEATURE  
<222> (11)..(12)  
<223> Xaa may independently be M, G, A, V, I, or L

<400> 1031

Ser Glu Ser Asn Xaa Asp Xaa Xaa Thr Asn Xaa Xaa Asn  
1 5 10

<210> 1032  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1032

A-1937-WO-PCT\_ST25

Ser Glu Ser Gln Ser Asp Ile Gly Thr Asn Ala Val Asn  
1 5 10

<210> 1033  
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<213> Artificial Sequence

<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1033

Ser Glu Ser Gln Ser Asp Xaa Xaa Thr Asn Xaa Xaa Asn  
1 5 10

<210> 1034  
<211> 11  
<212> PRT  
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<220>  
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<220>  
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A-1937-WO-PCT\_ST25

<220>  
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<220>  
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<400> 1034

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Thr | Trp | Asp | Asp | Asn | Xaa | Asn | Xaa | Pro | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1035  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 1035

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Trp | Asp | Asp | Asn | Leu | Gln | Gly | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1036  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (11)..(11)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1036

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Thr | Trp | Asp | Asp | Asn | Xaa | Gln | Xaa | Pro | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1037  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1037

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| Xaa | Phe | Tyr | Xaa | His |
| 1   |     |     | 5   |     |

<210> 1038  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1038

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Asn | Pro | Asp | Xaa | Gly | Gly | Thr | Asn | Tyr | Ala | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1039

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1039

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Asn | Pro | Glu | Ser | Gly | Gly | Thr | Asn | Tyr | Ala | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1040

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> Synthetic polypeptide

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

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<220>

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<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1040

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Asn | Pro | Asp | Ser | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 1041

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (6)..(8)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE



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<222> (12)..(12)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1041

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Asn | Pro | Asp | Xaa | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 1042

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (12)..(12)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1042

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Asn | Pro | Glu | Ser | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 1043  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (2)..(7)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1043

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Thr | Tyr |
| 1   |     |     |     | 5   |     |     |     |     |

<210> 1044  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

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<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1044

Arg Xaa Ser Gln Ser Xaa Ser Ser Tyr Xaa Asn  
 1 5 10

<210> 1045  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (1)..(1)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1045

Xaa Tyr Tyr Trp Ser  
 1 5

<210> 1046  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (2)..(2)  
 <223> Xaa may independently be M, G, A, V, I, or L

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)

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<223> A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Xaa may independently be M, G, A, V, I, or L

<220>

<221> MISC\_FEATURE

<222> (14)..(14)

<223> Xaa may independently be M, G, A, V, I, or L

<400> 1046

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Asn | Xaa | Ser | Xaa | Arg | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1047

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1047

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Gln | His | Ser | Gly | Arg | Thr | Asn | Tyr | Asn | Pro | Ser | Leu | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1048

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

A-1937-WO-PCT\_ST25

<222> (6)..(6)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (14)..(14)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1048

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Gln | His | Ser | Xaa | Arg | Thr | Asn | Tyr | Asn | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1049

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1049

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Xaa | Gly | Trp | His | Phe | Ser | Phe | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 1050

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1050

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Gly | Trp | His | Phe | Ser | Phe | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

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<210> 1051  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1051

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Xaa | Trp | His | Phe | Ser | Phe | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 1052  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1052

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Xaa | Trp | His | Phe | Ser | Phe | Asp | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 1053  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1053

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Ser | Gln | Xaa | Xaa | Arg | Asn | Asp | Leu | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |

<210> 1054  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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<222> (4)..(5)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
 <221> MISC\_FEATURE  
 <222> (7)..(7)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1054

Xaa Xaa Ser Xaa Xaa Gln Xaa  
 1 5

<210> 1055  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (1)..(1)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1055

Xaa Gln His Asn Ser Tyr Pro Thr Trp Thr  
 1 5 10

<210> 1056  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1056

Leu Gln His Gln Ser Tyr Pro Thr Trp Thr  
 1 5 10



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<210> 1057  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (1)..(1)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1057

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Gln | His | Gln | Ser | Tyr | Pro | Thr | Trp | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |

<210> 1058  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (6)..(6)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<400> 1058

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Phe | Asp | Xaa | Ser | Asn | Glu | Tyr | Tyr | Ala | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Gly

A-1937-WO-PCT\_ST25

<210> 1059  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1059

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Phe | Glu | Gly | Ser | Asn | Glu | Tyr | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1060  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1060

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Phe | Asp | Gly | Ser | Asn | Glu | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1061  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1061

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Trp | Phe | Glu | Gly | Ser | Asn | Glu | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

1 5 10 15

Gly

<210> 1062  
 <211> 16  
 <212> PRT  
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<220>  
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<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<400> 1062

Xaa Trp Phe Asp Xaa Ser Asn Glu Tyr Tyr Xaa Asp Ser Xaa Lys Xaa  
 1 5 10 15

<210> 1063

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<211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (5)..(5)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (7)..(8)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1063

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Trp | Phe | Xaa | Glu | Xaa | Xaa | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

<210> 1064  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (6)..(6)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

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<400> 1064

Arg Xaa Ser Gln Ser Xaa Ser Tyr Tyr Xaa Asn  
1 5 10

<210> 1065

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (7)..(7)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1065

Gln Gln Ser Tyr Ser Ser Xaa Thr  
1 5

<210> 1066

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC\_FEATURE

<222> (14)..(14)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1066

Gly Ile Ser Gly Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Xaa Val Lys  
1 5 10 15

Gly

<210> 1067  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1067

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ser | Gly | Gly | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1068  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1068

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Xaa | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Ser | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1069  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(15)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1069

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Xaa | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Xaa | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1070

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (1)..(2)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

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<222> (4)..(7)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

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<220>

<221> MISC\_FEATURE

<222> (15)..(15)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1070



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Xaa Xaa Ser Xaa Xaa Xaa Xaa Ser Thr Tyr Tyr Xaa Glu Ser Xaa Lys  
1 5 10 15

Xaa

<210> 1071  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
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<220>  
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<222> (2)..(5)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
<221> MISC\_FEATURE  
<222> (8)..(8)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1071

Glu Xaa Xaa Xaa Xaa Phe Asp Xaa  
1 5

<210> 1072  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

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<221> MISC\_FEATURE  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (10)..(10)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1072

Arg Xaa Ser Gln Asn Xaa Ser Ser Tyr Xaa Asn  
 1 5 10

<210> 1073  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <222> (2)..(2)  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1073

Thr Xaa Ser Ser Xaa Gln Ser  
 1 5

<210> 1074  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (14)..(14)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1074

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Asn | Pro | Xaa | Xaa | Arg | Thr | Asn | Tyr | Lys | Pro | Ser | Xaa | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 1075  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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 <222> (10)..(10)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1075

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Asp Asn Xaa Trp His Tyr Xaa Phe Asp Xaa  
1 5 10

<210> 1076  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1076

Asp Gln Gly Trp His Tyr Ala Phe Asp Ile  
1 5 10

<210> 1077  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<222> (7)..(7)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1077

Asp Gln Xaa Trp His Tyr Xaa Phe Asp Xaa  
1 5 10

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<210> 1078  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<220>  
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<220>  
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 <222> (15)..(15)  
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1078

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Xaa | Xaa | Tyr | Ser | Asp | Xaa | Asn | Thr | Tyr | Xaa | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1079  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1079

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Leu | Val | Tyr | Ser | Asp | Gly | Gln | Thr | Tyr | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1080  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1080

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Xaa | Xaa | Tyr | Ser | Asp | Xaa | Gln | Thr | Tyr | Xaa | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1081  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<220>  
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<222> (7)..(7)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1081

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Ser | Asn | Trp | Asp | Xaa |
| 1   |     |     | 5   |     |     |     |

<210> 1082  
<211> 7

<212> PRT  
 <213> Artificial Sequence  
  
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 <400> 1082

Lys Val Ser Asn Trp Glu Ser  
 1 5

<210> 1083  
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 <220>  
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 <400> 1083

Lys Xaa Ser Asn Trp Asp Ser  
 1 5

<210> 1084  
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<222> (7)..(7)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1084

Lys Xaa Ser Asn Trp Asp Xaa  
1 5

<210> 1085

<211> 7

<212> PRT

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<220>

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<400> 1085

Lys Xaa Ser Asn Trp Glu Ser  
1 5

<210> 1086

<211> 7

<212> PRT

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<220>

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<222> (3)..(3)

<223> Each Xaa is independently selected from M, G, A, V, I and L.



<400> 1086

Xaa Gln Xaa Thr His Trp Pro  
1 5

<210> 1087

<211> 5

<212> PRT

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<223> Synthetic polypeptide

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<222> (4)..(4)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1087

Xaa Tyr Tyr Xaa His  
1 5

<210> 1088

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<222> (2)..(2)

<223> Xaa may independently be M, G, A, V, I, or L

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<222> (6)..(6)

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<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<220>

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<222> (7)..(8)

<223> Xaa may independently be M, G, A, V, I, or L

<220>

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<223> Xaa may independently be M, G, A, V, I, or L

<220>

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<222> (17)..(17)

<223> Xaa may independently be M, G, A, V, I, or L

<400> 1088

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Asn | Pro | Asn | Xaa | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1089

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1089

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Asn | Pro | Gln | Ser | Gly | Gly | Thr | Asn | Tyr | Ala | Gln | Lys | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 1090

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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<400> 1090

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Asn | Pro | Gln | Ser | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 1091

<211> 9

<212> PRT

<213> Artificial Sequence

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<220>

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<222> (6)..(6)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1091

Xaa Xaa Ser Trp Glu Xaa Phe Asp Tyr

1 5

<210> 1092

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<222> (5)..(5)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1092

Xaa Xaa Ser Arg Xaa Gln Ser

1 5

<210> 1093

<211> 9

<212> PRT

<213> Artificial Sequence

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Gln Gln Ser Asp Ser Thr Pro Xaa Thr  
 1 5

<210> 1094  
 <211> 8  
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<400> 1094

Gln Gln Ser Phe Ser Thr Xaa Thr  
 1 5

<210> 1095  
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<400> 1095

Gly Ile Ser Gly Ser Gly Gly Ser Arg Tyr Tyr Ala Asp Xaa Val Lys  
 1 5 10 15

Gly

<210> 1096  
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 <212> PRT  
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<400> 1096

Xaa Xaa Ser Xaa Ser Xaa Xaa Ser Arg Tyr Tyr Xaa Asp Ser Xaa Lys

Xaa

<210> 1097

<211> 17

<212> PRT

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<220>

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<222> (17)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1097

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Xaa Xaa Ser Xaa Ser Xaa Xaa Ser Arg Tyr Tyr Xaa Asp Xaa Xaa Lys  
 1 5 10 15

Xaa

<210> 1098  
 <211> 7  
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 <213> Artificial Sequence

<220>  
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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

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<400> 1098

Xaa Xaa Ser Arg Xaa Gln Ser  
 1 5

<210> 1099  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1099



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Gln Gln Ser Asp Xaa Thr Pro Ile Thr  
1 5

<210> 1100  
<211> 9  
<212> PRT  
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<220>  
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<220>  
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<400> 1100

Gln Gln Ser Asp Thr Thr Pro Xaa Thr  
1 5

<210> 1101  
<211> 9  
<212> PRT  
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<220>  
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<222> (5)..(5)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<222> (8)..(8)  
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1101

Gln Gln Ser Asp Xaa Thr Pro Xaa Thr  
1 5

<210> 1102  
 <211> 17  
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<220>  
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<220>  
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 <222> (2)..(3)  
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<220>  
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 <222> (6)..(6)  
 <223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

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<220>  
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<400> 1102

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Xaa | Pro | Asn | Xaa | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Xaa

<210> 1103  
 <211> 17

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1103

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Ile | Pro | Gln | Ser | Gly | Gly | Thr | Asn | Tyr | Ala | Gln | Lys | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Gly

<210> 1104  
<211> 17  
<212> PRT  
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<400> 1104

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Xaa | Pro | Gln | Ser | Xaa | Xaa | Thr | Asn | Tyr | Xaa | Gln | Lys | Phe | Gln |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

1 5 10 15

Xaa

<210> 1105  
 <211> 9  
 <212> PRT  
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<220>  
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<220>  
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<400> 1105

Xaa Ser Ser Trp Glu Xaa Phe Asp Tyr  
 1 5

<210> 1106  
 <211> 11  
 <212> PRT  
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<220>  
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<220>  
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<222> (6)..(6)  
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<400> 1106

Arg Xaa Ser Gln Ser Xaa Ser His Tyr Xaa Asn  
 1 5 10

<210> 1107  
 <211> 8  
 <212> PRT  
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<220>  
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<220>  
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<400> 1107

Gln Gln Ser Phe Ser Ser Xaa Thr  
 1 5

<210> 1108  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

&lt;400&gt; 1108

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ser | Gly | Arg | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

&lt;210&gt; 1109

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1109

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Ser | Gly | Arg | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

&lt;210&gt; 1110

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(2)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(4)

&lt;223&gt; Each Xaa is independently selected from M, G, A, V, I and L.

&lt;220&gt;

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<220>  
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>  
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<400> 1110

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Arg | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1111  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
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<400> 1111

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Arg | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Asp | Xaa | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1112  
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 <212> PRT  
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<220>  
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<220>  
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<220>  
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<220>  
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<400> 1112

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Ser | Xaa | Arg | Xaa | Xaa | Ser | Thr | Tyr | Tyr | Xaa | Glu | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Xaa

<210> 1113  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1113

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asn | Gly | Tyr | Asn | Tyr | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 1114  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1114

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Ser | Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly

<210> 1115  
 <211> 645  
 <212> DNA  
 <213> Homo sapiens

<400> 1115  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gggcattaga aatgacttag gctggatatca ggagaaacca 120  
 gggaaagccc ctaagcgcct gatctatgct gcatccggtt tacaagggtg ggacccatca 180  
 aggttcagcg gcagtggatc tgggacagaa ttactctca caatcagcag cctgcagcct 240  
 gaagattttg caacttatta ctgtctacag cataatagtt accccacgtg gacgttcggc 300  
 caagggacca aggtggaaat caaacgaact gtggctgcac catctgtctt catcttcccg 360  
 ccatctgatg agcagttgaa atctggaact gctagcgttg tgtgcctgct gaataacttc 420  
 tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc 480  
 caggagagtgc tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540  
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600  
 ggcttgagct cgcccgtcac aaagagcttc aacagggggag agtgt 645

<210> 1116  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 1116

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 Arg Ala Ser Gln Gly Ile Arg Asn Asp  
 20 25 30

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Leu Gly Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile  
35 40 45

Tyr Ala Ala Ser Gly Leu Gln Gly Gly Asp 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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Thr  
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  
210 215

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<210> 1117

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 1117

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtgcagc tgggtggagtc cggggcaggc gtggtccagc ctgggaggtc cctgagactc | 60   |
| tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct  | 120  |
| ccaggcatgg ggctggagtg ggtggcagtt atatggtttg atggaagtaa tgaatactat  | 180  |
| gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat  | 240  |
| ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagagcga  | 300  |
| tggttcgggg agttattaga ctactggggc cagggaaccc tggtcaccgt ctctcagcc   | 360  |
| tccaccaagg gcccatcggg cttccccctg gcgccctgct ctagaagcac ctccgagagc  | 420  |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg  | 480  |
| aactcaggcg ctctgaccag cggcgtgcac accttcccag ctgtcctaca gtcctcagga  | 540  |
| ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac  | 600  |
| acatgcaacg tagatcaciaa gccagcaac accaagggtgg acaagacagt tgagcgcaaa | 660  |
| tgttggtgctg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc | 720  |
| ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtgcgtg  | 780  |
| gtggtggacg tgagccacga agaccccag gtccagttca actggtacgt ggacggcgtg   | 840  |
| gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg  | 900  |
| gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgcaag  | 960  |
| gtctccaaca aaggcctccc agcccccatc gagaaaacca tctccaaaac caaagggcag  | 1020 |
| ccccgagaac cacagggtgta caccctgccc ccatcccggg aggagatgac caagaaccag | 1080 |
| gtcagcctga cctgcctggg caaaggcttc taccacagcg acatcgccgt ggagtgggag  | 1140 |
| agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc  | 1200 |
| tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc  | 1260 |

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ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtaaa 1335

<210> 1118

<211> 445

<212> PRT

<213> Homo sapiens

<400> 1118

Gln Val Gln Leu Val Glu Ser Gly Ala 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

Gly Met His Trp Val Arg Gln Ala Pro Gly Met Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Phe Asp Gly Ser Asn Glu 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 Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Arg Trp Phe Gly Glu Leu Leu Asp Tyr 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 Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu  
130 135 140

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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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
195 200 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln  
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 Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu  
290 295 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
325 330 335

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Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
340 345 350

Arg Glu Glu Met 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 Met 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 Lys  
435 440 445

<210> 1119

<211> 660

<212> DNA

<213> Homo sapiens

<400> 1119

gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagtca gaatatatta tacagctcca acaataaaaa ctacttagct 120

tggtagcagc agaaaccagg acagcctcct agcctgctca tttactgggc atctaccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

ctcagcagcc tgcaggctga agatgtggca gtttatttct gtcaacaata ttatagtatt 300

ccgtggacgt tcggccaagg gaccaagggtg gaaatcaaac gaactgtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgctag cgttgtgtgc 420

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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
 ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1120

<211> 220

<212> PRT

<213> Homo sapiens

<400> 1120

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Ile Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
 35 40 45

Pro Pro Ser Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Leu Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln  
 85 90 95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125



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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1121

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 1121

cagggtgcagt tgggtggagtc tggggggaggc gtgggtccagc ctgggagggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt acttatggca tgcactgggt cgcagggt 120

ccaggcaagg ggctggagtg ggtggcagtt atttggatg atggaagtaa taaagactat 180

gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgttgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaggaa 300

agggattcgt actaccatta cgggatggac gtctggggcc aagggaccac ggtcaccgtc 360

tcttcagcct ccaccaaggg cccatcggtc ttccccctgg cgccctgctc tagaagcacc 420

tccgagagca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc tctgaccagc ggcgtgcaca ctttcccagc tgtcctacag 540

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcaa cttcggcacc  | 600  |
| cagacctaca catgcaacgt agatcacaag cccagcaaca ccaaggtgga caagacagtt  | 660  |
| gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc  | 780  |
| acgtgcgtgg tgggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg  | 900  |
| ttccgtgtgg tcagcgtcct caccgttgtg caccaggact ggctgaacgg caaggagtac  | 960  |
| aagtgcgaagg tctccaacaa aggccctcca gccccatcg agaaaaccat ctccaaaacc  | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct accccagcga catcgccgtg | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac  | 1200 |
| tccgacggct ctttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg taaa                                         | 1344 |

<210> 1122

<211> 448

<212> PRT

<213> Homo sapiens

<400> 1122

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Thr | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

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Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asp Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Arg Asp Thr Leu Tyr  
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 Glu Glu Arg Asp Ser Tyr Tyr His Tyr Gly Met Asp Val Trp  
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro  
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys  
210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser  
225 230 235 240

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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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val  
290 295 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Met 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

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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440 445

<210> 1123  
 <211> 651  
 <212> DNA  
 <213> Homo sapiens

<400> 1123  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcggctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 cttccaggaa cagcccccaa actcctcatc tatggtaata gtcacgcggc ctcagggatc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300  
 gtcttcggaa ctgggaccaa ggtcaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1124  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 1124

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Gly Ser Asn Ile Gly Ala Gly  
 20 25 30

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Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Gly Asn Ser His Arg Pro Ser Gly Ile Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

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<210> 1125

<211> 1338

<212> DNA

<213> Homo sapiens

<400> 1125

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtgcagc tgttggaatc tgggggaggc ttggtacagc cggggggggtc cctgagactc  | 60   |
| tcctgtgcag cctctggatt cacctttagc aactatgcca tgaactgggt ccgccaggct   | 120  |
| ccagggaagg ggctggagtg ggtctcagtc attagtggtc gtgggtggtag tacatactat  | 180  |
| gcagactccg tgaagggccg gttcaccatc tccagagaca attccaggaa cacgctgtat   | 240  |
| ctgcaaatga acagcctgag agccgaggac acggccatat attactgtgc gaaagacggg   | 300  |
| tatagcagtg cctggttctt tgactactgg ggccaggga cctgatcac cgtctcctca     | 360  |
| gcctccacca agggcccatc ggtcttcccc ctggcgccct gctctagaag cacctccgag   | 420  |
| agcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 480  |
| tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca   | 540  |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcaacttcgg caccagacc   | 600  |
| tacacatgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc   | 660  |
| aaatgttgtg tcgagtgtcc accgtgtcca gcaccacctg tggcaggacc gtcagtcttc   | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc    | 780  |
| gtgggtgggtg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc  | 840  |
| gtggaggtgc ataatgcaa gacaaagcca cgggaggagc agttcaacag cacgttccgt    | 900  |
| gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc   | 960  |
| aaggtctcca acaaaggcct cccagcccc atcgagaaaa ccatctccaa aaccaaaggg    | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcg cgtggagtgg     | 1140 |
| gagagcaatg ggagccgga gaacaactac aagaccacac ctcccatgct ggactccgac    | 1200 |
| ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac  | 1260 |

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gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 1126

<211> 446

<212> PRT

<213> Homo sapiens

<400> 1126

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 Asn Tyr  
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Val Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Lys Asp Gly Tyr Ser Ser Ala Trp Phe Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Ile Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
130 135 140



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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335

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Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met 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 Met 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 Lys  
435 440 445

<210> 1127

<211> 657

<212> DNA

<213> Homo sapiens

<400> 1127

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tacctgcaga agccagggca gtctccacag ctctgatct atttgggttc tagtcgggcc 180

tccgggggtcc ctgacagggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttgggggtt tattactgca tgcaacctct acaaactccg 300

ctcactttcg gcggagggac caaggtggag atcaaacgaa ctgtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgctagcgt tgtgtgcctg 420

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ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480  
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agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600  
gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 1128

<211> 219

<212> PRT

<213> Homo sapiens

<400> 1128

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser  
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Ser Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Pro  
85 90 95

Leu Gln Thr Pro Leu Thr 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

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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> 1129

<211> 1353

<212> DNA

<213> Homo sapiens

<400> 1129

gaggtgcagc tgggtggagtc tgggggaggc ctggtcaagc ctgggggggtc cctgagactc 60

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ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtagttt catatactac 180

gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtat attactgtgc gagagaccgt 300

atagcagcac ctggtacata ctactactac ggtatggacg tctggggcca agggaccacg 360

gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc gccctgctct 420

agaagcacct ccgagagcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgct ctgaccagcg gcgtgcacac cttcccagct 540

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gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcaac 600  
 ttcggcaccc agacctacac atgcaacgta gatcacaagc ccagcaacac caaggtggac 660  
 aagacagttg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc acctgtggca 720  
 ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780  
 cctgagggtca cgtgcgtggt ggtggacgtg agccacgaag accccgaggt ccagttcaac 840  
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccacggga ggagcagttc 900  
 aacagcacgt tccgtgtggt cagcgtcctc accgttgtgc accaggactg gctgaacggc 960  
 aaggagtaca agtgcaaggt ctccaacaaa ggctcccag ccccatcga gaaaaccatc 1020  
 tccaaaacca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag 1080  
 gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta ccccagcgac 1140  
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 atgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260  
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 acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 1130

<211> 451

<212> PRT

<213> Homo sapiens

<400> 1130

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Phe Ser Thr Tyr  
 20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Ser Ile Ser Ser Ser Ser Ser Phe Ile Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
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 Arg Ile Ala Ala Pro Gly Thr Tyr Tyr Tyr Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser  
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys  
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu  
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala  
225 230 235 240

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe  
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Lys  
 450

<210> 1131  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<400> 1131  
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 gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180  
 aggttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagtt ccatcacctt cggccaaggg 300  
 acacgactgg agattaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360  
 gatgagcagt tgaaatctgg aactgctagc gttgtgtgcc tgctgaataa cttctatccc 420  
 agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag 480  
 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540  
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600  
 agctcgcccc tcacaaagag cttcaacagg ggagagtgt 639

<210> 1132  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 1132

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15



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Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Tyr Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Ser Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
195 200 205

Asn Arg Gly Glu Cys  
210

<210> 1133

<211> 1329

<212> DNA

<213> Homo sapiens

<400> 1133

|                                                                      |      |
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| tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct    | 120  |
| ccagggaagg ggctggagtg ggtctcaggt attagtgtg gtggtggtag cacatactac     | 180  |
| gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat    | 240  |
| ctgcaaatga acagcctgag agccgagaac acggccgtat attactgtgc gatagaaatg    | 300  |
| gctggggctt ttgatattctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc  | 360  |
| aaggggcccat cggctcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg  | 420  |
| gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca  | 480  |
| ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac    | 540  |
| tccctcagca gcgtgggtgac cgtgccctcc agcaacttcg gcaccagac ctacacatgc    | 600  |
| aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt    | 660  |
| gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtcct cctcttcccc    | 720  |
| ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtgggtggtg   | 780  |
| gacgtgagcc acgaagaccc cgagggtccag ttcaactgggt acgtggacgg cgtggagggtg | 840  |
| cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtggtcagc    | 900  |
| gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc    | 960  |
| aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga    | 1020 |
| gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc     | 1080 |
| ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat   | 1140 |

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gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc 1200  
 ttctcttaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260  
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1320  
 ccgggtaaa 1329

<210> 1134  
 <211> 443  
 <212> PRT  
 <213> Homo sapiens

<400> 1134

Glu Val His 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 Tyr  
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Ser Gly Gly Gly Gly Ser Thr 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 Asn Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Glu Met Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

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Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn  
180 185 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn  
195 200 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro  
210 215 220

Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln 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 Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val  
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
305 310 315 320

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Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
340 345 350

Glu Met 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 Met 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 Lys  
435 440

<210> 1135

<211> 648

<212> DNA

<213> Homo sapiens

<400> 1135

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

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gggaaagccc ctaacctcct gctctttact gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcaacag tctgcaacct 240

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ggccagggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc      360
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ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac      480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc      540
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat      600
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<210> 1136

<211> 216

<212> PRT

<213> Homo sapiens

<400> 1136

```

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 Arg Ala Ser Gln Asn Ile Ser Ser Tyr
20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Asn Leu Leu Leu
35           40           45

```

```

Phe Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Pro
85           90           95

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```

Glu Ser Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
100          105          110

```

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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> 1137

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 1137

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acctgcgctg tctatgggtgg gtccttcagt ggggtactact ggagctggat ccgccagcct 120

ccagggaagg ggctggagtg gattggggaa atcaatcctg ttggaagaac caactacaaa 180

ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aagctgagtt ctgtgaccgc cgcggacacg gctctgtatt actgtgcgag ggacaatggg 300

tggcactatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttcagcctcc 360

accaagggcc catcggctctt ccccttggcg ccctgtctta gaagcacctc cgagagcaca 420

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gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac      480
tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc      540
tactccctca gcagcgtggg gaccgtgccc tccagcaact tcggcaccca gacctacaca      600
tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaattg      660
tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc      720
ccccaaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac gtgcgtgggtg      780
gtggacgtga gccacgaaga ccccgagggtc cagttcaact ggtacgtgga cggcgtggag      840
gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc      900
agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc      960
tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc     1020
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc     1080
agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc     1140
aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc     1200
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc     1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg     1320
tctccgggta aa                                                                1332

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<210> 1138

<211> 444

<212> PRT

<213> Homo sapiens

<400> 1138

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Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1           5           10           15

```

```

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
      20           25           30

```



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Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn Pro Val Gly Arg Thr Asn Tyr Lys Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Tyr Cys Ala  
85 90 95

Arg Asp Asn Gly Trp His Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr  
100 105 110

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220

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Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

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Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 435 440

<210> 1139  
 <211> 651  
 <212> DNA  
 <213> Homo sapiens

<400> 1139  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagctc caacatcggg gcagggttata atgttcactg gtaccagcag 120  
 cttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggactc 240  
 cagactgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540  
 agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1140  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 1140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

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Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1141  
<211> 1347  
<212> DNA  
<213> Homo sapiens

<400> 1141  
gaaatacagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactt 60  
tcctgtgtag cctctggatt cacctttagc agctatgtca tgagctgggt ccgccaggct 120  
ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtgtag cacatactac 180  
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cacgctgtat 240  
ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgt 300  
accaactatt actactacta ctccggtatg gacgtctggg gccaaaggac cacggtcacc 360  
gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc 420  
acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480  
acggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta 540  
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc 600  
acccagacct acacatgcaa cgtagatcac aagcccagca acaccaagggt ggacaagaca 660  
gttgagcgca aatgttgtgt cgagtgtcca ccgtgtccag caccacctgt ggaggaccg 720  
tcagtcttcc tcttcccccc aaaacccaag gacacctca tgatctccc gacctctgag 780  
gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtccagtt caactggtag 840  
gtggacggcg tggagggtgca taatgccaag acaaagccac gggaggagca gttcaacagc 900  
acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag 960  
tacaagtgca aggtctccaa caaaggcctc ccagcccca tcgagaaaac catctccaaa 1020  
accaaagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggaggagatg 1080  
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140

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gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1200  
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260  
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320  
aagagcctct ccctgtctcc gggtaaa 1347

<210> 1142

<211> 449

<212> PRT

<213> Homo sapiens

<400> 1142

Glu Ile Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Thr Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Gly Gly Thr Asn Tyr Tyr Tyr Tyr Tyr Ser Gly Met Asp Val  
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

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Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val  
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315 320

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Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys  
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met 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 Met 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

Lys

<210> 1143

<211> 639

<212> DNA

<213> Homo sapiens

<400> 1143

gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca acagaaacca 120

gggaaagccc ctaaattcct gatctatgct gcatccagtt tacaaagtgg ggtcccttca 180



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aggtttagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agtttcagta ccatcacctt cggccaaggg 300  
acacgactgg agattaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360  
gatgagcagt tgaaatctgg aactgctagc gttgtgtgcc tgctgaataa cttctatccc 420  
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag 480  
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540  
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600  
agctcgccccg tcacaaagag cttcaacagg ggagagtgt 639

<210> 1144

<211> 213

<212> PRT

<213> Homo sapiens

<400> 1144

Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Phe Ser Thr Ile Thr  
85 90 95

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Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
195 200 205

Asn Arg Gly Glu Cys  
210

<210> 1145

<211> 1329

<212> DNA

<213> Homo sapiens

<400> 1145

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttagt agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtgtag cagatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gatagaagtg 300

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gctggggctt ttgatattctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc | 360  |
| aagggcccat cggctcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg  | 420  |
| gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca | 480  |
| ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac   | 540  |
| tccctcagca gcgtgggtgac cgtgccctcc agcaacttcg gcacccagac ctacacatgc  | 600  |
| aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt   | 660  |
| gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtcctt cctcttcccc  | 720  |
| ccaaaaccca aggacacctt catgatctcc cggacccctg aggtcacgtg cgtgggtggg   | 780  |
| gacgtgagcc acgaagaccc cgaggtccag ttcaactggg acgtggacgg cgtggagggtg  | 840  |
| cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtgggtcagc  | 900  |
| gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc   | 960  |
| aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga   | 1020 |
| gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc   | 1080 |
| ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat  | 1140 |
| gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc   | 1200 |
| ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca  | 1260 |
| tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct   | 1320 |
| ccgggtaaa                                                           | 1329 |

<210> 1146

<211> 443

<212> PRT

<213> Homo sapiens

<400> 1146

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Leu | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Arg 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 Val Tyr Tyr Cys  
85 90 95

Ala Ile Glu Val Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met  
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn  
180 185 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn  
195 200 205

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Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro  
210 215 220

Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln 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 Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val  
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
340 345 350

Glu Met 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 Met Leu Asp Ser Asp Gly Ser Phe  
385 390 395 400

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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 Lys  
 435 440

<210> 1147

<211> 642

<212> DNA

<213> Homo sapiens

<400> 1147

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc gggcaagtca gagcgttacc agctatttaa attggtatca gcagaaacca  | 120 |
| gggaaagccc ctaaactcct gatctatact gcatccagtt tgcaaagtgg gatcccatca  | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct  | 240 |
| gaagattttg caacttactt ctgtcaacag agttacagta cccctcgcag ttttggccag  | 300 |
| gggaccaagc tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca  | 360 |
| tctgatgagc agttgaaatc tggaactgct agcgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                     | 642 |

<210> 1148

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1148

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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 Arg Ala Ser Gln Ser Val Thr 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 Thr Ala Ser Ser Leu Gln Ser Gly Ile 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 Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

A-1937-W0-PCT\_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1149

<211> 1347

<212> DNA

<213> Homo sapiens

<400> 1149

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtagcgc tgcagcagtc aggtccagga ctggtgaagc cctcgagac cctctcactc   | 60   |
| acctgtgcca tctccgggga cagtgtctct agcaacagtg ctacttggaa ctggatcagg  | 120  |
| cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagttgtat   | 180  |
| aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac  | 240  |
| cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca  | 300  |
| agagaagtag tggctggccc gaggtgggtc gaccctggg gccagggaac cctggtcacc   | 360  |
| gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc   | 420  |
| acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg  | 480  |
| acgggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta | 540  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc  | 600  |
| accagacct acacatgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca   | 660  |
| gttgagcgca aatgttgtgt cgagtggcca ccgtgcccag caccacctgt ggcaggaccg  | 720  |
| tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctccc gaccctgag    | 780  |
| gtcacgtgcg tgggtgggga cgtgagccac gaagaccccg aggtccagtt caactggtac  | 840  |
| gtggacggcg tggaggtgca taatgccaag acaaagccac gggaggagca gttcaacagc  | 900  |
| acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag  | 960  |
| tacaagtgca aggtctccaa caaaggcctc ccagcccca tcgagaaaac catctccaaa   | 1020 |



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accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080  
 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140  
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1200  
 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260  
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320  
 aagagcctct ccctgtctcc gggtaaa 1347

<210> 1150

<211> 449

<212> PRT

<213> Homo sapiens

<400> 1150

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn  
 20 25 30

Ser Ala Thr Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Leu Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro  
 100 105 110

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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val  
290 295 300

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Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys  
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met 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 Met 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

Lys

<210> 1151

<211> 648

<212> DNA

<213> Homo sapiens

<400> 1151

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

60

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```

atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta atcctcagga gtgcagtttt      300
ggccagggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc      360
ccgccatctg atgagcagtt gaaatctgga actgctagcg ttgtgtgcct gctgaataac      420
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac      480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc      540
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat      600
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt      648

```

<210> 1152

<211> 216

<212> PRT

<213> Homo sapiens

<400> 1152

```

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 Arg Ala Ser Gln Ser Ile Ser 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 Val Ala Ser Ser Leu Gln 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

```

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Gln  
85 90 95

Glu Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val  
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
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> 1153

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 1153

caggagcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tctatggtgg gtccttcagt gggtactact ggagctggat ccgccagccc 120

ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaagaac caactacaac 180

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| ccgtccctca agagtcgagt caccatatca gtggacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc cgcggaacacg gctgtgtatt actgtgagag ggacagtggc | 300  |
| tggcactttt cttttgatata ctgggaccaa gggacaatgg tcaccgtctc ttcagcctcc | 360  |
| accaagggcc catcggctct cccctggcg ccctgctcta gaagcacctc cgagagcaca   | 420  |
| gcggcccttg gctgcctggc caaggactac ttccccgaac cggtagcggg gtcgtggaac  | 480  |
| tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc  | 540  |
| tactccctca gcagcgtggg gaccgtgccc tccagcaact tcggcaccca gacctacaca  | 600  |
| tgcaacgtag atcacaagcc cagcaacacc aaggtaggaca agacagttga gcgcaaatgt | 660  |
| tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc  | 720  |
| ccccaaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac gtgcgtgggtg | 780  |
| gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag  | 840  |
| gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt cctgtgtggc  | 900  |
| agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc  | 960  |
| tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc  | 1020 |
| cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc  | 1080 |
| agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc | 1140 |
| aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc   | 1200 |
| ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc  | 1260 |
| tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg  | 1320 |
| tctccgggta aa                                                      | 1332 |

<210> 1154

<211> 444

<212> PRT

<213> Homo sapiens

<400> 1154

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Gln Glu Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ser Gly Arg Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Asp Ser Gly Trp His Phe Ser Phe Asp Ile Trp Asp Gln Gly Thr  
100 105 110

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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

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Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380



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Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
435 440

<210> 1155

<211> 651

<212> DNA

<213> Homo sapiens

<400> 1155

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc  | 60  |
| tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag  | 120 |
| cttccaggaa cagcccccaa actcctcatc tatggtaaca gccatcggcc ctcaggggtc  | 180 |
| cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc  | 240 |
| caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttat | 300 |
| gtcttcggaa ctgggaccaa ggtcaccgtc ctaggtcagc ccaaggctgc cccctcggtc  | 360 |
| actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc  | 420 |
| ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc  | 480 |
| aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc  | 540 |
| agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc   | 600 |
| acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a           | 651 |

<210> 1156

<211> 217

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<212> PRT

<213> Homo sapiens

<400> 1156

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Tyr Gly Asn Ser His Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

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Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
 195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
 210 215

<210> 1157

<211> 1338

<212> DNA

<213> Homo sapiens

<400> 1157

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctaagactc  | 60  |
| tcctgtgcag cctctggatt cacctttagc aactatgcca tgagctgggt ccgccaggct   | 120 |
| ccagggaagg ggctgcagtg ggtctcagtt attagtggta gaggtggtag cacatactac   | 180 |
| gcagactccg tgaagggccg gttcaccatc tccagagaca actccaagaa cacgctgtat   | 240 |
| ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagacggg   | 300 |
| tatagcagtg cctgggtactt tgactactgg ggccaggga ccctgggtcac cgtctcctca  | 360 |
| gcctccacca agggcccatc ggtcttcccc ctggcgccct gctctagaag cacctccgag   | 420 |
| agcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 480 |
| tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca   | 540 |
| ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcaacttcgg cacccagacc  | 600 |
| tacacatgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc   | 660 |
| aaatgttgtg tcgagtgtcc accgtgtcca gcaccacctg tggcaggacc gtcagtcttc   | 720 |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggacacgtgc    | 780 |
| gtgggtgggtg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc  | 840 |
| gtggagggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt  | 900 |

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```

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc      960
aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg      1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac      1080
caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcg cgtggagtgg      1140
gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac      1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac      1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc      1320
tccctgtctc cgggtaaa                                     1338

```

<210> 1158

<211> 446

<212> PRT

<213> Homo sapiens

<400> 1158

```

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 Asn Tyr
20           25           30

```

```

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gln Trp Val
35           40           45

```

```

Ser Val Ile Ser Gly Arg Gly Gly Ser Thr 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 Val Tyr Tyr Cys
85           90           95

```

A-1937-W0-PCT\_ST25

Ala Lys Asp Gly Tyr Ser Ser Ala Trp Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val  
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
275 280 285

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Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val  
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met 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 Met 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 Lys  
435 440 445

<210> 1159

<211> 651

<212> DNA

<213> Homo sapiens

<400> 1159

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc

60

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```

tcctgcactg ggagcagctc caacatcggg gcaggttata atgttcactg gtaccagcag      120
cttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggactc      240
cagactgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttgg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc      540
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a                651

```

<210> 1160

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1160

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20           25           30

```

```

Tyr Asn Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
          35           40           45

```

```

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50           55           60

```

```

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65           70           75           80

```

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Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1161

<211> 1347

<212> DNA

<213> Homo sapiens

<400> 1161

gaaatacagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactt 60

tcctgtgtag cctctggatt cacctttagc agctatgtca tgagctgggt cgcaggct 120

ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtggtag cacatactac 180



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cacgctgtat  | 240  |
| ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgt  | 300  |
| accaactatt actactacta ctccggtatg gacgtctggg gccaaaggac cacggtcacc  | 360  |
| gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc   | 420  |
| acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccgggtg | 480  |
| acgggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta | 540  |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc  | 600  |
| accagagact acacatgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca  | 660  |
| gttgagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggaggaccg   | 720  |
| tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag   | 780  |
| gtcacgtgcg tgggtgtgga cgtgagccac gaagaccccg aggtccagtt caactggtac  | 840  |
| gtggacggcg tggagggtgca taatgccaa acaaagccac gggaggagca gttcaacagc  | 900  |
| acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag  | 960  |
| tacaagtgca aggtctccaa caaaggcctc ccagcccca tcgagaaaac catctccaaa   | 1020 |
| accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg  | 1080 |
| accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc  | 1140 |
| gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg  | 1200 |
| gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag  | 1260 |
| caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag  | 1320 |
| aagagcctct ccctgtctcc gggtaaa                                      | 1347 |

<210> 1162

<211> 449

<212> PRT

<213> Homo sapiens

<400> 1162

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Glu Ile Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Val Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Thr Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Gly Gly Thr Asn Tyr Tyr Tyr Tyr Tyr Ser Gly Met Asp Val  
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
180 185 190

A-1937-W0-PCT\_ST25

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val  
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys  
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met 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

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Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met 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

Lys

<210> 1163

<211> 642

<212> DNA

<213> Homo sapiens

<400> 1163

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc gggcaagtca gagctttagc agttatttaa attggtatca gcagaaacca  | 120 |
| gggaaagccc ctgagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca  | 180 |
| aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct   | 240 |
| gaagattttg caagttactt ctgtcaacag agttacagta cccctcgag ttttggccag   | 300 |
| gggaccaagc tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcga  | 360 |
| tctgatgagc agttgaaatc tggaactgct agcgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                     | 642 |

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<210> 1164

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1164

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 Arg Ala Ser Gln Ser Phe Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1165

<211> 1347

<212> DNA

<213> Homo sapiens

<400> 1165

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| caggtacaac tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc  | 60  |
| acctgtgccca tctccgggga cagtgtctct agcagcagtg ctacttggaa ctggatcagg | 120 |
| cagtcccat cgagaggcct tgagtggctg ggaaggacat accagaggtc caagtggaat   | 180 |
| aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaggaac  | 240 |
| cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca  | 300 |
| agagaagtag tggctggccc gaggtggttc gaccttggg gccagggaac cctggtcacc   | 360 |
| gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc   | 420 |
| acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg  | 480 |
| acgggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta | 540 |
| cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc  | 600 |
| accagacct acacatgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca   | 660 |
| gttgagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggaggaccg   | 720 |
| tcagtcttcc tcttcccccc aaaacccaag gacacctca tgatctcccg gaccttgag    | 780 |

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gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtccagtt caactggtac 840  
 gtggacggcg tggaggtgca taatgccaag acaaagccac gggaggagca gttcaacagc 900  
 acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag 960  
 tacaagtgca aggtctccaa caaaggcctc ccagcccca tcgagaaaac catctccaaa 1020  
 accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080  
 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140  
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1200  
 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260  
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320  
 aagagcctct ccctgtctcc gggtaaa 1347

<210> 1166

<211> 449

<212> PRT

<213> Homo sapiens

<400> 1166

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Ser  
 20 25 30

Ser Ala Thr Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu  
 35 40 45

Trp Leu Gly Arg Thr Tyr Gln Arg Ser Lys Trp Asn Asn Asp Tyr Ala  
 50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Arg Asn  
 65 70 75 80

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Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro  
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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



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Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val  
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu  
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys  
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met 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 Met 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

Lys

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<210> 1167  
 <211> 648  
 <212> DNA  
 <213> Homo sapiens

<400> 1167  
 cagtctgtgc tgactcaacc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60  
 tcttgttctg aaagcaactc cgacatcgga actaatgctg taaactggta ccagcagttc 120  
 ccaggaacgg cccccaaatt cctcatctat agtaataata agcggccctc aggagtccct 180  
 gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240  
 tctgaggatg aggctgatta ttactgtgca acatgggatg acaacctcaa tgggtccgta 300  
 ttcggcggag ggaccaagct gaccgtccta ggtcagccca aggctgcccc ctcggtcact 360  
 ctgttcccg cctctagcga ggagcttcaa gccacaagg ccacactggg gtgtctcata 420  
 agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtaag 480  
 gcgggagtg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540  
 tatctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 600  
 catgaaggga gcaccgtgga gaagacagtg gccctacag aatgttca 648

<210> 1168  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 1168

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Glu Ser Asn Ser Asp Ile Gly Thr Asn  
 20 25 30

Ala Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Phe Leu  
 35 40 45

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Ile Tyr Ser Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Asn Leu  
85 90 95

Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln  
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys  
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1169

<211> 1332

<212> DNA

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&lt;213&gt; Homo sapiens

&lt;400&gt; 1169

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtgcaac tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgagggtc | 60   |
| tcctgcaagg cttctggata caccttcacc ggcttctata tgcactgggt gcgacaggcc  | 120  |
| cctggacaag ggcttgagt gatgggatgg atcaaccctg acagtgggtg cacaaactat   | 180  |
| gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac  | 240  |
| atggagttga gtaggctgag atctgacgac acggccgtat attactgtgc gagagagggt  | 300  |
| atagcagtgg ctcttaccta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggcttt cccctggcg ccctgtctta gaagcacctc cgagagcaca   | 420  |
| gcggccctgg gctgcctgg caaggactac ttccccgaac cggtgacggt gtcgtggaac   | 480  |
| tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc  | 540  |
| tactccctca gcagcgtgg gaccgtgccc tccagcaact tcggcaccca gacctacaca   | 600  |
| tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaagt  | 660  |
| tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc  | 720  |
| ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgagggtcac gtgcgtgggtg | 780  |
| gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag  | 840  |
| gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc  | 900  |
| agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc  | 960  |
| tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc  | 1020 |
| cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc  | 1080 |
| agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc | 1140 |
| aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc   | 1200 |
| ttcttctct acagcaagct caccgtggac aagagcaggt ggacgcaggg gaacgtcttc   | 1260 |
| tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg  | 1320 |
| tctccgggta aa                                                      | 1332 |

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<210> 1170  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

<400> 1170

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Phe  
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45

Gly Trp Ile Asn Pro Asp Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Glu Gly Ile Ala Val Ala Leu Thr 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 Cys Ser Arg Ser Thr Ser Glu Ser 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

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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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

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Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
435 440

<210> 1171

<211> 660

<212> DNA

<213> Homo sapiens

<400> 1171

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatcgtga tgacccagtc tccagactcc ctgactgtgt ctctgggcga gggggccacc  | 60  |
| atcaactgca agtccagcca gagggtttta tacagctcca acaataaaaa ctacttagct  | 120 |
| tggtagcagc agaaaccagg acagcctcct agcctgctca tttactgggc atctaccgg   | 180 |
| gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc  | 240 |
| atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtatt  | 300 |
| ccgtggacgt tcggccaagg gaccaagggtg gaaatcaaac gaactgtggc tgcaccatct | 360 |
| gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgctag cgttgtgtgc  | 420 |
| ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc | 480 |
| caatcgggta actcccagga gagggtcaca gagcaggaca gcaaggacag cacctacagc  | 540 |

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ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1172

<211> 220

<212> PRT

<213> Homo sapiens

<400> 1172

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly  
1 5 10 15

Glu Gly Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Ser Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140



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Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1173

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 1173

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc | 60  |
| tcctgtgcag cgtctggatt catcttcagt agttatggca tgcactgggt ccgccaggct  | 120 |
| ccaggcaagg ggctggagtg ggtggcagtt atttggatatg atggaagtaa taaagactat | 180 |
| gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgttgtat  | 240 |
| ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaggaa  | 300 |
| agggattcct actaccacta cggtatggac gtctggggcc aagggaccac ggtcaccgtc  | 360 |
| tcttcagcct ccaccaaggg cccatcggtc ttccccctgg cgccctgctc tagaagcacc  | 420 |
| tccgagagca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 480 |
| gtgtcgtgga actcaggcgc tctgaccagc ggcgtgcaca ctttcccagc tgtcctacag  | 540 |
| tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcaa cttcggcacc  | 600 |
| cagacctaca catgcaacgt agatcacaag cccagcaaca ccaaggtgga caagacagtt  | 660 |

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gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acgtgcgtgg tgggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 900  
ttccgtgtgg tcagcgtcct caccgttgtg caccaggact ggctgaacgg caaggagtac 960  
aagtgcaagg tctccaacaa aggcctccca gccccatcg agaaaacat ctccaaaacc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080  
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1140  
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 1200  
tccgacggct ctttcttct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg taaa 1344

<210> 1174

<211> 448

<212> PRT

<213> Homo sapiens

<400> 1174

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 Ile Phe Ser Ser Tyr  
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asp Tyr Ala Asp Ser Val  
50 55 60

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Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Arg Asp Thr Leu Tyr  
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 Glu Glu Arg Asp Ser Tyr Tyr His Tyr Gly Met Asp Val Trp  
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro  
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys  
210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly 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

A-1937-W0-PCT\_ST25

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val  
290 295 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Met 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 Lys  
435 440 445

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<210> 1175  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<400> 1175  
 gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattagc cactatttaa attggtatca gcagaaacca 120  
 gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180  
 aggttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agtttcagta gcatcacctt cggccaaggg 300  
 acacgactgg agattaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360  
 gatgagcagt tgaaatctgg aactgctagc gttgtgtgcc tgctgaataa cttctatccc 420  
 agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480  
 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540  
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600  
 agctcgcccc tcacaaagag cttcaacagg ggagagtgt 639

<210> 1176  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 1176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Ile | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Ser | Ile | Ser | His | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Phe | Leu | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |

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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Phe Ser Ser Ile Thr  
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
195 200 205

Asn Arg Gly Glu Cys  
210

<210> 1177

<211> 1329

<212> DNA

## A-1937-W0-PCT\_ST25

&lt;213&gt; Homo sapiens

&lt;400&gt; 1177

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtgcacc tgttggagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc  | 60   |
| tcttgtgcag cctctggatt cacctttagc agttatgcca tgagttgggt cgcaggtt     | 120  |
| ccagggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac   | 180  |
| gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   | 240  |
| ctgcaaatgg acagcctgag agccgaggac acggccgtat ataactgtgc gatagaagtg   | 300  |
| gctggggctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc  | 360  |
| aaggggcccat cggctcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg | 420  |
| gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca | 480  |
| ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac   | 540  |
| tccctcagca gcgtgggtgac cgtgccctcc agcaacttcg gcacccagac ctacacatgc  | 600  |
| aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt   | 660  |
| gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtcctt cctcttcccc  | 720  |
| ccaaaacca aggacacctt catgatctcc cggacccttg aggtcacgtg cgtgggtggtg   | 780  |
| gacgtgagcc acgaagaccc cgagggtccag ttcaactgggt acgtggacgg cgtggaggtg | 840  |
| cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtgggtcagc  | 900  |
| gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc   | 960  |
| aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga   | 1020 |
| gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc    | 1080 |
| ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat  | 1140 |
| gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc   | 1200 |
| ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca   | 1260 |
| tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct   | 1320 |
| ccgggtaaa                                                           | 1329 |

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<210> 1178  
 <211> 443  
 <212> PRT  
 <213> Homo sapiens

<400> 1178

Glu Val His 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 Tyr  
 20 25 30

Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gly Ile Ser Gly Arg Gly Gly Ser Thr 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 Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Asn Cys  
 85 90 95

Ala Ile Glu Val Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met  
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
 115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys  
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 145 150 155 160



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Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn  
180 185 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn  
195 200 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro  
210 215 220

Pro Cys Pro Ala Pro Pro Val Ala Gly 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 Gln 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 Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val  
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
340 345 350

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Glu Met 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 Met 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 Lys  
435 440

<210> 1179

<211> 642

<212> DNA

<213> Homo sapiens

<400> 1179

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc | 60  |
| atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca | 120 |
| gggacagccc ctaagttcct gatctatggc gcatcccggt tgcaaagtgg ggtcccatca | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcacttca ccatcagcag tctgcaacct  | 240 |
| gaagactttg caacttacta ctgtcaacag agtgacacta ccccgatcac cttcggccaa | 300 |
| gggacacgac tggagattaa acgaactgtg gctgcacat ctgtcttcat cttcccgcca  | 360 |
| tctgatgagc agttgaaatc tggaactgct agcgttgtgt gcctgctgaa taacttctat | 420 |
| cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg | 540 |

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1180

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1180

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 Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Gly Ala Ser Arg Leu Gln 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 Ser Asp Thr Thr Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

A-1937-W0-PCT\_ST25

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1181

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 1181

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| cagggtgcagc tgggtgcaatc tggggctgag gtgaagaagc ctggggcctc agtgcaggtc | 60  |
| tcctgcaagg cttctggata caccttcacc ggctactata tgcactggat tcgacaggcc   | 120 |
| cctgggcaag ggcttgagtg gctgggatgg atcatcccta acagtgggtgg cacaaattat  | 180 |
| gcccagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac   | 240 |
| atggaactga gcaggctgag atctgacgac acggccgttt attactgtgc gactggcagc   | 300 |
| agctgggagg gatttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc   | 360 |
| accaagggcc catcggctctt ccccctggcg ccctgctcta gaagcacctc cgagagcaca  | 420 |
| gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac   | 480 |
| tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc   | 540 |
| tactccctca gcagcgtggg gaccgtgccc tccagcaact tcggcaccca gacctacaca   | 600 |
| tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaagt   | 660 |

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```

tgtgtcgagt gccacccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc      720
ccccaaaaac ccaaggacac cctcatgata tcccggaccc ctgagggtcac gtgcgtgggtg      780
gtggacgtga gccacgaaga ccccgagggtc cagttcaact ggtacgtgga cggcgtggag      840
gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc      900
agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaagggtc      960
tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc     1020
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccagggtc     1080
agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc     1140
aatgggcagc cggagaacaa ctacaagacc acacctccca tgctggactc cgacggctcc     1200
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc     1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg     1320
tctccgggta aa                                                                1332

```

<210> 1182

<211> 444

<212> PRT

<213> Homo sapiens

<400> 1182

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10          15

```

```

Ser Val Gln Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20           25           30

```

```

Tyr Met His Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
35           40          45

```

```

Gly Trp Ile Ile Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50           55          60

```

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Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Thr Gly Ser Ser Trp Glu Gly 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 Cys Ser Arg Ser Thr Ser Glu Ser 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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

A-1937-W0-PCT\_ST25

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
435 440

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<210> 1183

<211> 651

<212> DNA

<213> Homo sapiens

<400> 1183

```

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc      60
atctcctgca ggtctagtca aagcctcgta tacagtgacg gaaacaccta cttgaattgg      120
tttcagcaga ggccaggccg atctccaagg cgcttaattt ataaggtttc taactgggac      180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgattccac actgataatc      240
agcaggggtgg aggctgagga tgttgggggtt tattactaca tgcaaggtag aactggcct      300
ctcggcggag ggaccaaggt ggagatcaaa cgaactgtgg ctgcaccatc tgtcttcac      360
ttcccgccat ctgatgagca gttgaaatct ggaactgcta gcgttgtgtg 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> 1184

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1184

```

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1           5           10           15

```

```

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20           25           30

```

```

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Arg Ser
35           40           45

```



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Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Ser Thr Leu Ile Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Tyr Met Gln Gly  
85 90 95

Thr His Trp Pro Leu 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> 1185

<211> 1332

<212> DNA

## A-1937-W0-PCT\_ST25

&lt;213&gt; Homo sapiens

&lt;400&gt; 1185

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagggacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc | 60   |
| tcctgccagg cttctggata caccttcacc gcctactata tgcactgggt gcgacaggcc  | 120  |
| cctggacaag ggcttgagt gatgggttg atcaacccta acagtgggtg cacaactat     | 180  |
| gcacagaagt ttcggggcag ggtcaccatg accagggaca cgtccatcag cacagcctac  | 240  |
| atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gactggcggc  | 300  |
| agctgggagg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggcttt cccctggcg ccctgtctta gaagcacctc cgagagcaca   | 420  |
| gcggccctgg gctgcctgg caaggactac ttccccgaac cggtgacggt gtcgtggaac   | 480  |
| tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc  | 540  |
| tactccctca gcagcgtgg gaccgtgccc tccagcaact tcggcaccca gacctacaca   | 600  |
| tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaagt  | 660  |
| tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc  | 720  |
| ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgagggtcac gtgcgtggtg  | 780  |
| gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag  | 840  |
| gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtggtc  | 900  |
| agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc  | 960  |
| tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc  | 1020 |
| cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc  | 1080 |
| agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc | 1140 |
| aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc   | 1200 |
| ttcttctct acagcaagct caccgtggac aagagcaggt ggacgaggg gaacgtcttc    | 1260 |
| tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg  | 1320 |
| tctccgggta aa                                                      | 1332 |

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<210> 1186  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

<400> 1186

Gln Gly Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Ala Tyr  
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
 50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Thr Gly Gly Ser Trp Glu Gly 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 Cys Ser Arg Ser Thr Ser Glu Ser 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

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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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

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Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
435 440

<210> 1187

<211> 642

<212> DNA

<213> Homo sapiens

<400> 1187

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| gacatccaga tgacccagtc tccatcgtcc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca  | 120 |
| gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca  | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcacttca ccatcagtag tctgcaacct   | 240 |
| gaagattttg caacttacta ctgtcaacag agtgacagta ccccgatcac cttcggccaa  | 300 |
| gggacacgac tggagattaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcc   | 360 |
| tctgatgagc agttgaaatc tggaactgct agcgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg  | 540 |

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 1188

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1188

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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile  
35 40 45

Tyr Ala Ala Ser Arg Leu Gln 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 Ser Asp Ser Thr Pro Ile  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1189  
<211> 33  
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<220>  
<223> Synthetic oligonucleotide

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33

<210> 1190  
<211> 444  
<212> PRT  
<213> Homo sapiens

<400> 1190

Gln Gly Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
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Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Ala Tyr  
20 25 30

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Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe  
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Thr Gly Gly Ser Trp Glu Gly 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 Cys Ser Arg Ser Thr Ser Glu Ser 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

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys  
210 215 220



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Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe  
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe  
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr  
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser  
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
405 410 415

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |

<210> 1191  
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<400> 1191  
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<210> 1192  
 <211> 25  
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<220>  
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<400> 1192  
 caccatggac tggacctgga gcatc 25

<210> 1193  
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<400> 1193  
 caccatggac tgcacctgga ggatc 25

<210> 1194  
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<220>  
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<400> 1194  
 caccatggac tggacctgga gaatc 25

<210> 1195  
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<400> 1195  
 caccatggac tggacctgga ggg 23

<210> 1196  
 <211> 26  
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<220>  
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<400> 1196  
 caccatggac tggatttgga ggatcc 26

<210> 1197  
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<400> 1197  
 caccatggac acactttgct ccacg 25

<210> 1198  
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<400> 1198  
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<400> 1199  
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<210> 1200  
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<400> 1200  
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<400> 1201  
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<210> 1202  
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<400> 1202  
caccatggaa ctggggctcc gc 22

<210> 1203  
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<400> 1203  
caccatggaa tttgggctga gctgg 25

<210> 1204  
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<400> 1204  
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<210> 1205  
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<400> 1205  
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<210> 1206  
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<210> 1207  
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 <400> 1208  
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<210> 1209  
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 <400> 1209  
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<210> 1210  
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<400> 1210  
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<210> 1211  
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<400> 1211  
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<210> 1212  
<211> 28  
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<400> 1212  
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<210> 1213  
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<400> 1213  
caccatggac atgagggtcc ccg 23

<210> 1214  
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<400> 1214  
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<400> 1216  
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<210> 1217  
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<400> 1217  
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<210> 1218  
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<220>  
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<400> 1218  
caccatggaa accccagcgc agc 23

<210> 1219  
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<400> 1219  
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<210> 1220  
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<220>  
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<400> 1220  
caccatggaa gccccagctc ag 22

<210> 1221  
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<400> 1221  
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<210> 1222  
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&lt;400&gt; 1222

caccatggtg ttgcagaccc aggtc

25

&lt;210&gt; 1223

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1223

caccatgggg tcccagggtc acc

23

&lt;210&gt; 1224

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1224

caccatgttg ccatcacaac tcattggg

28

&lt;210&gt; 1225

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1225

caccatggtg tccccgttgc aattc

25

&lt;210&gt; 1226

&lt;211&gt; 25

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&lt;213&gt; Artificial Sequence

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<210> 1227  
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<210> 1234  
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<400> 1238  
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<210> 1239  
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<400> 1239  
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<210> 1240  
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<400> 1240  
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<210> 1241  
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<400> 1241  
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<210> 1242  
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<400> 1242  
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<210> 1243  
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<400> 1244  
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<400> 1245  
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<210> 1246  
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<400> 1246  
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<400> 1247  
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<220>  
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<400> 1249  
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<210> 1250  
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&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1250

caccatggcc tgggctcctc tg

22

&lt;210&gt; 1251

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1251

caccatgccc tgggctctgc tc

22

&lt;210&gt; 1252

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (8)..(8)

&lt;223&gt; K is G or T.

&lt;400&gt; 1252

ggagggtktg gtggtctcca ctccc

25

&lt;210&gt; 1253

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1253

gatatcaaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg

60

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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
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aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<210> 1254  
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<220>  
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<400> 1254

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20          25          30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45

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Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1255

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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```

<400> 1255
gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggtagcgcc tctgtttgtg gcctgctgaa taactttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

```

<210> 1256
<211> 214
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Synthetic polypeptide

```

<400> 1256

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10          15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45

```

```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50           55           60

```

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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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1257

<211> 2046

<212> DNA

<213> Artificial Sequence

<220>

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&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1257

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt  | 60   |
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg | 120  |
| cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct  | 360  |
| agtcctcca ccaagggccc atcggcttc cccctggcac cctcctcaa gagcacctct      | 420  |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg   | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag   | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag   | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc     | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag   | 1380 |

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gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc 1440  
 tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggattcg ccagccacca 1500  
 gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg 1560  
 tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg 1620  
 ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga 1680  
 agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctctcagcc 1740  
 tccaccaagg gcccatcggg cttccccctg gcaccctcct ccaagagcac ctctgggggc 1800  
 acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860  
 aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 1920  
 ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 1980  
 atctgcaacg tgaatcaciaa gccagcaac accaaggtgg acaagaaagt tgagcccaaa 2040  
 tcttgt 2046

<210> 1258  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1258

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240



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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
 450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
 465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
 485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
 500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
 515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
 530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
 545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
 580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
 595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
 610 615 620

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Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1259  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1259  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttcag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcga 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

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<210> 1260  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1260

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1261  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1261  
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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1262  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1262

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1263  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1263  
gaggtagaac tggtagaac aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360  
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacg 600

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc  | 780  |
| cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac  | 1140 |
| atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagctgc aggagtctggg cccaggactg gtgaagcctt cggagaccct gtccctcacc | 1440 |
| tgactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagcccca    | 1500 |
| ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc  | 1560 |
| tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag  | 1620 |
| ctgagctctg tgaccgtgc ggacacggcc gtgtattact gtgcgagaga aactgggagc   | 1680 |
| tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc agcctccacc | 1740 |
| aaggggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg   | 1800 |
| gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca | 1860 |
| ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac  | 1920 |
| tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc  | 1980 |
| aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt  | 2040 |



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<210> 1264  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1264

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

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Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1265

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1265
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg      60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc      120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgccca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

```

<210> 1266
<211> 214
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic polypeptide

```

<400> 1266

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1267

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1267

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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc      480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

```

<210> 1268

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1268

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35           40           45

```

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Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1269

<211> 2061

<212> DNA

<213> Artificial Sequence



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&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1269

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| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg | 120  |
| cctggaaaag ggctcgagtg gggttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct | 360  |
| agtgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct | 420  |
| gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag   | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag   | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc     | 780  |
| cctgaggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atgcccggtg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc   | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |

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acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380  
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc 1440  
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag 1500  
ccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat 1560  
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 1620  
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 1680  
gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc 1740  
accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag 1800  
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaaccg 1860  
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920  
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980  
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aaagttgagc ccaaattctt t 2061

<210> 1270  
<211> 687  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1270

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

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Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1271  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1271  
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1272  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1272

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

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Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1273  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1273  
gaaatttgtt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtc gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgt ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600



ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

642

&lt;210&gt; 1274

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1274

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1275  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1275  
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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540

## A-1937-W0-PCT\_ST25

|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| ctcaaaagcg  | tggtgaccgt | gccctccagc | agcttgggca | cccagaccta  | catctgcaac | 600  |
| gtgaatcaca  | agcccagcaa | caccaaggtg | gacaagaaag | ttgagcccaa  | atcttgtgac | 660  |
| aaaactcaca  | catgcccacc | gtgcccagca | cctgaactcc | tgggggggacc | gtcagtcttc | 720  |
| ctcttcccc   | caaaacccaa | ggacaccctc | atgatctccc | ggacccctga  | ggtcacatgc | 780  |
| gtggtggtgg  | acgtgagcca | cgaagaccct | gaggtcaagt | tcaactggta  | cgtggacggc | 840  |
| gtggagggtgc | ataatgccaa | gacaaagccg | tgtgaggagc | agtacggcag  | cacgtaccgt | 900  |
| tgtgtcagcg  | tcctcaccgt | cctgcaccag | gactggctga | atggcaagga  | gtacaagtgc | 960  |
| aaggtctcca  | acaaagccct | cccagcccc  | atcgagaaaa | ccatctccaa  | agccaaaggg | 1020 |
| cagccccgag  | aaccacaggt | gtacaccctg | cccccatccc | gggaggagat  | gaccaagaac | 1080 |
| caggtcagcc  | tgacctgcct | ggtcaaaggc | ttctatccca | gcgacatcgc  | cgtggagtgg | 1140 |
| gagagcaatg  | ggcagccgga | gaacaactac | aagaccacgc | ctcccgtgct  | ggactccgac | 1200 |
| ggctccttct  | tcctctatag | caagctcacc | gtggacaaga | gcaggtggca  | gcaggggaac | 1260 |
| gtcttctcat  | gctccgtgat | gcatgaggct | ctgcacaacc | actacacgca  | gaagagcctc | 1320 |
| tcctgtctc   | cgggtggtgg | cggatcggga | ggtggcggat | cccaggtgca  | gttacagcag | 1380 |
| tcgggcgcag  | gactgttgaa | gccttcggag | accctgtccc | tcacctgcgc  | tgtccatggt | 1440 |
| gggtccttca  | gtggttacta | ctggaactgg | attcgccagc | caccagggaa  | ggggctagag | 1500 |
| tggattgggg  | aaatcaatca | tgctggaaac | accaactaca | acccgtccct  | caagagtcga | 1560 |
| gtcaccatat  | cattagacac | gtccaagaac | cagttctccc | tgacgctgac  | ctctgtgacc | 1620 |
| gccgcggaca  | cggctgtgta | ttactgtgcg | agaggatatt | gtagaagtac  | cacctgctac | 1680 |
| tttgactact  | ggggccaggg | aaccctagtc | accgtctcct | cagcctccac  | caagggccca | 1740 |
| tcggtcttcc  | ccctggcacc | ctcctccaag | agcacctctg | ggggcacagc  | ggccctgggc | 1800 |
| tgctgtgtca  | aggactactt | ccccgaaccg | gtgacggtgt | cgtggaactc  | aggcgccctg | 1860 |
| accagcggcg  | tgcacacctt | cccggctgtc | ctacagtcct | caggactcta  | ctccctcgag | 1920 |
| agcgtggtga  | ccgtgccctc | cagcagcttg | ggcaccacga | cctacatctg  | caacgtgaat | 1980 |

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

2031

<210> 1276

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1276

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335

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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

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Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1277

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1277

```

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg gagggaccaaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag      540
agctatctga gcctgacgcc tgagcagtgga aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a                651

```

&lt;210&gt; 1278

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1278

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35          40          45

```



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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1279

<211> 642

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 1279

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

<210> 1280

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1280

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1281

<211> 2025

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1281

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| cccggaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac    | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctctg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag  | 360  |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc  | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc  | 540  |
| ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac  | 600  |
| gtgaatcaca agccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac   | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc  | 720  |
| ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc     | 780  |
| gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc | 840  |
| gtggaggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt   | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggtctcca acaaagccct ccagcccc atcgagaaaa ccatctcaa agccaaaggg     | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg    | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac  | 1260 |

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gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320  
 tccctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtgca gctgcaggag 1380  
 tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt 1440  
 ggctccatca gtagttactt ctggagctgg attcggcagc cccaggtaa gggactggag 1500  
 tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga 1560  
 gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc 1620  
 gctgcggaca cggccgtgta ttactgtgcg agagaaactg ggagctacta cggctttgac 1680  
 tactggggcc agggaaacct ggtcaccgtc tcctcagcct ccaccaaggg cccatcggtc 1740  
 ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 1800  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 1860  
 ggctgtcaca ccttcccggc tgcctacag tcctcaggac tctactccct cgagagcgtg 1920  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 1980  
 cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt 2025

<210> 1282  
 <211> 675  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1282

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

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Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly  
435 440 445

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620



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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
660 665 670

Lys Ser Cys  
675

<210> 1283  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1283  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1284  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1284

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

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Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1285  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1285  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

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gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1286  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1286

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140

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Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1287  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1287  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540

## A-1937-W0-PCT\_ST25

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| ctcaaaagcg | tggtgaccgt | gccctccagc | agcttgggca | cccagaccta  | catctgcaac | 600  |
| gtgaatcaca | agcccagcaa | caccaaggtg | gacaagaaag | ttgagcccaa  | atcttgtgac | 660  |
| aaaactcaca | catgcccacc | gtgcccagca | cctgaactcc | tgggggggacc | gtcagtcttc | 720  |
| ctcttcccc  | caaaacccaa | ggacaccctc | atgatctccc | ggacccctga  | ggtcacatgc | 780  |
| gtggtggtgg | acgtgagcca | cgaagaccct | gaggtcaagt | tcaactggta  | cgtggacggc | 840  |
| gtggaggtgc | ataatgccaa | gacaaagccg | tgtgaggagc | agtacggcag  | cacgtaccgt | 900  |
| tgtgtcagcg | tcctcaccgt | cctgcaccag | gactggctga | atggcaagga  | gtacaagtgc | 960  |
| aaggtctcca | acaaagccct | cccagcccc  | atcgagaaaa | ccatctccaa  | agccaaaggg | 1020 |
| cagccccgag | aaccacaggt | gtacaccctg | cccccatccc | gggaggagat  | gaccaagaac | 1080 |
| caggtcagcc | tgacctgcct | ggtcaaaggc | ttctatccca | gcgacatcgc  | cgtggagtgg | 1140 |
| gagagcaatg | ggcagccgga | gaacaactac | aagaccacgc | ctcccgtgct  | ggactccgac | 1200 |
| ggctccttct | tcctctatag | caagctcacc | gtggacaaga | gcaggtggca  | gcaggggaac | 1260 |
| gtcttctcat | gctccgtgat | gcatgaggct | ctgcacaacc | actacacgca  | gaagagcctc | 1320 |
| tcctgtctc  | cgggtggtgg | cggatcggga | ggtggcggat | cccaggtaca  | gttgaggag  | 1380 |
| tcaggtccag | gactggtgaa | gccctcggag | accctctcac | tcacctgtac  | catctccggg | 1440 |
| gacagtgtct | ctaccaacag | tgttgcttgg | aactggatta | ggcagcccc   | agggaaaggc | 1500 |
| cttgagtgga | taggaaggac | atactacagg | tccaagtggg | ataatgatta  | tgcagtttct | 1560 |
| ctgaaaagtc | gagtaaccat | cagcccagac | acatccaaga | accagttctc  | cctgaagctg | 1620 |
| agctctgtga | ctgccgcgga | cacggctgtg | tattactgtg | caagagagga  | tggggatagc | 1680 |
| tactaccgct | acggtatgga | cgtctggggc | caagggacca | cggtcaccgt  | ctcctcagcc | 1740 |
| tccaccaagg | gcccacgggt | cttccccctg | gcaccctcct | ccaagagcac  | ctctgggggc | 1800 |
| acagcggccc | tgggctgcct | ggtcaaggac | tacttccccg | aaccggtgac  | ggtgtcgtgg | 1860 |
| aactcaggcg | ccctgaccag | cggcgtgcac | accttcccgg | ctgtcctaca  | gtcctcagga | 1920 |
| ctctactccc | tcgagagcgt | ggtgaccgtg | ccctccagca | gcttgggcac  | ccagacctac | 1980 |

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atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 2040

tcttgt 2046

<210> 1288

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1288

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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



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Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

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Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1289

<211> 642

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 1289

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1290

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1290

```

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 Arg Ser Ser
20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45

```

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1291

<211> 642

A-1937-W0-PCT\_ST25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1291

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg  | 60  |
| attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc  | 120 |
| ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg  | 180 |
| aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc  | 240 |
| gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa  | 300 |
| gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc  | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                     | 642 |

<210> 1292

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1292

|                                                                    |  |
|--------------------------------------------------------------------|--|
| 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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr    |  |
| 20                    25                    30                     |  |

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

## A-1937-W0-PCT\_ST25

<210> 1293  
 <211> 2046  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1293  
 caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatggtgg gtccttcagt gggttactact ggaactggat ccgccagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 gcctccacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900  
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080  
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg 1200

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|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| ctggactccg | acggctcctt  | cttcctctat | agcaagctca | ccgtggacaa | gagcaggtgg | 1260 |
| cagcagggga | acgtcttctc  | atgctccgtg | atgcatgagg | ctctgcacaa | ccactacacg | 1320 |
| cagaagagcc | tctccctgtc  | tccgggtggg | ggcggatcgg | gaggtggcgg | atccgaggta | 1380 |
| caactgggtg | aatcaggtgg  | aggtttggtg | cagccgggga | gatcgtcag  | gcttagctgt | 1440 |
| gcggcatcgg | ggttttacttt | cgatgattat | gcgatgcatt | gggtccggca | agcgcctgga | 1500 |
| aaagggctcg | agtgggtttc  | cgccattacg | tggaatagcg | gacacatcga | ttatgcagac | 1560 |
| agtgtggagg | gcagattcac  | aatctcacga | gacaatgcta | agaacagcct | gtaccttcag | 1620 |
| atgaactcac | ttcgcgcgga  | agataaccgc | gtatactact | gcgccaaagt | ctcctacttg | 1680 |
| tctacagctt | cgtcgctcga  | ctattggggg | caaggaacgt | tggtcaccgt | ctctagtgcc | 1740 |
| tccaccaagg | gcccacggt   | cttccccctg | gcaccctcct | ccaagagcac | ctctgggggc | 1800 |
| acagcggccc | tgggctgcct  | ggtcaaggac | tacttccccg | aaccggtgac | ggtgtcgtgg | 1860 |
| aactcaggcg | ccctgaccag  | cggcgtgcac | accttcccgg | ctgtcctaca | gtcctcagga | 1920 |
| ctctactccc | tcgagagcgt  | ggtgaccgtg | ccctccagca | gcttgggcac | ccagacctac | 1980 |
| atctgcaacg | tgaatcacia  | gcccagcaac | accaaggtgg | acaagaaagt | tgagcccaaa | 2040 |
| tcttgt     |             |            |            |            |            | 2046 |

|       |                     |
|-------|---------------------|
| <210> | 1294                |
| <211> | 682                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1294

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30



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Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

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Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

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Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

A-1937-W0-PCT\_ST25

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1295  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1295  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtaaccgc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540

A-1937-W0-PCT\_ST25

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1296

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1296

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

A-1937-W0-PCT\_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1297  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1297  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

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aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1298  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1298

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

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Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1299  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1299  
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acctgcgctg tccatgggtgg gtccttcagt gggtactact ggaactggat ccgccagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 480  |
| tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 540  |
| ggactctact ccctcaaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc  | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 660  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    | 780  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc  | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 960  |
| gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1020 |
| aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1080 |
| atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg   | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1320 |
| cagaagagcc tctccctgtc tccgggtggg gccggatcgg gaggtggcgg atccgagggtg  | 1380 |
| cagctgggtgc agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatctcctgt | 1440 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg  | 1500 |
| aaaggcctgg agtggatggg gatcatctat cttgggtgact cagataccag atacagcccg  | 1560 |
| tccttccaag gccagggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag  | 1620 |
| tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt  | 1680 |
| cttgactact ggggccaggg aaccctgggt accgtctcta gtgcctccac caagggccca   | 1740 |
| tcgggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 1800 |
| tgcttggtca aggactactt cccgaaccg gtgacgggtgt cgtggaactc aggcgcctg    | 1860 |

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accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag 1920  
 agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1980  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 2031

<210> 1300  
 <211> 677  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1300

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

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Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

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Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1301

<211> 642

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1301

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca  | 120 |
| gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca  | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct  | 240 |
| gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa  | 300 |
| gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc  | 360 |
| tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt                    | 642 |

<210> 1302

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1302

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

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<210> 1303  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1303  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1304  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1304

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30



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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1305  
 <211> 2040  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1305  
 cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
 acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
 ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
 ccttccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
 accaagggcc catcggctctt ccccttgga cctcctcca agagcacctc tgggggcaca 420  
 gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
 tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
 tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gccc aaatct 660  
 tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga cctgaggtc 780  
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900  
 taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
 aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc 1020  
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 1080  
 aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg 1140

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gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200  
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260  
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
agcctctccc tgtctccggg tgggtggcgga tcgggaggtg gcggatccga ggtacaactg 1380  
gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca 1440  
tcgggggttta ctttcgatga ttatgcgatg cattgggtcc ggcaagcgcc tggaaaaggg 1500  
ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg 1560  
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac 1620  
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680  
gcttcgtcgc tcgactattg gggtaagga acgttgggtca ccgtctctag tgcctccacc 1740  
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg 1800  
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860  
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 1980  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1306

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1306

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

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Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

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His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
450 455 460

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

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Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1307  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1307  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtaaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1308

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1308

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125



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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1309  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1309  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

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aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1310  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1310

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

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Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1311  
<211> 2025  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1311  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc  | 540  |
| tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga cctgagggtc     | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcgga tcgggagggtg gcggatccga ggtgcagctg | 1380 |
| gtgcagtctg gagcagaggt gaaaaagccc ggggagcttc tgaagatctc ctgtaagact   | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc   | 1500 |
| ctggagtgga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc   | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc   | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac  | 1680 |
| tactggggcc agggaaacct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc   | 1740 |
| ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg    | 1800 |
| gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc   | 1860 |

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ggcgtgcaca ctttcccggc tgcctacag tcctcaggac tctactccct cgagagcgtg 1920  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 1980  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 2025

<210> 1312  
 <211> 675  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1312

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

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Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

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Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
660 665 670

Lys Ser Cys  
675

<210> 1313

<211> 660



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<212> DNA

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 1313

gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtggggcga taggggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggg 180

gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480

caatcgggta actcccagga gagtggtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

$\langle 210 \rangle$  1314

$\langle 211 \rangle$      $220$

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 1314

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

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Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

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<210> 1315  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1315  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1316  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1316

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

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<210> 1317  
 <211> 2061  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1317  
 cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120  
 cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
 agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
 gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc 420  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540  
 gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660  
 aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720  
 gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 780  
 atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840  
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt 900  
 gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac 960  
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc 1020  
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080  
 ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc 1140

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg   | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt   | 1380 |
| ggcggatccg aggtacaact ggtggaatca ggtggagggtt tgggtgcagcc ggggagatcg | 1440 |
| ctcaggctta gctgtgcggc atcgggggtt actttcgatg attatgcatg gcattgggtc   | 1500 |
| cggcaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac   | 1560 |
| atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac   | 1620 |
| agcctgtacc ttcagatgaa ctacttcgc gcggaagata ccgccgtata ctactgcgcc    | 1680 |
| aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtcaagg aacgttggtc   | 1740 |
| accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag    | 1800 |
| agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt cccgaaccg    | 1860 |
| gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc   | 1920 |
| ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg   | 1980 |
| ggcaccacga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag   | 2040 |
| aaagttgagc ccaaattcttg t                                            | 2061 |

<210> 1318  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1318

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

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Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400



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Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1319

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1319

gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480

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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1320  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1320

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1321  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1321  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

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ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1322  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1322

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

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Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1323  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1323  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc  | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct  | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg    | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agacctgag    | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc    | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtga caccctgccc  | 1080 |
| ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt  | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct  | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg  | 1500 |
| cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat  | 1560 |
| accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt  | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcgga cccgcatgta ttactgtgcg    | 1680 |
| agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtgcc  | 1740 |
| tccaccaagg gcccacgtgt cttccccctg gcaccctcct ccaagagcac ctctgggggc  | 1800 |

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acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860  
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 1920  
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 1980  
atctgcaacg tgaatcaciaa gcccagcaac accaagggtg acaagaaagt tgagcccaaa 2040  
tcttgt 2046

<210> 1324  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1324

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110



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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

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Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

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Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

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<210> 1325  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1325  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1326  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1326

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1327  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1327  
gagggtacaac tgggtggaatc aggtggagggt ttgggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaag ggctcgagtg gggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660  
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac 780  
ttccggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc 840  
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900  
gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960  
ctgaatggca aggagtacaa gtgcaaggct tccaacaaag ccctcccagc ccccatcgag 1020  
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ttccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc   | 1380 |
| ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg   | 1440 |
| tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc | 1500 |
| cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac   | 1560 |
| tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc   | 1620 |
| tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga   | 1680 |
| tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc   | 1740 |
| tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc   | 1800 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg   | 1860 |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag   | 1920 |
| tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc   | 1980 |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt   | 2040 |
| gagcccaaatt cttgt                                                   | 2055 |

<210> 1328  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1328

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205



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Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

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Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

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Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1329  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1329  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

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ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1330  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1330

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1331  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1331  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360

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tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1332  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1332

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1333  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1333  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt cggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggg caccgtctct  | 360  |
| agtacgggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct  | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac  | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc   | 780  |
| tcccggaacc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc  | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg   | 1440 |
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg  | 1500 |
| cagccccag gtaagggtact ggagtggatt ggctatatct attacagtgg gcagacaaaa   | 1560 |
| tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc    | 1620 |
| tccctgaagc tgagctctgt gaccgtgctg gacacggccg tgtattactg tgcgagagaa   | 1680 |
| actgggagct actacggctt tgactactgg ggccaggga ccttggtcac cgtctcctca    | 1740 |



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```
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 1800
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 1860
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 1920
ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 1980
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 2040
aaatcttgt 2049
```

<210> 1334  
 <211> 683  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1334

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1           5           10           15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20           25           30
```

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45
```

```
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50           55           60
```

```
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85           90           95
```

## A-1937-W0-PCT\_ST25

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
 130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
 145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
 165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
 180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
 195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
 210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

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Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

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Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

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Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1335  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1335  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1336  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1336

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1337  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1337  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1338  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1338

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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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190



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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1339  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1339  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt cggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 660  
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac 780  
tcccggaacc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 840  
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900  
gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960

# A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctgaatggca aggagtacaa gtgcaaggct tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  | 1080 |
| tcccgggagg agatgaccaa gaaccaggct agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac  | 1260 |
| aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc | 1380 |
| ggatcccagg tacagttgca ggagtcagggt ccaggactgg tgaagccctc ggagaccctc | 1440 |
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg  | 1500 |
| attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta cagggtccaag | 1560 |
| tggataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc   | 1620 |
| aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac  | 1680 |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg  | 1740 |
| accacggtca cagtctctc agcctccacc aaggggccat cggctcttccc cctggcaccc  | 1800 |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc | 1860 |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc  | 1920 |
| ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc | 1980 |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag  | 2040 |
| gtggacaaga aagttgagcc caaatcttgt                                   | 2070 |

<210> 1340

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1340

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
 130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
 145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
 165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
 180 185 190

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Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

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Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1341  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1341  
gatatccaaa tgacacaatc accatcgatcgt ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc ggcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

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aggttttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 1342  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1342

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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

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Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1343  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1343  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120



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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1344  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1344

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1345

<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1345

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc

60

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| ccccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaggcc  | 360  |
| aacccactg tcaactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca  | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtgcagtta  | 1380 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc   | 1440 |
| catggtgggt ccttcagtgg ttactactgg aactggattc gccagccacc aggggaagggg | 1500 |

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ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag 1560  
 agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct 1620  
 gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc 1680  
 tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcagc ctccaccaag 1740  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1800  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc 1860  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 1920  
 ctcgagagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1980  
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgt 2037

<210> 1346  
 <211> 679  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1346

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

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Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

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Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
580 585 590

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
595 600 605

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
610 615 620

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
625 630 635 640

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
645 650 655

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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
660 665 670

Lys Val Glu Pro Lys Ser Cys  
675

<210> 1347  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1347  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1348  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>



&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1348

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 165 170 175

A-1937-W0-PCT\_ST25

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1349  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1349  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 1350  
<211> 214  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1350

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

<210> 1351  
 <211> 2031  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1351  
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 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agccccgcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccgaaggcc 360  
 aacccccactg tactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
 ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
 ggagcccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540  
 tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac 600  
 agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660  
 tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc  | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tcgggagggtg gcggatccca ggtgcagctg | 1380 |
| caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc  | 1440 |
| tctggtggct ccatcagtag ttacttctgg agctggattc ggcagcccc aggtaaggga   | 1500 |
| ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag  | 1560 |
| agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct  | 1620 |
| gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc  | 1680 |
| tttgactact gggggccaggg aaccctggtc accgtctcct cagcctccac caagggccca | 1740 |
| tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 1800 |
| tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg   | 1860 |
| accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag  | 1920 |
| agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat | 1980 |
| cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          | 2031 |

<210> 1352

<211> 677

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1352

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

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Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
355 360 365

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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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560



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Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1353  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1353  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

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cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagt gagcccaa at cttgt 645

<210> 1354  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1354

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1355  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1355  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

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tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccg 180  
 gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
 cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360  
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
 ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1356  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1356

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

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Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1357

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1357

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc

60

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| ccccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaggcc  | 360  |
| aacccactg tcaactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca  | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tggtagcgga tcgggaggtg gcggatccca ggtacagttg  | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc  | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg   | 1500 |

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aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca 1560  
 gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg 1620  
 aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg 1680  
 gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc 1740  
 tcagcctcca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct 1800  
 gggggcacag cggccctggg ctgcctgggc aaggactact tccccgaacc ggtgacgggtg 1860  
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1920  
 tcaggactct actccctcga gagcgtgggt accgtgccct ccagcagctt gggcaccacag 1980  
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 2040  
 cccaaatctt gt 2052

<210> 1358  
 <211> 684  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1358

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

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Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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



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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510

Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
580 585 590

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
595 600 605

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
610 615 620

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
625 630 635 640

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Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser  
645 650 655

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
660 665 670

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1359  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1359  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca cttccccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaagggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1360  
<211> 215  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1360

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

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Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1361  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1361  
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1362  
<211> 214

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1362

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1363  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1363  
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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccaggga ccttagtcac cgtctcctca 360  
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
aagggtgata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

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|                                                                      |      |
|----------------------------------------------------------------------|------|
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc  | 780  |
| cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagaccc tgagggtcaag | 840  |
| ttcaactgggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg    | 960  |
| aatggcaagg agtacaagtg caaggctctcc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc    | 1080 |
| cgggaggaga tgaccaagaa ccaggctcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg    | 1200 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag    | 1260 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac   | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga   | 1380 |
| tccgaggtag aactgggtgga atcagggtgga ggtttgggtgc agccggggag atcgctcagg | 1440 |
| cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa    | 1500 |
| gcgcctggaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat     | 1560 |
| tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg    | 1620 |
| taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc    | 1680 |
| tcctacttgt ctacagcttc gtcgctcgac tattgggggtc aaggaacgtt ggtcaccgtc   | 1740 |
| tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc    | 1800 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg    | 1860 |
| gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca cttccccggc tgtcctacag     | 1920 |
| tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc    | 1980 |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt   | 2040 |
| gagcccaaatt cttgt                                                    | 2055 |



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<210> 1364  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1364

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
 115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 145 150 155 160

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Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

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Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

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Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1365

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1365

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc

60

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ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1366  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1366

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 Arg Ser Ser  
                     20                      25                      30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
                     35                      40                      45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
                     50                      55                      60

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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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1367

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1367
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcggggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag      540
agctatctga gcctgacgcc tgagcagtgga aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

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```

<210> 1368
<211> 217
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polypeptide

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<400> 1368

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
          35          40          45

```

```

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

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Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1369

<211> 2040

<212> DNA

<213> Artificial Sequence

<220>



&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1369

|                                                                     |      |
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| cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc  | 60   |
| acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca   | 120  |
| ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac   | 180  |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca    | 360  |
| acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 420  |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 480  |
| aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gtcgccccgt cacaaagagc   | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 720  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccctg aggtcacatg cgtggtgggtg gacgtgagcc acgaagacc tgaggtcaag   | 840  |
| ttcaactggt acgtggacgg cgtggagggtg cataatgcc aagacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa    | 1020 |
| accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc    | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag    | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac   | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |

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```

tccgaggtgc agctggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag      1440
atctcctgta agacttctga atacagcttt accagctact ggatcggctg ggtgcgccag      1500
atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga      1560
tacagcccgt ccttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc      1620
tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt      1680
aactggggtc ttgactactg gggccaggga accctgggtca ccgtctctag tgcctccacc      1740
aaggggccat cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      1800
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca      1860
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      1920
tccttcgaga gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      1980
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      2040

```

<210> 1370

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1370

```

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
1           5           10           15

```

```

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
          20           25           30

```

```

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35           40           45

```

```

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
50           55           60

```

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Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

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Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

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Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
485 490 495

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

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Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1371  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1371  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 1372  
<211> 211

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1372

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1373  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1373  
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttcag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642



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<210> 1374  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1374

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1375  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1375  
cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctgggtg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360  
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420  
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480  
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600  
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc  | 780  |
| cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tgttacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag  | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc  | 1440 |
| tgtgcggcat cggggtttac tttcgatgat tatgcgatgc attgggtccg gcaagcgctt  | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca  | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt  | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac   | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtcaaggaa cgttggtcac cgtctctagt  | 1740 |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg  | 1800 |
| ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg  | 1860 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 1920 |
| ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc   | 1980 |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc  | 2040 |
| aaatcttgt                                                          | 2049 |

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<210> 1376  
 <211> 683  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1376

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
 115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
 130 135 140

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Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
 450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
 465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
 485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
 500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
 515 520 525

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Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560

Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1377

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1377

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaatct tgt                                     633

```

<210> 1378

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1378

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20          25          30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
35          40          45

```

```

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60

```



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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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1379

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1379

```
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg gagggacca gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag      540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651
```

<210> 1380

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1380

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20          25          30
```

```
Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35          40          45
```

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1381

<211> 2034

<212> DNA

<213> Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1381

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc | 60   |
| acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc  | 120  |
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac  | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg  | 360  |
| gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc  | 420  |
| tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac  | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa  | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac  | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag  | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |

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```

acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag      1380
gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccg gggagtctct gaagatctcc      1440
tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg ccagatgccc      1500
gggaaaggcc tggagtggat ggggatcatc tatcttgggtg actcagatac cagatacagc      1560
ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg      1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgcgag aagtaactgg      1680
ggtcttgact actggggcca gggaaccctg gtcaccgtct ctagtgcctc caccaagggc      1740
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg      1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc      1860
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc      1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg      1980
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaadc ttgt          2034

```

<210> 1382  
 <211> 678  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1382

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1              5              10             15

```

```

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20              25             30

```

```

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35              40             45

```

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Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala  
565 570 575

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser  
580 585 590

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe  
595 600 605

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
610 615 620



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Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
625 630 635 640

Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr  
645 650 655

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys  
660 665 670

Val Glu Pro Lys Ser Cys  
675

<210> 1383  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1383  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggtatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

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<210> 1384  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1384

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1385  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1385  
gatatcaaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1386  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1386

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1387  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1387  
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540  
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg   | 660  |
| cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc   | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac    | 780  |
| accctcatga tctcccggac ccctgaggtc acatgcgtgg tggaggacgt gagccacgaa   | 840  |
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg   | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca    | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac   | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc   | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac   | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat   | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga   | 1380 |
| tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg   | 1440 |
| gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg   | 1500 |
| cattgggtcc ggcaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat    | 1560 |
| agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat   | 1620 |
| gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac   | 1680 |
| tactgcgcca aagtctccta cttgtctaca gcttcgtcgc tcgactattg ggggtcaagga  | 1740 |
| acgttgggtca ccgtctctag tgcctccacc aagggcccat cggctcttccc cctggcaccc | 1800 |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc  | 1860 |
| cccgaaccgg tgacgggtgc gtggaactca ggccgacctga ccagcggcgt gcacaccttc  | 1920 |
| ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc  | 1980 |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag   | 2040 |

gtggacaaga aagttgagcc caaatcttgt

2070

&lt;210&gt; 1388

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1388

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
 115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
 130 135 140

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Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335



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Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

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Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1389

<211> 651

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1389

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc  | 60  |
| atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt  | 120 |
| tgggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccgg | 180 |
| gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc | 240 |
| atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact  | 300 |
| cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca | 360 |
| tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 420 |
| tgcttggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgccctg   | 480 |
| accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa  | 540 |
| agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat  | 600 |
| cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          | 651 |

<210> 1390

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1390

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

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<210> 1391  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1391  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1392  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1392

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

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Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1393  
 <211> 2055  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1393  
 cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
 cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
 agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
 gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
 cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480  
 gccaaagtac agtggaaggg ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540  
 acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
 gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
 cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
 ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780  
 accctcatga tctcccgga cctgagggtc acatgcgtgg tggaggacgt gagccacgaa 840  
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900  
 aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960  
 caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacia agccctccca 1020  
 gccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080  
 accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1140

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggcggcgga | 1380 |
| tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc | 1440 |
| ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc | 1500 |
| ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggt | 1560 |
| gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag | 1620 |
| tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat | 1680 |
| tactgtgcga gaagtaactg gggctctgac tactggggcc agggaaacct ggtcaccgtc | 1740 |
| tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc | 1800 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg | 1860 |
| gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca cttccccggc tgtcctacag  | 1920 |
| tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc | 1980 |
| cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagtt | 2040 |
| gagcccaaatt cttgt                                                 | 2055 |

<210> 1394  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1394

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |



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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

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Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

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Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

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Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1395

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1395

gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360

tcggctcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420

tgccctgggtca aggactactt ccccgaaacc gtgacgggtg cgtggaactc aggcgccttg 480

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accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
 agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1396  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1396

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 115 120 125

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Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1397  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1397  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

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```

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

<210> 1398  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1398

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
          100          105          110

```

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1399  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1399  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360



## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| agtcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct   | 420  |
| gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcaccag   | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag   | 660  |
| cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc     | 780  |
| cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgagg    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag   | 1380 |
| gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc   | 1440 |
| tgcgctgtcc atggtgggtc cttcagtggt tactactgga actggattcg ccagccacca   | 1500 |
| gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg   | 1560 |
| tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg   | 1620 |
| ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga   | 1680 |
| agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctctcaact    | 1740 |
| gtggctgcac catctgtctt catcttcccc ccatctgatg agcagttgaa atctggaact   | 1800 |

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gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860  
 gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920  
 gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980  
 aaagtctacg cctgcgaagt cacccatcag ggcttgagct cgcccgtcac aaagagcttc 2040  
 aacaggggag agtgt 2055

<210> 1400  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1400

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

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Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

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<210> 1401  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1401  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1402  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1402

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Gly | Thr | Leu | Ser | Leu | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1403  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1403  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1404  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1404

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15



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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1405  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1405  
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacag 600  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660  
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780  
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840  
tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac 900  
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960  
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagcccca   | 1500 |
| ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc  | 1560 |
| tcctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag   | 1620 |
| ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc  | 1680 |
| tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc aactgtggct | 1740 |
| gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct  | 1800 |
| gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat  | 1860 |
| aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc  | 1920 |
| acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc  | 1980 |
| tacgcctgcg aagtcaccca tcagggcctg agctcgcccc tcacaaagag cttcaacagg  | 2040 |
| ggagagtgt                                                          | 2049 |

<210> 1406

<211> 683

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1406

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

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Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

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Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

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Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
595 600 605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
610 615 620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1407  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1407  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccctggca 360

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```

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

```

<210> 1408  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1408

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys
          100          105          110

```



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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1409  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1409  
gatatccaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

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```

gggacaaaag tcgagatcaa gcgtacgggtg gctgcacccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

```

<210> 1410  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1410

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1411  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1411  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc  | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct | 360  |
| agtgccctcca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct | 420  |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg  | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacag | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc     | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tcaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc   | 1440 |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag  | 1500 |
| ccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat   | 1560 |
| gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag  | 1620 |
| ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga  | 1680 |

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gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc 1740  
accgtctcct caactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 1800  
ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860  
aaagtacagt ggaagggtgga taacgccctc caatcgggta actcccagga gagtgtcaca 1920  
gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980  
gactacgaga aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040  
gtcacaaaga gcttcaacag gggagagtgt 2070

<210> 1412  
<211> 690  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1412

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

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Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

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His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

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Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670



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Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685

Glu Cys  
690

<210> 1413  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1413  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttacttgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcgggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgccctggta aggactactt ccccgaaacc gtgacgggtgt cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1414  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1414

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asn | Lys | Asn | Tyr | Leu | Val | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Lys | Thr | Pro | Leu | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1415  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1415  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccagggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1416  
<211> 217  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1416

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

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Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1417  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1417  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600  
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660  
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg   | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggaggca gcaggggaac  | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tcctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gttacagcag  | 1380 |
| tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt  | 1440 |
| gggtccttca gtggttacta ctggaactgg attcgccagc caccaggga ggggctagag   | 1500 |
| tggattgggg aaatcaatca tgctggaaac accaactaca acccgccct caagagtcga   | 1560 |
| gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc  | 1620 |
| gccgcggaca cggctgtgta ttactgtgcg agaggatatt gtagaagtac cacctgctac  | 1680 |
| tttgactact ggggccaggg aaccctagtc accgtctcct caactgtggc tgcaccatct  | 1740 |
| gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc  | 1800 |
| ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc | 1860 |
| caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc  | 1920 |
| ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc  | 1980 |
| gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt  | 2040 |

<210> 1418

<211> 680

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1418

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
355 360 365



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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

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Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1419

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1419

gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 1420  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1420

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1421

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1421

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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

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tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc   180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc   240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg   300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc   360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc   420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc   480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag   540
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc   600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a           651

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<210> 1422  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1422

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1423

<211> 2034

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1423

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60

## A-1937-W0-PCT\_ST25

|                                                                    |      |
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| ccccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag | 360  |
| ggcccatcgg tcttccccct ggacccctcc tccaagagca cctctggggg cacagcggcc  | 420  |
| ctgggctgcc tggtaagga ctacttcccc gaaccgggtga cgggtgctgt gaactcaggc  | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc  | 540  |
| ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc  | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc    | 780  |
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt  | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggctctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg  | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac | 1260 |
| gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gctgcaggag | 1380 |
| tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt  | 1440 |
| ggctccatca gtagttactt ctggagctgg attcggcagc cccaggtaa gggactggag   | 1500 |

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tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga 1560  
 gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc 1620  
 gctgcggaca cggccgtgta ttactgtgcg agagaaactg ggagctacta cggctttgac 1680  
 tactggggcc agggaaaccct ggtcaccgtc tcctcaactg tggctgcacc atctgtcttc 1740  
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 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 1860  
 ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcgaa 1920  
 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 1980  
 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 2034

<210> 1424  
 <211> 678  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1424

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
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Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80



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Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
275 280 285

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

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Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala  
565 570 575

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
580 585 590

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
595 600 605

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
610 615 620

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
625 630 635 640

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
645 650 655

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
660 665 670

Phe Asn Arg Gly Glu Cys  
675

<210> 1425  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1425  
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1426  
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<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1426

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Lys | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

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<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1427  
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccagggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1428  
<211> 217  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1428

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

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Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1429  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1429  
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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
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gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600  
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660  
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg   | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tcctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag   | 1380 |
| tcagggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg | 1440 |
| gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc   | 1500 |
| cttgagtgga taggaaggac atactacagg tccaagtgggt ataatgatta tgcagtttct | 1560 |
| ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg  | 1620 |
| agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc  | 1680 |
| tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctctcaact   | 1740 |
| gtggctgcac catctgtctt catcttccc ccatctgatg agcagttgaa atctggaact   | 1800 |
| gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag  | 1860 |
| gtggataacg ccctccaatc gggtaactcc caggagagtgc tcacagagca ggacagcaag | 1920 |
| gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac  | 1980 |
| aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc   | 2040 |
| aacaggggag agtgt                                                   | 2055 |

<210> 1430

<211> 685

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1430

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
165 170 175

Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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

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Ser Arg Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

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Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1431  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1431  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

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tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 180  
 gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
 cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360  
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
 tgcctgggtca aggactactt ccccgaaaccg gtgacgggtg cgtggaactc aggcgccttg 480  
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
 agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1432  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1432

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

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Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1433

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1433

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc

60

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```

ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggtagcgcc tctgtttgtg gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1434  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1434

```

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 Arg Ser Ser
          20          25          30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35          40          45

```

```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50          55          60

```



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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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1435

<211> 2055

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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&lt;400&gt; 1435

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc  | 60   |
| acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat ccgccagcca | 120  |
| ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac | 180  |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg  | 240  |
| acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgcgag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca  | 360  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg  | 420  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtc | 480  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 540  |
| ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc  | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc  | 660  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga  | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct   | 780  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc  | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag  | 960  |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag   | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg  | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg  | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg  | 1320 |
| cagaagagcc tctccctgtc tccgggtggg ggcggtcgg gaggtggcgg atccgaggta   | 1380 |
| caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt  | 1440 |

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gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga 1500  
aaagggctcg agtggggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560  
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620  
atgaactcac ttgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg 1680  
tctacagctt cgtcgctcga ctattgggggt caaggaacgt tggtcaccgt ctctagtact 1740  
gtggctgcac catctgtctt catcttcccc ccatctgatg agcagttgaa atctggaact 1800  
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860  
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920  
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980  
aaagtctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 2040  
aacaggggag agtgt 2055

<210> 1436

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1436

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

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Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

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Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1437  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1437  
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtcct ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtagcggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattc tgt 633

<210> 1438  
<211> 211

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1438

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160



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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1439  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1439  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

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<210> 1440  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1440

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1441  
<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1441  
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgccagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtagca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagagacc 600  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct   | 780  |
| gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc  | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag  | 960  |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag  | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc  | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg  | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg  | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg  | 1320 |
| cagaagagcc tctccctgtc tccgggtgtt ggcgatcgg gaggtggcgg atccgaggtg   | 1380 |
| cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt  | 1440 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg | 1500 |
| aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg  | 1560 |
| tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag  | 1620 |
| tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt | 1680 |
| cttgactact ggggccaggg aaccctggtc accgtctcta gtcagcccaa ggccaacccc  | 1740 |
| actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagt    | 1800 |
| tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc  | 1860 |
| cccgtcaagg cgggagtgga gaccaccaa cctccaac agagcaacaa caagtacgcg     | 1920 |
| gccgagagct acctgagcct gacgcccag cagtggaaagt cccacagaag ctacagctgc  | 1980 |
| caggtcacgc atgaaggag caccgtggag aagacagtgg cccctacaga atgttca      | 2037 |

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<210> 1442  
 <211> 679  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1442

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

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Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

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Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln Pro  
565 570 575

Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu  
580 585 590

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro  
595 600 605

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala  
610 615 620

Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala  
625 630 635 640

Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg  
645 650 655

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr  
660 665 670

Val Ala Pro Thr Glu Cys Ser  
675

<210> 1443

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1443

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc

60



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|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| tcctgcactg | ggagcagttc  | caacatcggg | gcaggttatg | atgtacactg | gtaccagcag | 120 |
| tttccaggaa | cagcccccaa  | actcctcatc | caaggtaaca | gcaatcggcc | ctcaggggtc | 180 |
| cctgaccgat | tctctggctc  | caagtctggc | acctcagcct | ccctggccat | cactgggctc | 240 |
| caggctgagg | atgaggctga  | ttattactgc | cagtcctatg | acagcagcct | gagtggttcg | 300 |
| gtgttcggcg | gagggaccaa  | gctgaccgtc | ctaggtgcct | ccaccaaggg | cccatcggtc | 360 |
| ttccccctgg | caccctcctc  | caagagcacc | tctgggggca | cagcggccct | gggctgcctg | 420 |
| gtcaaggact | acttccccga  | accggtgacg | gtgtcgtgga | actcaggcgc | cctgaccagc | 480 |
| ggcgtgcaca | ccttcccggc  | tgtcctacag | tcctcaggac | tctactccct | caaaagcgtg | 540 |
| gtgaccgtgc | cctccagcag  | cttgggcacc | cagacctaca | tctgcaacgt | gaatcacaag | 600 |
| cccagcaaca | ccaagggtgga | caagaaagtt | gagcccaaat | cttgt      |            | 645 |

|       |                     |
|-------|---------------------|
| <210> | 1444                |
| <211> | 215                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1444

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

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Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1445

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1445

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgccca      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1446

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1446

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

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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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1447

<211> 2049

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1447

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc | 60   |
| acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc  | 120  |
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac  | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggcttt cccctggca ccctcctcca agagcacctc tgggggcaca   | 420  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc   | 540  |
| tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gccc aaatct  | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgga cctgagggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc     | 1020 |
| aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc | 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 tgggtggcgga tcgggaggtg gcggatccga ggtacaactg | 1380 |

A-1937-W0-PCT\_ST25

|             |            |            |             |             |            |      |
|-------------|------------|------------|-------------|-------------|------------|------|
| gtggaatcag  | gtggagggtt | ggtgcagccg | gggagatcgc  | tcaggccttag | ctgtgcggca | 1440 |
| tcgggggttta | ctttcgatga | ttatgcgatg | cattgggtcc  | ggcaagcgcc  | tggaaaaggg | 1500 |
| ctcgagtggg  | tttccgccat | tacgtggaat | agcggacaca  | tcgattatgc  | agacagtgtg | 1560 |
| gagggcagat  | tcacaatctc | acgagacaat | gctaagaaca  | gcctgtacct  | tcagatgaac | 1620 |
| tcacttcgcg  | cggaagatac | cgccgtatac | tactgcgcca  | aagtctccta  | cttgtctaca | 1680 |
| gcttcgtcgc  | tcgactattg | gggtcaagga | acgttgggtca | ccgtctctag  | tactgtggct | 1740 |
| gcaccatctg  | tcttcatctt | cccgccatct | gatgagcagt  | tgaaatctgg  | aactgcctct | 1800 |
| gttgtgtgcc  | tgctgaataa | cttctatccc | agagaggcca  | aagtacagtg  | gaaggtggat | 1860 |
| aacgccctcc  | aatcgggtaa | ctcccaggag | agtgtcacag  | agcaggacag  | caaggacagc | 1920 |
| acctacagcc  | tcgaaagcac | cctgacgctg | agcaaagcag  | actacgagaa  | acacaaagtc | 1980 |
| tacgcctgcg  | aagtcaccca | tcagggcctg | agctcgcccg  | tcacaaagag  | cttcaacagg | 2040 |
| ggagagtgt   |            |            |             |             |            | 2049 |

|       |                     |
|-------|---------------------|
| <210> | 1448                |
| <211> | 683                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1448

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

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Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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



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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly  
 435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
 450 455 460

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
 465 470 475 480

Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala  
 485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
 500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
 515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
 530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
 545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 565 570 575

Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 595 600 605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 610 615 620

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Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1449  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1449  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagtcctt gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtagcggg gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

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<210> 1450  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1450

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1451  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1451  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcga 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1452  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1452

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1453  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1453  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gccc aaatct  | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttctctt tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcggga tcgggaggtg gcggatccga ggtgcagctg | 1380 |
| gtgcagtctg gagcagaggt gaaaaagccc ggggagtctc tgaagatctc ctgtaagact   | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc   | 1500 |
| ctggagtgga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc   | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc   | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctttgac   | 1680 |
| tactggggcc agggaaacct gggtcaccgtc tctagtcagc ccaaggccaa cccactgtc   | 1740 |
| actctgttcc cgccctcctc tgaggagctc caagccaaca aggccacact agtgtgtctg   | 1800 |
| atcagtgact tctaccggg agctgtgaca gtggcctgga aggagatgg cagccccgtc     | 1860 |
| aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccgag    | 1920 |
| agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccaggtc   | 1980 |
| acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a            | 2031 |

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<210> 1454  
 <211> 677  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1454

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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



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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

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Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln Pro Lys Ala  
565 570 575

Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
580 585 590

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala  
595 600 605

Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val  
610 615 620

Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu  
625 630 635 640

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr  
645 650 655

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala  
660 665 670

Pro Thr Glu Cys Ser  
675

<210> 1455

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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```

<400> 1455
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc      360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg      420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt                        645

```

```

<210> 1456
<211> 215
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic polypeptide

```

<400> 1456

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
          35          40          45

```

```

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

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Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1457

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1457

```

gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc      480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

```

&lt;210&gt; 1458

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1458

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35           40           45

```

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Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1459

<211> 2070

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1459

|                                                                    |      |
|--------------------------------------------------------------------|------|
| caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc  | 60   |
| acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg   | 120  |
| cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtgggtat  | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac  | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgtac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc  | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct   | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg  | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag   | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc    | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc  | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |



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cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtgggtggcgg atcgggaggt 1380  
ggcggatccg aggtacaact ggtggaatca ggtggagggtt tgggtgcagcc ggggagatcg 1440  
ctcaggctta gctgtgcggc atcgggggttt actttcgatg attatgcgat gcattggggtc 1500  
cggcaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac 1560  
atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac 1620  
agcctgtacc ttcagatgaa ctcaacttcgc gcggaagata ccgccgtata ctactgcgcc 1680  
aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtcaagg aacgttggtc 1740  
accgtctcta gtactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 1800  
ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860  
aaagtacagt ggaaggtgga taacgccctc caatcgggta actcccagga gagtgtcaca 1920  
gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980  
gactacgaga aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040  
gtcacaaaga gcttcaacag gggagagtgt 2070

<210> 1460

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1460

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

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Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

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Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

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Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685

Glu Cys  
690

<210> 1461  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1461  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540

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tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aagggtggaca agaaagttga gcccaaattct tgt 633

<210> 1462  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1462

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1463  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1463  
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1464  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1464

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125



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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1465  
<211> 2052  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1465  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggatat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgtac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa   | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct   | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc   | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac   | 660  |
| aagaaaagttg agcccaaatac ttgtgacaaa actcacacat gcccaccgtg cccagcacct | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg   | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag    | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt   | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac   | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc   | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc   | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg   | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt   | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct   | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg   | 1500 |
| cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat   | 1560 |
| accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt   | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg    | 1680 |
| agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtcag   | 1740 |
| cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac   | 1800 |
| aaggccacac tagtgtgtct gatcagtgac ttctaccgg gagctgtgac agtggcctgg    | 1860 |

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aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc 1920  
aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtcccac 1980  
agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct 2040  
acagaatgtt ca 2052

<210> 1466  
<211> 684  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1466

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

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Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

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Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro  
580 585 590

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
595 600 605

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly  
610 615 620

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser  
625 630 635 640

Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln  
645 650 655

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser  
660 665 670

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

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<210> 1467  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1467  
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 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
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 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagt gagcccaa at cttgt 645

<210> 1468  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1468

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

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Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215



<210> 1469  
 <211> 2064  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1469  
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 agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg 120  
 cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360  
 agtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 420  
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
 tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
 agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
 aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 660  
 agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
 ctcttggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac 780  
 tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc 840  
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900  
 gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960  
 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1020  
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080  
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aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 1440
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cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 1560
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 1620
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 1680
tattgtagaa gtaccacctg ctactttgac tactggggcc aggggaaccct agtcaccgtc 1740
tcctcaactg tggctgcacc atctgtcttc atcttcccgc catctgatga gcagttgaaa 1800
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta 1860
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 1920
gacagcaagg acagcaccta cagcctcgaa agcacctga cgctgagcaa agcagactac 1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca 2040
aagagcttca acaggggaga gtgt 2064

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<210> 1470  
 <211> 688  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1470

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

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Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
 210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 385 390 395 400

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Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

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Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1471

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1471

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| gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc  | 60  |
| ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa   | 120 |
| cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca  | 180 |
| gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag  | 240 |
| cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa  | 300 |
| gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccctggca  | 360 |
| ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac  | 420 |
| ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc | 480 |

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ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1472  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1472

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1473  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1473  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420



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```

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

```

<210> 1474  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1474

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys
          100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1475  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1475  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360

## A-1937-W0-PCT\_ST25

|                                   |                                   |      |
|-----------------------------------|-----------------------------------|------|
| agtacggtgg ctgcaccatc tgtcttcac   | ttcccggcat ctgatgagca gttgaaatct  | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat  | aacttctatc ccagagaggc caaagtacag  | 480  |
| tggaaggtgg ataacgccct ccaatcgggt  | aactcccagg agagtgtcac agagcaggac  | 540  |
| agcaaggaca gcacctacag cctcaagagc  | accctgacgc tgagcaaagc agactacgag  | 600  |
| aaacacaaaag tctacgcctg cgaagtcacc | catcagggcc tgagctcgcc cgtcacaaaag | 660  |
| agcttcaaca ggggagagtg tgacaaaact  | cacacatgcc caccgtgccc agcacctgaa  | 720  |
| ctcctggggg gaccgtcagt cttcctcttc  | ccccaaaaac ccaaggacac cctcatgac   | 780  |
| tcccggaccc ctgaggtcac atgcgtgggtg | gtggacgtga gccacgaaga ccctgaggtc  | 840  |
| aagttcaact ggtacgtgga cggcgtggag  | gtgcataatg ccaagacaaa gccgtgtgag  | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc  | agcgtcctca ccgtcctgca ccaggactgg  | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc  | tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc  | cgagaaccac aggtgtacac cctgccccca  | 1080 |
| tcccgggagg agatgaccaa gaaccaggtc  | agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc  | aatgggcagc cggagaacaa ctacaagacc  | 1200 |
| acgcctcccg tgctggactc cgacggctcc  | ttcttcctct atagcaagct caccgtggac  | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc  | tcatgctccg tgatgcatga ggctctgcac  | 1320 |
| aaccactaca cgcagaagag cctctccctg  | tctccgggtg gtggcggatc gggaggtggc  | 1380 |
| ggatcccagg tgcagctgca ggagtcgggc  | ccaggactgg tgaagccttc ggagaccctg  | 1440 |
| tccctcacct gcactgtctc tgggtggctcc | atcagtagtt acttctggag ctggattcgg  | 1500 |
| cagccccag gtaagggact ggagtggatt   | ggctatatct attacagtgg gcagacaaaa  | 1560 |
| tacaaccct ccctcaagag tcgagtcacc   | atatcaatag acacgtccaa gaaccagttc  | 1620 |
| tccctgaagc tgagctctgt gaccgtgcg   | gacacggccg tgtattactg tgcgagagaa  | 1680 |
| actgggagct actacggctt tgactactgg  | ggccagggaa ccctgggtcac cgtctcctca | 1740 |
| actgtggctg caccatctgt cttcatcttc  | ccgccatctg atgagcagtt gaaatctgga  | 1800 |

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actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 1860  
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 1920  
aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa 1980  
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 2040  
ttcaacaggg gagagtgt 2058

<210> 1476  
<211> 686  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1476

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

A-1937-W0-PCT\_ST25

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

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Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

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Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

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<210> 1477  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1477  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
 gggaaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
 ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1478  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1478

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |



## A-1937-W0-PCT\_ST25

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 195 200 205

Lys Ser Cys  
210

<210> 1479  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1479  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1480  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1480

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1481  
<211> 2079  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1481  
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agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt cgggcaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 660  
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgata 780  
tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc 840  
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900  
gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960  
ctgaatggca aggagtacaa gtgcaagggt tccaacaaaag ccctcccagc ccccatcgag 1020

# A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac    | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc   | 1440 |
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg   | 1500 |
| attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag   | 1560 |
| tgggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc  | 1620 |
| aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac   | 1680 |
| tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg   | 1740 |
| accacgggtca cagtctctc aactgtggct gcaccatctg tcttcatctt cccgccatct   | 1800 |
| gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc   | 1860 |
| agagaggcca aagtacagt gaaggtggat aacgccctcc aatcgggtaa ctcccaggag    | 1920 |
| agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg   | 1980 |
| agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg   | 2040 |
| agctcgcccc tcacaaagag cttcaacagg ggagagtgt                          | 2079 |

<210> 1482  
 <211> 693  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1482

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

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Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

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Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575



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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

<210> 1483  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1483  
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttactgggc atctaccg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

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atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgcctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1484  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1484

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

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Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1485  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1485  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc ggcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

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```

aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1486  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1486

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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

```

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Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1487  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1487  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| cccggaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac     | 180  |
| agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac   | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc   | 360  |
| aacccccactg tcaactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat   | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag   | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac   | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca    | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc     | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc      | 1020 |
| aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg   | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac   | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag   | 1320 |
| agcctctccc tgtctccggg tgggtggcga tcgggagggtg gcggatccca ggtgcagtta  | 1380 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc    | 1440 |
| catggtgggt ccttcagtgg ttactactgg aactggattc gccagccacc agggaaagggg  | 1500 |
| ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag   | 1560 |

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agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct 1620  
 gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc 1680  
 tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcaac tgtggctgca 1740  
 ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac tgcctctgtt 1800  
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 1860  
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 1920  
 tacagcctcg aaagcacctt gacgctgagc aaagcagact acgagaaaca caaagtctac 1980  
 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 2040  
 gagtgt 2046

<210> 1488  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1488

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

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Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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



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Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

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Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
580 585 590

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
595 600 605

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
610 615 620

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
625 630 635 640

Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
645 650 655

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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
660 665 670

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1489  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1489  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1490  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>

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&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1490

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 165 170 175

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1491  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1491  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1492  
<211> 215  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1492

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

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Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1493  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1493  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgaggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccgaaggcc 360  
aaccctactg tctctctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540  
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac 600  
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660  
tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc  | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tcgggagggtg gcggatccca ggtgcagctg | 1380 |
| caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc  | 1440 |
| tctggtggct ccatcagtag ttacttctgg agctggattc ggcagcccc aggtaaggga   | 1500 |
| ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag  | 1560 |
| agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct  | 1620 |
| gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc  | 1680 |
| tttgactact ggggccaggg aaccctggtc accgtctcct caactgtggc tgcaccatct  | 1740 |
| gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc  | 1800 |
| ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc | 1860 |
| caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc  | 1920 |
| ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc  | 1980 |
| gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt  | 2040 |

<210> 1494

<211> 680

<212> PRT

<213> Artificial Sequence



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<220>

<223> Synthetic polypeptide

<400> 1494

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

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Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
355 360 365

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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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560

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Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1495

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1495

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggc caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattc tgt 633

<210> 1496  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1496

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1497  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1497  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

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tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc   180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc   240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg   300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc   360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg   420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc   480
ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg   540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag   600
cccagcaaca ccaagggtga caagaaagtt gagcccaaat cttgt                      645

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<210> 1498  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1498

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1                      5                      10                      15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
                     20                      25                      30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
                     35                      40                      45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
                     50                      55                      60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65                      70                      75                      80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1499

<211> 2061

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1499

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc

60



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaggcc  | 360  |
| aacccactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca   | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc   | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtacagttg  | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc  | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg   | 1500 |

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aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca 1560  
 gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg 1620  
 aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg 1680  
 gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggc caccgtctcc 1740  
 tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 1800  
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 1860  
 tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 1920  
 agcaaggaca gcacctacag cctcgaaagc accctgacgc tgagcaaagc agactacgag 1980  
 aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 2040  
 agcttcaaca ggggagagtg t 2061

<210> 1500  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1500

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

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Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

## A-1937-W0-PCT\_ST25

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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510

Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
580 585 590

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
595 600 605

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
610 615 620

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
625 630 635 640

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Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys  
645 650 655

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
660 665 670

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1501  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1501  
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tgggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctacccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcgggtcttcc ccctggcacc ctcttccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctgggtca aggactactt ccccgaaaccg gtgacgggtg cgtggaactc aggcgccttg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1502  
<211> 217  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1502

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asn | Lys | Asn | Tyr | Leu | Val | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Lys | Thr | Pro | Leu | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1503  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1503  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaaagt gagcccaaatt cttgt 645

<210> 1504  
<211> 215



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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1504

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

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Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1505  
<211> 2064  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1505  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccaggga ccttagtcac cgtctcctca 360  
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc  | 780  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgaggtcaag   | 840  |
| ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc    | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag   | 1260 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |
| tccgaggtag aactgggtgga atcagggtgga ggtttggtgc agccggggag atcgctcagg | 1440 |
| cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa   | 1500 |
| gcgcctggaa aagggtctga gtgggtttcc gccattacgt ggaatagcgg acacatcgat   | 1560 |
| tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg   | 1620 |
| taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc   | 1680 |
| tcctacttgt ctacagcttc gtcgctcgac tattgggggtc aaggaacgtt ggtcaccgtc  | 1740 |
| tctagtactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa    | 1800 |
| tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta   | 1860 |
| cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag   | 1920 |
| gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac   | 1980 |
| gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca   | 2040 |
| aagagcttca acaggggaga gtgt                                          | 2064 |

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<210> 1506  
 <211> 688  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1506

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
 115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 145 150 155 160

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Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

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Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

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Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1507

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1507

gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg

60

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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagtga gccc aaatct tgt 633

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<210> 1508  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1508

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10          15

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```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20          25          30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45

```

```

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

```



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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1509  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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<400> 1509  
gaaatttgtt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattc tgt 633

<210> 1510  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1510

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ala | Pro | Arg | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Tyr | Gly | Ala | Ser | Ser | Arg | Ala | Thr | Gly | Ile | Pro | Asp | Arg | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

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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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1511

<211> 2046

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1511

|                                                                     |      |
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| cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc  | 60   |
| acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca   | 120  |
| ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac   | 180  |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca    | 360  |
| acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 420  |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 480  |
| aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gtcgccccgt cacaaagagc   | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 720  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccctg aggtcacatg cgtggtgggtg gacgtgagcc acgaagaccc tgaggtcaag  | 840  |
| ttcaactggt acgtggacgg cgtggagggtg cataatgcc aagacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc  | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag    | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac   | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |

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|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| tccgaggtgc | agctggtgca  | gtctggagca  | gaggtgaaaa  | agcccgggga | gtctctgaag | 1440 |
| atctcctgta | agactttctga | atacagcttt  | accagctact  | ggatcggctg | ggtgcgccag | 1500 |
| atgcccggga | aaggcctgga  | gtggatgggg  | atcatctatc  | ttggtgactc | agataccaga | 1560 |
| tacagcccgt | ccttccaagg  | ccaggtcacc  | atctcagccg  | acaagtccat | cagtaccgcc | 1620 |
| tacctgcagt | ggagcagcct  | gaaggcctcg  | gacaccgcca  | tgtattactg | tgcgagaagt | 1680 |
| aactggggtc | ttgactactg  | gggccaggga  | accctgggtca | ccgtctctag | tcagcccaag | 1740 |
| gccaaaccca | ctgtcactct  | gttcccggcc  | tcctctgagg  | agctccaagc | caacaaggcc | 1800 |
| acactagtgt | gtctgatcag  | tgactttctac | ccgggagctg  | tgacagtggc | ctggaaggca | 1860 |
| gatggcagcc | ccgtcaaggc  | gggagtggag  | accaccaaac  | cctccaaaca | gagcaacaac | 1920 |
| aagtacgcgg | ccgagagcta  | cctgagcctg  | acggccgagc  | agtggaagtc | ccacagaagc | 1980 |
| tacagctgcc | aggtcacgca  | tgaaggggagc | accgtggaga  | agacagtggc | ccctacagaa | 2040 |
| tgttca     |             |             |             |            |            | 2046 |

|       |                     |
|-------|---------------------|
| <210> | 1512                |
| <211> | 682                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1512

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

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Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

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Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

## A-1937-W0-PCT\_ST25

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
 450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
 465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
 485 490 495

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
 500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
 515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
 530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
 545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 565 570 575

Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser  
 580 585 590

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp  
 595 600 605

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro  
 610 615 620



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Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn  
625 630 635 640

Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys  
645 650 655

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val  
660 665 670

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

<210> 1513  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1513  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctccagggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcctt caaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagt gagcccaaatt cttgt 645

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<210> 1514  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1514

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 145 150 155 160

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Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1515  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1515  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480  
ttccccgctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 1516  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1516

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1517  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1517  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360  
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 420  
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480  
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac  | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc  | 780  |
| cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaaagaca agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag  | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc  | 1440 |
| tgtgcggcat cggggtttac tttcgatgat tatgcgatgc attgggtccg gcaagcgct   | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca  | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt  | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac   | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtcaaggaa cgttgggtcac cgtctctagt | 1740 |
| actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 1800 |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg  | 1860 |
| aagggtgata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 1920 |
| aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa  | 1980 |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc  | 2040 |

ttcaacaggg gagagtgt

2058

<210> 1518  
 <211> 686  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1518

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
 115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
 130 135 140

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Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335



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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
515 520 525

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Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560

Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1519

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

A-1937-W0-PCT\_ST25

<223> Synthetic polynucleotide

<400> 1519

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gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg      60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc      120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtcg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1520

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1520

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

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Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1521

<211> 633

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 1521

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1522

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1522

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1523

<211> 2040

## A-1937-WO-PCT\_ST25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1523

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcgagac cctgtccctc  | 60   |
| acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc  | 120  |
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac  | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg  | 360  |
| gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc  | 420  |
| tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac  | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa  | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac  | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggc ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag  | 1080 |
| gagatgacca agaaccaggc cagcctgacc tgcctggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |

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|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| tggcagcagg | ggaacgtctt  | ctcatgtctc | gtgatgcatg | aggctctgca | caaccactac | 1320 |
| acgcagaaga | gcctctccct  | gtctccgggt | ggtggcggat | cgggaggtgg | cggatccgag | 1380 |
| gtgcagctgg | tgcagtctgg  | agcagaggtg | aaaaagcccg | gggagtctct | gaagatctcc | 1440 |
| tgtaaactt  | ctgaatacag  | ctttaccagc | tactggatcg | gctgggtgcg | ccagatgccc | 1500 |
| gggaaaggcc | tggagtggat  | ggggatcatc | tatcttggtg | actcagatac | cagatacagc | 1560 |
| ccgtccttcc | aaggccaggt  | caccatctca | gccgacaagt | ccatcagtac | cgcctacctg | 1620 |
| cagtggagca | gcctgaaggc  | ctcggacacc | gccatgtatt | actgtgcgag | aagtaactgg | 1680 |
| ggtcttgact | actggggcca  | gggaaccctg | gtcaccgtct | ctagtcagcc | caaggccaac | 1740 |
| cccactgtca | ctctgtttcc  | gccctcctct | gaggagctcc | aagccaacaa | ggccacacta | 1800 |
| gtgtgtctga | tcagtgactt  | ctacccggga | gctgtgacag | tggcctggaa | ggcagatggc | 1860 |
| agccccgtca | aggcggggagt | ggagaccacc | aaaccctcca | aacagagcaa | caacaagtac | 1920 |
| gcggccgaga | gctacctgag  | cctgacgccc | gagcagtgga | agtcccacag | aagctacagc | 1980 |
| tgccaggtca | cgcataaagg  | gagcaccgtg | gagaagacag | tggcccctac | agaatgttca | 2040 |

|       |                     |
|-------|---------------------|
| <210> | 1524                |
| <211> | 680                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1524

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45



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Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln  
565 570 575

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
580 585 590

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
595 600 605

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys  
610 615 620

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Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
625 630 635 640

Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
645 650 655

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
660 665 670

Thr Val Ala Pro Thr Glu Cys Ser  
675 680

<210> 1525  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1525  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 1526  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1526

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1527  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1527  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aagggtggaca agaaaagttga gccc aaatct tgt

633

&lt;210&gt; 1528

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1528

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1529  
<211> 2079  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1529  
cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtgggaagg ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540



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|                                                                   |      |
|-------------------------------------------------------------------|------|
| acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa | 600  |
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg | 660  |
| cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac  | 780  |
| accctcatga tctcccggac ccctgaggct acatgcgtgg tggaggacgt gagccacgaa | 840  |
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacia agccctccca  | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggct | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagggggaga gcaatgggca gccggagaac | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag  | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga | 1380 |
| tcgggagggt gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg | 1440 |
| gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg | 1500 |
| cattgggtcc ggcaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat  | 1560 |
| agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat | 1620 |
| gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac | 1680 |
| tactgcgcca aagtctccta cttgtctaca gcttcgtcgc tcgactattg gggtaagga  | 1740 |
| acgttggtca ccgtctctag tactgtggct gcaccatctg tcttcatctt cccgccatct | 1800 |
| gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc | 1860 |
| agagaggcca aagtacagtg gaaggaggat aacgccctcc aatcgggtaa ctcccaggag | 1920 |
| agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg | 1980 |

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agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 2040

agctcgcccg tcacaaagag cttcaacagg ggagagtgt 2079

<210> 1530

<211> 693

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1530

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

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Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

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His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
500 505 510

A-1937-W0-PCT\_ST25

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

A-1937-WO-PCT\_ST25

<210> 1531  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1531  
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 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 1532  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1532

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

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<210> 1533  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1533  
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 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
 tggtagcagc agaaaccagg aaagggttct aaactgctca tttactgggc atctaccg 180  
 gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
 cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
 tgcctgggtca aggactactt ccccgaaccg gtgacgggtg cgtggaactc aggcgccctg 480  
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
 agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

<210> 1534  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1534

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |



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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

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Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1535  
 <211> 2061  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1535  
 caggtagct tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
 acctgtacca tctccgggga cagtgtctct accaaccagtg ttgcttgga ctggattagg 120  
 cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtgggtat 180  
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
 agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
 gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
 cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480  
 gccaaagtac agtggaagggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540  
 acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
 gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
 cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
 ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780  
 accctcatga tctcccgga cctgaggtc acatgcgtgg tggaggacgt gagccacgaa 840  
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900  
 aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960  
 caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacia agccctccca 1020  
 gccccatcg agaaaacat ctcaaagcc aaagggcagc ccgagaacc acaggtgtac 1080

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accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc      1140
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aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag      1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat      1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggtagcgga      1380
tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc      1440
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc      1500
ggctgggtgc gccagatgcc cgggaaaaggc ctggagtgga tggggatcat ctatcttgg      1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag      1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat      1680
tactgtgcga gaagtaactg gggctttgac tactggggcc agggaaacct ggtcaccgtc      1740
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc      1800
caagccaaca aggccacact agtgtgtctg atcagtgact tctacccggg agctgtgaca      1860
gtggcctgga aggcagatgg cagccccgtc aaggcgggag tggagaccac caaacctcc      1920
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg      1980
aagtcaccaca gaagctacag ctgccaggtc acgcatgaag ggagcaccgt ggagaagaca      2040
gtggccccta cagaatgttc a                                          2061

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<210> 1536  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1536

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

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Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

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Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu  
580 585 590

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Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val  
595 600 605

Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys  
610 615 620

Ala Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser  
625 630 635 640

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr  
645 650 655

Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His  
660 665 670

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680 685

<210> 1537

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1537

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| tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag | 120 |
| tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc | 180 |
| cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc | 240 |
| caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg | 300 |
| gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc | 360 |
| ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg | 420 |

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gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 1538  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1538

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110



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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1539  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1539  
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360

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tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
 tgcctgggtca aggactactt ccccgaaaccg gtgacgggtgt cgtggaactc aggcgccttg 480  
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
 agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1540  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1540

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

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Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1541  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1541  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

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gggacaaaag tcgagatcaa gcgtacgggtg gctgcacccat ctgtcttcat cttcccgccca    360
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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag    480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg    540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc    600
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<210> 1542  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1542

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1543  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1543  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtggt gtctggggaca gacttcactc tcaccatcag cagactggag 240

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cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tgggtaccgcc tctgtttgtgt gcctgctgaa taactttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1544  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1544

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

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Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1545  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1545  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac  | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc  | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct | 360  |
| agtcctcca ccaagggccc atcggcttcc cccctggcac cctcctcaa gagcacctct    | 420  |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg  | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 540  |
| tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag  | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc   | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag  | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atgcccggtg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggattcg caagccacca  | 1500 |
| gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg  | 1560 |
| tcctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg   | 1620 |



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ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga 1680  
 agtaccacct gctactttga ctactggggc caggggaaccc tagtcaccgt ctctcagcc 1740  
 tccaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 1800  
 acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860  
 aactcaggcg ccctgaccag cggcgtgcac accttcccg ctgtcctaca gtcctcagga 1920  
 ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 1980  
 atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tgagcccaaa 2040  
 tcttgt 2046

<210> 1546  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1546

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

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Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

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Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1547  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1547  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1548  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1548

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1549  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1549  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1550  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1550

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
 165 170 175



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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1551  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1551  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtgccctcca ccaaggggccc atcggctctt cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacag 600  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660  
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780  
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag   | 1380 |
| gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc   | 1440 |
| tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gaagcccca    | 1500 |
| ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc   | 1560 |
| tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag   | 1620 |
| ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc   | 1680 |
| tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc agcctccacc  | 1740 |
| aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg  | 1800 |
| gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca | 1860 |
| ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac   | 1920 |
| tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc  | 1980 |
| aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt   | 2040 |

<210> 1552

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1552

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175

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Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

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Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1553  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1553  
gatatcaaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240

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```

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaaag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

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<210> 1554  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1554

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95

```

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1555  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1555  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180



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gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1556  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1556

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

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Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1557  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1557  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaagcg 120

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat  | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac  | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc  | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct | 360  |
| agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct | 420  |
| gggggacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg   | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 540  |
| tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag  | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg  | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc   | 1440 |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggaag  | 1500 |
| ccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat   | 1560 |

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gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 1620  
 ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 1680  
 gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc 1740  
 accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag 1800  
 agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg 1860  
 gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920  
 ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980  
 ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040  
 aaagttgagc ccaaattcttg t 2061

<210> 1558  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1558

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

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Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495

Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1559  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1559  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1560  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>



&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1560

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 165 170 175

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Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
 195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
 210 215

<210> 1561  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1561  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 1562  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1562

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

<210> 1563  
 <211> 2031  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1563  
 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
 ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600  
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660  
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg   | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggaggca gcaggggaac  | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tcctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gttacagcag  | 1380 |
| tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt  | 1440 |
| gggtccttca gtggttacta ctggaactgg attcgcaagc caccaggga ggggctagag   | 1500 |
| tggattgggg aaatcaatca tgctggaaac accaactaca acccgctcct caagagtcga  | 1560 |
| gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc  | 1620 |
| gccgcggaca cggctgtgta ttactgtgcg agaggatatt gtagaagtac cacctgctac  | 1680 |
| tttgactact ggggccaggg aaccctagtc accgtctcct cagcctccac caagggccca  | 1740 |
| tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 1800 |
| tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgcctg    | 1860 |
| accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag  | 1920 |
| agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat  | 1980 |
| cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          | 2031 |

<210> 1564

<211> 677

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1564

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
355 360 365

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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560



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Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1565  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1565  
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tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

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cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1566  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1566

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1567

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1567

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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

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```

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1568  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1568

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

```

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln 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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1569

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1569

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc

60

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg  | 120  |
| ccccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac | 180  |
| agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag | 360  |
| ggcccatcgg tcttccccct ggacccctcc tccaagagca cctctggggg cacagcggcc  | 420  |
| ctgggctgcc tggtaagga ctacttcccc gaaccgggtga cgggtgctgt gaactcaggc  | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc  | 540  |
| ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc  | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc    | 780  |
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt  | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggctctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg  | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac | 1260 |
| gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gctgcaggag | 1380 |
| tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt  | 1440 |
| ggctccatca gtagttactt ctggagctgg attcgggaag ccccaggtaa gggactggag  | 1500 |

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|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| tggattggct | atatctatta  | cagtgggcag | accaaataca | acctctccct | caagagtcga | 1560 |
| gtcaccatat | caatagacac  | gtccaagaac | cagttctccc | tgaagctgag | ctctgtgacc | 1620 |
| gctgcggaca | cggccgtgta  | ttactgtgcg | agagaaactg | ggagctacta | cggctttgac | 1680 |
| tactggggcc | agggaaccct  | ggtcaccgtc | tcctcagcct | ccaccaaggg | cccatcggtc | 1740 |
| ttccccctgg | caccctcctc  | caagagcacc | tctgggggca | cagcggccct | gggctgcctg | 1800 |
| gtcaaggact | acttccccga  | accggtgacg | gtgtcgtgga | actcaggcgc | cctgaccagc | 1860 |
| ggcgtgcaca | ccttcccggc  | tgtcctacag | tcctcaggac | tctactccct | cgagagcgtg | 1920 |
| gtgaccgtgc | cctccagcag  | cttgggcacc | cagacctaca | tctgcaacgt | gaatcacaag | 1980 |
| cccagcaaca | ccaagggtgga | caagaaagtt | gagcccaa   | attgt      |            | 2025 |

|       |                     |
|-------|---------------------|
| <210> | 1570                |
| <211> | 675                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1570

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

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Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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



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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
275 280 285

Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

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Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 660 665 670

Lys Ser Cys  
 675

<210> 1571  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1571  
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 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1572  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1572

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 165 170 175

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Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1573  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1573  
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tggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctacccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1574  
<211> 220  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1574

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asn | Lys | Asn | Tyr | Leu | Val | Trp | Tyr | Gln | Glu | Lys | Pro | Gly | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Lys | Thr | Pro | Leu | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1575  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1575  
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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600  
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660  
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtgggtgggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc | 840  |
| gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt   | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc   | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg     | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg    | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac   | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc   | 1320 |
| tcctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag   | 1380 |
| tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg   | 1440 |
| gacagtgtct ctaccaacag tgttgcttgg aactggatta ggaagcccc agggaaaggc    | 1500 |
| cttgagtgga taggaaggac atactacagg tccaagtgggt ataattgatta tgcagtttct | 1560 |
| ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg   | 1620 |
| agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc   | 1680 |
| tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctctcagcc    | 1740 |
| tccaccaagg gcccatcgggt cttccccctg gcaccctcct ccaagagcac ctctgggggc  | 1800 |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg   | 1860 |
| aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga   | 1920 |
| ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac   | 1980 |
| atctgcaacg tgaatcacia gccagcaac accaaggtgg acaagaaagt tgagcccaaa    | 2040 |
| tcttgt                                                              | 2046 |

<210> 1576

<211> 682



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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1576

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
165 170 175

Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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

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Ser Arg Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Lys Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

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Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1577  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1577  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccaggagaaa 120

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1578  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1578

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1579

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1579

gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg

60

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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc      120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcga      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

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<210> 1580  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1580

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1581

<211> 2046

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide



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&lt;400&gt; 1581

|                                                                     |      |
|---------------------------------------------------------------------|------|
| caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc   | 60   |
| acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgcaagcca   | 120  |
| ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac   | 180  |
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgcgag aggatattgt    | 300  |
| agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca    | 360  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 420  |
| ggcacagcgg ccctgggctg cctggtaag gactacttcc ccgaaccggg gacgggtgtc    | 480  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 540  |
| ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc    | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 660  |
| aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga   | 720  |
| ccgtcagtct tcctcttccc cccaaaacc aaggacacc tcgatgctc ccggaccct       | 780  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 960  |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   | 1020 |
| aaagccaaag ggagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag     | 1080 |
| atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg   | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1320 |
| cagaagagcc tctccctgtc tccgggtggg ggcggtcgg gaggtggcgg atccgaggta    | 1380 |
| caactggtgg aatcagggtg aggtttggtg cagccgggga gatcgctcag gcttagctgt   | 1440 |

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gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggaa agcgcctgga 1500  
aaagggctcg agtggggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560  
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620  
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg 1680  
tctacagctt cgtcgctcga ctattgggggt caaggaacgt tggtcaccgt ctctagtgcc 1740  
tccaccaagg gcccatcgggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 1800  
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860  
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 1920  
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 1980  
atctgcaacg tgaatcaciaa gcccagcaac accaagggtgg acaagaaagt tgagcccaaa 2040  
tcttgt 2046

<210> 1582  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1582

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

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Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

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Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

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Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1583  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1583  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagccg tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1584  
<211> 214

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1584

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1585  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1585  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctccagggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651



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<210> 1586  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1586

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

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Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1587  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1587  
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgcaagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtagca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagagacc 600  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt  | 780  |
| gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc  | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag  | 960  |
| gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag  | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc  | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccggtg | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg  | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg  | 1320 |
| cagaagagcc tctccctgtc tccgggtgtt ggcggtatcg gaggtggcgg atccgaggtg  | 1380 |
| cagctgggtc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt  | 1440 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcaa gatgcccggg | 1500 |
| aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg  | 1560 |
| tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag  | 1620 |
| tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt | 1680 |
| cttgactact ggggccaggg aaccctggtc accgtctcta gtgcctccac caagggccca  | 1740 |
| tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 1800 |
| tgcttggtca aggactactt ccccgaaccg gtgacgggtg cgtggaactc aggcgccctg  | 1860 |
| accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag  | 1920 |
| agcgtgggtg ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat  | 1980 |
| cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaactctg t           | 2031 |

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<210> 1588  
 <211> 677  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1588

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

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Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

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Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1589

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1589

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

60

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```

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcga      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

<210> 1590  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1590

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20          25          30

```

```

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45

```

```

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

```



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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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1591

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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```

<400> 1591
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg      60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc      120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

```

<210> 1592
<211> 214
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic polypeptide

```

<400> 1592

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20           25           30

```

```

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1593  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1593

|                                                                    |      |
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| caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc  | 60   |
| acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc  | 120  |
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac  | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca   | 420  |
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  | 480  |
| tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc   | 540  |
| tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gccc aaatct  | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgga cctgagggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctcca gccccatcg agaaaacat ctccaaagcc      | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag    | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtacaactg  | 1380 |

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gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca 1440  
tcgggggttta ctttcgatga ttatgcgatg cattgggtcc ggaaagcgcc tggaaaaggg 1500  
ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg 1560  
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac 1620  
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680  
gcttcgctcg tcgactattg gggtaagga acgttggtca ccgtctctag tgcctccacc 1740  
aaggggcccat cggctttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 1800  
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860  
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
tccttcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1594

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1594

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

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Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
450 455 460

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Lys Ala  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640



A-1937-W0-PCT\_ST25

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1595  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1595  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1596  
<211> 214

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1596

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1597  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1597  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctccagggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

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<210> 1598  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1598

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

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Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1599  
<211> 2025  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1599  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 660

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcgaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc   | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tccggagggtg gcggatccga ggtgcagctg | 1380 |
| gtgcagtctg gagcagaggt gaaaaagccc ggggagctct tgaagatctc ctgtaagact  | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gcaagatgcc cgggaaaggc  | 1500 |
| ctggagtgga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc  | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc  | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac | 1680 |
| tactggggcc agggaaacct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc  | 1740 |
| ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg   | 1800 |
| gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc  | 1860 |
| ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactccct cgagagcgtg   | 1920 |
| gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag  | 1980 |
| cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt                 | 2025 |

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<210> 1600  
 <211> 675  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1600

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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



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Pro Pro Ser Arg Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Lys Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

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Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
660 665 670

Lys Ser Cys  
675

<210> 1601  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1601  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

60

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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tgggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg      180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc      480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

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<210> 1602  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1602

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
          20          25          30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys
          35          40          45

```

```

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50          55          60

```

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Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1603

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1603

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg  | 60  |
| attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc  | 120 |
| ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg  | 180 |
| aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc | 240 |
| gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa  | 300 |
| gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc   | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                     | 642 |

<210> 1604

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1604

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Gly | Ile | Arg | Asn | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Trp | Tyr | Gln | Glu | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Thr | Leu | Gln | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1605

<211> 2061

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1605

|                                                                     |      |
|---------------------------------------------------------------------|------|
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| acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg   | 120  |
| aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat     | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac   | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca   | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc  | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa  | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct   | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc   | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac   | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct   | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg     | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag    | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt   | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac   | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     | 1020 |
| gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc   | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg   | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt   | 1380 |

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```

ggcggatccg aggtacaact ggtggaatca ggtggagggtt tggtgcagcc ggggagatcg      1440
ctcaggctta gctgtgcggc atcgggggttt actttcgatg attatgcgat gcattggggtc      1500
cggaaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac      1560
atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac      1620
agcctgtacc ttcagatgaa ctacttcgc gcggaagata ccgccgtata ctactgcgcc      1680
aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtcaagg aacgttggtc      1740
accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag      1800
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg      1860
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc      1920
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg      1980
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag      2040
aaagttgagc ccaaattcttg t                                     2061

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<210> 1606  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1606

```

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1           5           10           15

```

```

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
20           25           30

```

```

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu
35           40           45

```



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Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

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Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1607  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1607  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

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<210> 1608  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1608

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 145 150 155 160

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Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1609  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1609  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1610  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1610

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

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Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1611  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1611  
caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540  
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct  | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg  | 780  |
| atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag  | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc    | 1020 |
| gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc  | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt  | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct  | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg  | 1500 |
| cgcaagatgc ccgggaaaagg cctggagtgg atggggatca tctatcttgg tgactcagat | 1560 |
| accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt  | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg   | 1680 |
| agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtgcc  | 1740 |
| tccaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc   | 1800 |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg  | 1860 |
| aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga  | 1920 |
| ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac  | 1980 |
| atctgcaacg tgaatcacia gcccagcaac accaaggtgg acaagaaagt tgagcccaaa  | 2040 |

tcttgt

2046

&lt;210&gt; 1612

&lt;211&gt; 682

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1612

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

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Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

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Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1613

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1613

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gaaatttgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1614

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1614

```

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 Arg Ser Ser
20          25          30

```

```

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu
35          40          45

```

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1615

<211> 2055

<212> DNA

<213> Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1615

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt | 60   |
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaaagcg | 120  |
| cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct | 360  |
| agtacgggtg ctgcaccatc tgtcttcac tccccgcat ctgatgagca gttgaaatct     | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc   | 780  |
| tccccgaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc  | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag   | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tccccggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat  | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |



A-1937-W0-PCT\_ST25

aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc 1380  
ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 1440  
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 1500  
aagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 1560  
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 1620  
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 1680  
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc 1740  
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 1800  
tctggggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 1860  
gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca ctttcccggc tgtcctacag 1920  
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980  
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2040  
gagcccaaatt cttgt 2055

<210> 1616  
<211> 685  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1616

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

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Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

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Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

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Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1617  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1617  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1618  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1618

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1619  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1619  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

642

&lt;210&gt; 1620

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1620

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Glu | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |



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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1621  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1621  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag  | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag  | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa  | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatk  | 780  |
| tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag  | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg  | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  | 1080 |
| tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac  | 1260 |
| aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc | 1380 |
| ggatcccagg tgcaagtga ggagtcgggc ccaggactgg tgaagccttc ggagaccctg   | 1440 |
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg | 1500 |
| aagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa   | 1560 |
| tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc  | 1620 |
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa  | 1680 |
| actgggagct actacggctt tgactactgg ggccagggaa ccctgggtcac cgtctcctca | 1740 |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg  | 1800 |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtc | 1860 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 1920 |
| ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc  | 1980 |

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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 2040

aaatcttgt 2049

<210> 1622

<211> 683

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1622

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

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Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

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Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

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Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1623

<211> 633

<212> DNA

<213> Artificial Sequence

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 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 1623

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| gatatccaaa  | tgacacaatc  | accatcgtcg  | ctttcagcgt | ctgttggcga  | ccgtgtgacg | 60  |
| attacctgtc  | gcgcgtccca  | gggaatccgg  | aattacctcg | catggtatca  | ggaaaaaccc | 120 |
| ggaaaagcac  | cgaagctcct  | gatctatgcc  | gcctcgactc | ttcagagtgg  | tgtgccgtcg | 180 |
| aggttttagcg | ggtccgggtc  | aggtacggac  | tttactctca | caattttccag | cctgcagccc | 240 |
| gaagatgtag  | ctacctatta  | ctgccagaga  | tacaaccgag | cgccttacac  | attcggacaa | 300 |
| gggacaaaag  | tcgagatcaa  | gcgtgcctcc  | accaagggcc | catcgggtctt | ccccctggca | 360 |
| ccctcctcca  | agagcacctc  | tgggggcaca  | gcggccctgg | gctgcctgggt | caaggactac | 420 |
| ttccccgaac  | cggtgacgggt | gtcgtggaac  | tcaggcgccc | tgaccagcgg  | cgtgcacacc | 480 |
| ttcccggctg  | tcctacagtc  | ctcaggactc  | tactccctcg | aaagcgtgggt | gaccgtgccc | 540 |
| tccagcagct  | tgggcaccca  | gacctacatc  | tgcaacgtga | atcacaagcc  | cagcaacacc | 600 |
| aaggtgggaca | agaaaagttga | gccccaaatct | tgt        |             |            | 633 |

<210> 1624

$\langle 211 \rangle$  211

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 1624

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

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Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1625

<211> 660



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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1625

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc   | 60  |
| atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt   | 120 |
| tgggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctacccgg | 180 |
| gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc  | 240 |
| atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact   | 300 |
| cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct | 360 |
| gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc   | 420 |
| ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc  | 480 |
| caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc   | 540 |
| ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc   | 600 |
| gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt   | 660 |

<210> 1626

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1626

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

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<210> 1627  
 <211> 2070  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1627  
 gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
 agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaaagcg 120  
 cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
 agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct 420  
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
 tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
 agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
 aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 660  
 agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
 ctcttggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc 780  
 tcccggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc 840  
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900  
 gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960  
 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaaag ccctcccagc ccccatcgag 1020  
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080  
 tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat 1140  
 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200

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acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac 1260  
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320  
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380  
ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 1440  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 1500  
attaggaagc cccaggggaa aggccttgag tggataggaa ggacatacta caggtccaag 1560  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 1620  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 1680  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 1740  
accacggtca ccgtctcctc agcctccacc aaggggcccat cggctcttccc cctggcaccc 1800  
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 1860  
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 1920  
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtggtgac cgtgccctcc 1980  
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 2040  
gtggacaaga aagttgagcc caaatcttgt 2070

<210> 1628

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1628

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

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Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

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Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

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Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1629  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1629  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420



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```

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                  633

```

<210> 1630  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1630

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys
          100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1631  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide"=

<400> 1631  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcga 360

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|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| tctgatgagc | agttgaaatc | tggtaccgcc  | tctgtttgtgt | gcctgctgaa | taacttctat | 420 |
| cccagagagg | ccaaagtaca | gtggaagggtg | gataacgcc   | tccaatcggg | taactcccag | 480 |
| gagagtgtca | cagagcagga | cagcaaggac  | agcacctaca  | gcctcaagag | caccctgacg | 540 |
| ctgagcaaag | cagactacga | gaaacacaaa  | gtctacgcct  | gcgaagtcac | ccatcagggc | 600 |
| ctgagctcgc | ccgtcacaaa | gagcttcaac  | aggggagagt  | gt         |            | 642 |

|       |                     |
|-------|---------------------|
| <210> | 1632                |
| <211> | 214                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1632

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1633  
<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1633  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaggcc    | 360  |
| aacccccactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca  | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat   | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag   | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac   | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcgga tcgggagggtg gcggatccca ggtgcagtta | 1380 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc   | 1440 |
| catggtgggt ctttcagtgg ttactactgg aactggattc gcaagccacc aggggaagggg  | 1500 |
| ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag   | 1560 |
| agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct   | 1620 |
| gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc   | 1680 |
| tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcagc ctccaccaag   | 1740 |

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ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1800  
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 1860  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 1920  
ctcgagagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1980  
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgt 2037

<210> 1634  
<211> 679  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1634

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

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Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Lys Pro  
485 490 495



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Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
580 585 590

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
595 600 605

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
610 615 620

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
625 630 635 640

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
645 650 655

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
660 665 670

Lys Val Glu Pro Lys Ser Cys  
675

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<210> 1635  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1635  
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 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
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 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttccggc tgcctacag tcctcaggac tctactccct cgaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 1636  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1636

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

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Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1637  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1638  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1638

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys

210

&lt;210&gt; 1639

&lt;211&gt; 2031

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1639

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg   | 120  |
| cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac   | 180  |
| agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac   | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc   | 360  |
| aacccccactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca  | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat   | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag   | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac    | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |

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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc      1080
aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct atcccagcga catcgccgtg      1140
gagtgggaga gcaatgggca gccgggagaac aactacaaga ccacgcctcc cgtgctggac      1200
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag      1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1320
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tctggtggct ccatcagtag ttacttctgg agctggattc ggaagcccc aggtaaggga      1500
ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag      1560
agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct      1620
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc      1680
tttgactact ggggccaggg aaccctgggtc accgtctcct cagcctccac caagggccca      1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      1800
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg      1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag      1920
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      1980
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<210> 1640  
 <211> 677  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1640

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| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205



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Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Lys Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

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Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
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<210> 1641  
<211> 645  
<212> DNA  
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<223> Synthetic polynucleotide

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tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

A-1937-W0-PCT\_ST25

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
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 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
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<210> 1642  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1642

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1643  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1643  
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tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360

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gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
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 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
 ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1644  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1644

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1645  
<211> 2052  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1645  
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cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
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| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat   | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag   | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac   | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtagctg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcgga tcgggaggtg gcggatccca ggtacagttg  | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc   | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggaa gccccagg     | 1500 |
| aaaggccttg agtggatagg aaggacatac tacaggtcca agtggataa tgattatgca    | 1560 |
| gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg   | 1620 |
| aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg    | 1680 |
| gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc   | 1740 |



A-1937-W0-PCT\_ST25

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 gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 1860  
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1920  
 tcaggactct actccctcga gagcgtgggtg accgtgccct ccagcagctt gggcaccag 1980  
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 2040  
 cccaaatctt gt 2052

<210> 1646  
 <211> 684  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1646

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

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Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
 115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
 130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
 145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
 165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
 180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
 195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

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Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510

Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
580 585 590

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
595 600 605

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
610 615 620

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
625 630 635 640

Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser  
645 650 655

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
660 665 670

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Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1647  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1647  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1648  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1648

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1649  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1649  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1650  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1650

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190



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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

<210> 1651  
 <211> 2055  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1651  
 cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat tcgcaagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgagag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
 aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
 aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
 ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720  
 ctgggggggac cgtcagtctt cctcttcccc ccaaaacca aggacaccct catgatctcc 780  
 cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840  
 ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag 900  
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa  | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc   | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg  | 1200 |
| cctcccgtagc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag  | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga | 1380 |
| tccgaggtac aactgggtga atcaggtgga ggtttggtagc agccggggag atcgctcagg | 1440 |
| cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggaaa  | 1500 |
| gcgcctggaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat   | 1560 |
| tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg  | 1620 |
| taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc  | 1680 |
| tcctacttgt ctacagcttc gtcgctcgac tattgggggtc aaggaacgtt ggtcaccgtc | 1740 |
| tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc  | 1800 |
| tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg  | 1860 |
| gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag  | 1920 |
| tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc  | 1980 |
| cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt   | 2040 |
| gagcccaaat cttgt                                                   | 2055 |

<210> 1652

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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&lt;400&gt; 1652

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
 115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
 165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
 180 185 190

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Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

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Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

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Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1653  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1653  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gatttactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300

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gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                  633

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<210> 1654  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1654

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

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Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1655  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1655  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240



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caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcaccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1656  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1656

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

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Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1657  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1657  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtgg gtccttcagt gggttactact ggaactggat tcgcaagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccaggga cctagtcac cgtctcctca     | 360  |
| acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 420  |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 480  |
| aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc   | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 720  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgagggtcaag  | 840  |
| ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagtg caaggctctc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag    | 1260 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |
| tccgagggtgc agctgggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag | 1440 |
| atctcctgta agacttctga atacagcttt accagctact ggatcggtg ggtgcgcaag    | 1500 |
| atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga   | 1560 |
| tacagcccgt ccttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc   | 1620 |

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tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt 1680  
aactgggggtc ttgactactg gggccaggga accctgggtca ccgtctctag tgcctccacc 1740  
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800  
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860  
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1658  
<211> 680  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1658

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

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Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

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Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
465 470 475 480

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Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
485 490 495

Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
 675 680

<210> 1659  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1659  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcg cggtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 1660  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1660



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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1661  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1661  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1662  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1662

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1663  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1663  
cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggaagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360  
gctgcaccat ctgtcttcat cttcccgcc a tctgatgagc agttgaaatc tggaactgcc 420  
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480  
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600  
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660  
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780  
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840  
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac 900

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag   | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc   | 1440 |
| tgtgcggcat cgggggtttac tttcgatgat tatgcatgac attgggtccg gaaagcgct   | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca   | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt   | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac    | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtcaaggaa cgttggtcac cgtctctagt   | 1740 |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 1800 |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg | 1860 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 1920 |
| ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 1980 |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 2040 |
| aaatcttgt                                                           | 2049 |

<210> 1664

<211> 683

<212> PRT

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1664

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
 115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
 130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
 145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
 165 170 175

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Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
485 490 495

Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560



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Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1665  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1665  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagatTTTg caacttacta ctgtcaacag agttacagta CCCctcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aagggtggaca agaaagttga gccc aaatct tgt 633

<210> 1666  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1666

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1667  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1667  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

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cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1668  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1668

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

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Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1669

<211> 2034

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1669

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggaagccc 120

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac   | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg   | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg   | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacgggtg  | 360  |
| gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc   | 420  |
| tctgtttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac   | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa   | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac   | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac   | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atgcccggtg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag   | 1380 |
| gtgcagctgg tgcagtctgg agcagagggtg aaaaagcccc gggagtctct gaagatctcc  | 1440 |
| tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg caagatgccc   | 1500 |
| gggaaaggcc tggagtggat ggggatcatc tatcttgggtg actcagatac cagatacagc  | 1560 |

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```

ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg      1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg      1680
ggctcttgact actggggcca gggaaccctg gtcaccgtct ctagtgacct caccaagggc      1740
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg      1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgctgtggaa ctcaggcgcc      1860
ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc      1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg      1980
aatcacaagc ccagcaacac caaggtggac aagaaaagtg agcccaaata ttgt          2034

```

<210> 1670  
 <211> 678  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1670

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1           5           10           15

```

```

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
          20           25           30

```

```

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35           40           45

```

```

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys
50           55           60

```

```

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
65           70           75           80

```

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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270



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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

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Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala  
565 570 575

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser  
580 585 590

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe  
595 600 605

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
610 615 620

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
625 630 635 640

Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr  
645 650 655

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Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys  
660 665 670

Val Glu Pro Lys Ser Cys  
675

<210> 1671  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1671  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaaagttga gccc aaatct tgt 633

<210> 1672  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1672

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 195 200 205

Lys Ser Cys  
 210

<210> 1673  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1673  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1674  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1674

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
 165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1675  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1675  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540  
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780  
accctcatga tctcccgac ccctgagggtc acatgcgtgg tgggtggacgt gagccacgaa 840

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg   | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca    | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac   | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc   | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac   | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct ttcacatgctc cgtgatgcat  | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcgg   | 1380 |
| tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg   | 1440 |
| gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg   | 1500 |
| cattgggtcc ggaaaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat   | 1560 |
| agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat   | 1620 |
| gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac   | 1680 |
| tactgcgcca aagtctccta cttgtctaca gtttcgtcgc tcgactattg gggtaagga    | 1740 |
| acgttgggtca ccgtctctag tgccctccacc aaggggccat cggctctccc cctggcaccc | 1800 |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc  | 1860 |
| cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc   | 1920 |
| ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc  | 1980 |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag   | 2040 |
| gtggacaaga aagttgagcc caaatcttgt                                    | 2070 |

<210> 1676

<211> 690

<212> PRT

<213> Artificial Sequence



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<220>

<223> Synthetic polypeptide

<400> 1676

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

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Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

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Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

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Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1677  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1677  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

60

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```

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tgggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctacccgg      180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaggcctccac caagggccca      360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      420
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccttg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa      540
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651

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<210> 1678  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1678

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
          20          25          30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys
          35          40          45

```

```

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50          55          60

```

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Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1679

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1679

```

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag      120
tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag      540
agctatctga gcctgacgcc tgagcagtg aagtcaccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

```

<210> 1680

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1680

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
          35          40          45

```

```

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

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Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1681

<211> 2055

<212> DNA

<213> Artificial Sequence

<220>



&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1681

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc | 60   |
| acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg   | 120  |
| aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat    | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac  | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg  | 360  |
| gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag  | 420  |
| cagttgaaat ctggaactgc ctctgttgtg tgctgtgta ataacttcta tcccagagag   | 480  |
| gccaaagtac agtgggaagg ggataacgcc ctccaatcgg gtaactcca ggagagtgtc   | 540  |
| acagagcagg acagcaagga cagcacctac agcctcaaga gcacctgac gctgagcaaa   | 600  |
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg  | 660  |
| cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc  | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac    | 780  |
| accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa  | 840  |
| gacctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg  | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctcca    | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac  | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc  | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac  | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaaacgtct tctcatgctc cgtgatgcat | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggtggcgga  | 1380 |

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|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| tcggggaggtg | gcggatccga | ggtgcagctg | gtgcagtctg | gagcagaggt | gaaaaagccc | 1440 |
| ggggagtctc  | tgaagatctc | ctgtaagact | tctgaataca | gctttaccag | ctactggatc | 1500 |
| ggctgggtgc  | gcaagatgcc | cgggaaaggc | ctggagtgga | tggggatcat | ctatcttgg  | 1560 |
| gactcagata  | ccagatacag | cccgtccttc | caaggccagg | tcaccatctc | agccgacaag | 1620 |
| tccatcagta  | ccgcctacct | gcagtggagc | agcctgaagg | cctcggacac | cgccatgtat | 1680 |
| tactgtgcga  | gaagtaactg | gggtcttgac | tactggggcc | agggaaccct | ggtcaccgtc | 1740 |
| tctagtgcct  | ccaccaaggg | cccatcggtc | ttccccctgg | caccctcctc | caagagcacc | 1800 |
| tctgggggca  | cagcggccct | gggctgcctg | gtcaaggact | acttccccga | accggtgacg | 1860 |
| gtgtcgtgga  | actcaggcgc | cctgaccagc | ggcgtgcaca | ccttcccggc | tgtcctacag | 1920 |
| tcctcaggac  | tctactccct | cgagagcgtg | gtgaccgtgc | cctccagcag | cttgggcacc | 1980 |
| cagacctaca  | tctgcaacgt | gaatcacaag | cccagcaaca | ccaaggtgga | caagaaagtt | 2040 |
| gagcccaa    | attgt      |            |            |            |            | 2055 |

|       |                     |
|-------|---------------------|
| <210> | 1682                |
| <211> | 685                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1682

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu

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Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

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Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

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Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1683  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1683  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctgggtca aggactactt ccccgaaccg gtgacgggtgt cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

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<210> 1684  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1684

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
 130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
 145 150 155 160

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Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1685  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1685  
gatatcaaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642



<210> 1686  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1686

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1687  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1687  
gaggatcaac tggatgaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt cgggaaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tggggatcaag gaacgttggt caccgtctct 360  
agtgcctcca ccaaggggcc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag 600

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg | 720  |
| ggaccgtcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc    | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcgctgtcc atggtgggtc cttcagtgggt tactactgga actggattcg caagccacca | 1500 |
| gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg  | 1560 |
| tcctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg   | 1620 |
| ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga  | 1680 |
| agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctctcaact   | 1740 |
| gtggctgcac catctgtctt catcttccc ccatctgatg agcagttgaa atctggaact   | 1800 |
| gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag  | 1860 |
| gtggataacg ccctccaatc gggtaactcc caggagagtgc tcacagagca ggacagcaag | 1920 |
| gacagcacct acagcctcga aagcaccctg acgtgagca aagcagacta cgagaaacac   | 1980 |
| aaagtctacg cctgcgaagt caccatcag gccctgagct cgcccgtcac aaagagcttc   | 2040 |

aacaggggag agtgt

2055

&lt;210&gt; 1688

&lt;211&gt; 685

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1688

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

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Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1689

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1689

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagtga gccc aaatct tgt                                633

```

<210> 1690

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1690

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10          15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20          25          30
Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu
35          40          45

```



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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1691  
<211> 642  
<212> DNA  
<213> Artificial Sequence

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 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 1691

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| gatatccaaa | tgacacaatc | accatcgtcg  | ctttcagcgt  | ctgtttggcga | ccgtgtgacg | 60  |
| attacctgtc | gcgcgtccca | gggaatccgg  | aattacctcg  | catggtatca  | ggaaaaaccc | 120 |
| ggaaaagcac | cgaagctcct | gatctatgcc  | gcctcgactc  | ttcagagtgg  | tgtgccgtcg | 180 |
| aggtttagcg | ggtccgggtc | aggtagcgac  | tttactctca  | caatttccag  | cctgcagccc | 240 |
| gaagatgtag | ctacctatta | ctgccagaga  | tacaaccgag  | cgccttacac  | attcggacaa | 300 |
| gggacaaaag | tcgagatcaa | gcgtacggtg  | gctgcaccat  | ctgtcttcat  | cttcccgcc  | 360 |
| tctgatgagc | agttgaaatc | tggaaactgcc | tctgtttgtgt | gcctgctgaa  | taacttctat | 420 |
| cccagagagg | ccaaagtaca | gtggaagggtg | gataacgccc  | tccaatcggg  | taactcccag | 480 |
| gagagtgtca | cagagcagga | cagcaaggac  | agcacctaca  | gcctcgaaag  | caccctgacg | 540 |
| ctgagcaaag | cagactacga | gaaacacaaa  | gtctacgcct  | gcgaagtcac  | ccatcagggc | 600 |
| ctgagctcgc | ccgtcacaaa | gagcttcaac  | aggggagagt  | gt          |            | 642 |

<210> 1692

$\langle 211 \rangle$  214

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 1692

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

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Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1693

<211> 2049

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1693

```

gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt      60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaaagcg      120
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat      180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac      240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc      300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct      360
agtgccctca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct      420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg      480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc      540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacag      600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc      780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac      900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1020
tcaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag     1080
gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc     1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg     1260

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gaagcccca   | 1500 |
| ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc  | 1560 |
| tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag  | 1620 |
| ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc  | 1680 |
| tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc aactgtggct | 1740 |
| gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct  | 1800 |
| gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaagggtggat | 1860 |
| aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc  | 1920 |
| acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc  | 1980 |
| tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg  | 2040 |
| ggagagtgt                                                          | 2049 |

<210> 1694  
 <211> 683  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1694

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln | Pro | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Arg | Leu | Ser | Cys | Ala | Ala | Ser | Gly | Phe | Thr | Phe | Asp | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
595 600 605



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Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
610 615 620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1695  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1695  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtagcggg gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aagggtggaca agaaaagttga gcccaaactct tgt

633

&lt;210&gt; 1696

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1696

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Glu | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1697  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1697  
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ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540

A-1937-WO-PCT\_ST25

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1698

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1698

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1699  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1699  
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agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtcctcca ccaaggggcc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcaccacag | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag   | 660  |
| cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac   | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag   | 1380 |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc    | 1440 |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggaag   | 1500 |
| ccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat    | 1560 |
| gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag   | 1620 |
| ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga   | 1680 |
| gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc   | 1740 |
| accgtctcct caactgtggc tgcacatct gtcttcatct tccgccatc tgatgagcag     | 1800 |
| ttgaaatctg gaactgcctc tggtgtgtgc ctgctgaata acttctatcc cagagaggcc   | 1860 |
| aaagtacagt ggaaggtgga taacgccctc caatcgggta actcccagga gagtgtcaca   | 1920 |

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gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980  
gactacgaga aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040  
gtcacaaaaga gcttcaacag gggagagtgt 2070

<210> 1700  
<211> 690  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1700

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

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Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320



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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495

Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

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Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685

Glu Cys  
690

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<210> 1701  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1701  
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 tggtagcagg agaaaccagg aaagggttct aaactgctca ttactgggc atctaccg 180  
 gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
 atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
 cctctcactt tcggcggagg gaccaagggt gagatcaaac gagcctccac caagggccca 360  
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
 tgcctgggtca aggactactt ccccgaaacc gtgacgggtgt cgtggaactc aggcgccctg 480  
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
 agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t 651

<210> 1702  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1702

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

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Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1703  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1703  
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctaccggg agccgtgaca gtggcctgga aggagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1704  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1704

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
 210 215

<210> 1705  
 <211> 2040  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1705  
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 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
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 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac 660  
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780  
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840  
 gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt 900  
 tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960  
 aaggctctca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020

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cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1080  
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140  
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200  
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tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt 1440  
gggtccttca gtggttacta ctggaactgg attcgcaagc caccagggaa ggggctagag 1500  
tggattgggg aaatcaatca tgctggaaac accaactaca acccgtcctt caagagtcga 1560  
gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc 1620  
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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 1860  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 1920  
ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 1980  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 2040

<210> 1706

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1706

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15



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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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

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Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

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Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1707

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1707

|                                                                   |     |
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| ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa  | 120 |
| cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca | 180 |
| gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag | 240 |
| cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa | 300 |
| gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccctggca | 360 |
| ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac | 420 |

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ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                  633

```

<210> 1708  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1708

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45

```

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50           55           60

```

```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65           70           75           80

```

```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85           90           95

```

```

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys
100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1709  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1709  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360

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actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1710  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1710

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

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Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1711  
<211> 2034  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1711  
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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tggggtcttg actactgggg ccaggggaacc ctggtcaccg tctctagtgc ctccaccaag  | 360  |
| ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc  | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc   | 540  |
| ctcaaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac  | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc  | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc     | 780  |
| gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt   | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc   | 960  |
| aagggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg    | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg     | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac   | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc   | 1320 |
| tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtgca gctgcaggag   | 1380 |
| tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt   | 1440 |
| ggctccatca gtagttactt ctggagctgg attcggaagc cccaggtaa gggactggag    | 1500 |
| tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga   | 1560 |
| gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc   | 1620 |
| gctgcggaca cggccgtgta ttactgtgag agagaaactg ggagctacta cggctttgac   | 1680 |
| tactggggcc agggaaaccct ggtcaccgtc tcctcaactg tggctgcacc atctgtcttc  | 1740 |

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atcttcccg c catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 1800  
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 1860  
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcgaa 1920  
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 1980  
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 2034

<210> 1712  
<211> 678  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1712

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val  
290 295 300

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Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
305 310 315 320

Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly  
485 490 495

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Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala  
565 570 575

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
580 585 590

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
595 600 605

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
610 615 620

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
625 630 635 640

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
645 650 655

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
660 665 670

Phe Asn Arg Gly Glu Cys  
675

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<210> 1713  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1713  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
 gggaaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1714  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1714

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1715  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1715  
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1716  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1716

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15



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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
 210 215

<210> 1717  
 <211> 2055  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1717  
 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
 ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600  
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac 660  
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780  
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840  
 gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt 900  
 tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960  
 aaggctctca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg  | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac  | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag | 1380 |
| tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg  | 1440 |
| gacagtgtct ctaccaacag tgttgcttgg aactggatta ggaagcccc agggaaaggc   | 1500 |
| cttgagtgga taggaaggac atactacagg tccaagtggg ataatgatta tgcagtttct  | 1560 |
| ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg  | 1620 |
| agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc  | 1680 |
| tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctctcaact   | 1740 |
| gtggctgcac catctgtctt catcttcccc ccatctgatg agcagttgaa atctggaact  | 1800 |
| gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag  | 1860 |
| gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag  | 1920 |
| gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac  | 1980 |
| aaagtctacg cctgcgaagt caccatcag ggctgagct cgcccgtcac aaagagcttc    | 2040 |
| aacaggggag agtgt                                                   | 2055 |

<210> 1718

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1718

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu  
180 185 190

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Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Lys Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr  
565 570 575

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Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1719  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1719  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360

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|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tcggtctttcc | ccctggcacc | ctcctccaag | agcacctctg | ggggcacagc | ggccctgggc | 420 |
| tgcctggtca  | aggactactt | ccccgaaccg | gtgacggtgt | cgtggaactc | aggcgccctg | 480 |
| accagcggcg  | tgcacacctt | cccggctgtc | ctacagtcct | caggactcta | ctccctcaaa | 540 |
| agcgtggtga  | ccgtgccctc | cagcagcttg | ggcacccaga | cctacatctg | caacgtgaat | 600 |
| cacaagccca  | gcaacaccaa | ggtggacaag | aaagttgagc | ccaaatcttg | t          | 651 |

|       |                     |
|-------|---------------------|
| <210> | 1720                |
| <211> | 217                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1720

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110



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Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1721  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1721  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gatttactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300

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```

gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

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<210> 1722  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1722

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

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Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1723  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1723  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgcaagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240

## A-1937-W0-PCT\_ST25

acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900  
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080  
 atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200  
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg 1260  
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320  
 cagaagagcc tctccctgtc tccgggtggg ggcgatcgg gaggtggcgg atccgaggta 1380  
 caactgggtg aatcagggtg aggtttgggtg cagccgggga gatcgctcag gcttagctgt 1440  
 gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggtccggaa agcgcttggg 1500  
 aaagggtcag agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560  
 agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620  
 atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg 1680

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tctacagctt cgtcgtcga ctattggggt caaggaacgt tggtcaccgt ctctagtact 1740  
 gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 1800  
 gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860  
 gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920  
 gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980  
 aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc 2040  
 aacaggggag agtgt 2055

<210> 1724  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1724

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

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Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

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Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

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Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670



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Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1725  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1725  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1726  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1726

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1727  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1727  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtaaccgc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1728  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1728

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

A-1937-W0-PCT\_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1729  
<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1729  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtg gtccttcagt ggttactact ggaactggat ccgcaagcca 120  
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
aaatcttgtg acaaaaactca cacatgccc cctgcccag cacctgaact cctgggggga 720  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780  
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 960  |
| gagtacaagt gcaaggctctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   | 1080 |
| atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg   | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1320 |
| cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgagggtg  | 1380 |
| cagctgggtgc agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatctcctgt | 1440 |
| aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcaa gatgcccggg  | 1500 |
| aaaggcctgg agtggatggg gatcatctat cttgggtgact cagataccag atacagccccg | 1560 |
| tccttccaag gccaggctcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag  | 1620 |
| tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt  | 1680 |
| cttgactact gggggccaggg aaccctgggtc accgtctcta gtcagcccaa ggccaacccc | 1740 |
| actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagt     | 1800 |
| tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc   | 1860 |
| cccgtcaagg cgggagtgga gaccaccaa cctccaac agagcaacaa caagtacgcg      | 1920 |
| gccgagagct acctgagcct gacgcccag cagtgggaagt cccacagaag ctacagctgc   | 1980 |
| caggtcacgc atgaaggag caccgtggag aagacagtgg cccctacaga atgttca       | 2037 |

<210> 1730

<211> 679

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1730

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
 180 185 190

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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380



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Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln Pro  
565 570 575

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Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu  
580 585 590

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro  
595 600 605

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala  
610 615 620

Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala  
625 630 635 640

Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg  
645 650 655

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr  
660 665 670

Val Ala Pro Thr Glu Cys Ser  
675

<210> 1731  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1731  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300

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gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1732  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1732

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

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Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1733

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1733

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gaagatTTTg caacttacta ctgtcaacag agttacagta CCCtcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
 CCCagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1734  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1734

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1735  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1735  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggctct ccccttgga cctctctcca agagcacctc tgggggcaca   | 420  |
| gcggccctgg gctgcctgg caaggactac ttccccgaac cggtgacggg gtcgtggaac   | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc | 540  |
| tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagtga gcccaaatct | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctgggc 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 tgggtggcga tcgggagggtg gcggatccga ggtacaactg | 1380 |
| gtggaatcag gtggagggtt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca  | 1440 |
| tcggggttta ctttcgatga ttatgcgatg cattgggtcc ggaaaagcgc tggaaaagg   | 1500 |
| ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg   | 1560 |
| gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac  | 1620 |

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|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| tcacttcgcg | cggaagatac | cgccgtatac | tactgcgcca  | aagtctccta | cttgtctaca | 1680 |
| gcttcgtcgc | tcgactattg | gggtcaagga | acgttgggtca | ccgtctctag | tactgtggct | 1740 |
| gcaccatctg | tcttcattct | cccgccatct | gatgagcagt  | tgaaatctgg | aactgcctct | 1800 |
| gttgtgtgcc | tgctgaataa | cttctatccc | agagaggcca  | aagtacagtg | gaaggtggat | 1860 |
| aacgccctcc | aatcgggtaa | ctcccaggag | agtgtcacag  | agcaggacag | caaggacagc | 1920 |
| acctacagcc | tcgaaagcac | cctgacgctg | agcaaagcag  | actacgagaa | acacaaagtc | 1980 |
| tacgcctgcg | aagtcaccca | tcagggcctg | agctcgcccc  | tcacaaagag | cttcaacagg | 2040 |
| ggagagtgt  |            |            |             |            |            | 2049 |

|       |                     |
|-------|---------------------|
| <210> | 1736                |
| <211> | 683                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1736

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80



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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
275 280 285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
450 455 460

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Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Lys Ala  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
595 600 605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
610 615 620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

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Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1737  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1737  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtcct ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 1738  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1738

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 195 200 205

Lys Ser Cys  
 210

<210> 1739  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1739  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120  
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1740  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1740

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
 165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1741  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1741  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540  
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac | 960  |
| aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaacccat ctccaaagcc | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tggTggcgga tcgggagggtg gcggatccga ggtgcagctg | 1380 |
| gtgcagtctg gagcagaggT gaaaaagccc ggggagTctc tgaagatctc ctgtaagact  | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gcaagatgcc cgggaaaggc  | 1500 |
| ctggagtgga tggggatcat ctatcttggT gactcagata ccagatacag cccgtccttc  | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc  | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggTcttgac  | 1680 |
| tactggggcc agggaaacct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc   | 1740 |
| actctgttcc cgccctctc tgaggagctc caagccaaca aggccacact agtgtgtctg   | 1800 |
| atcagtgact tctacccggg agctgtgaca gtggcctgga aggcagatgg cagccccgtc  | 1860 |
| aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccgag   | 1920 |
| agctacctga gcctgacgcc cgagcagtgg aagTcccaca gaagctacag ctgccaggTc  | 1980 |
| acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a           | 2031 |

<210> 1742

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1742

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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

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Ser Ser Gly Leu Tyr Ser Leu Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
355 360 365

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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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Lys Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

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Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln Pro Lys Ala  
565 570 575

Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
580 585 590

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala  
595 600 605

Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val  
610 615 620

Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu  
625 630 635 640

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr  
645 650 655

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala  
660 665 670

Pro Thr Glu Cys Ser  
675

<210> 1743  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1743  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

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caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaagggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1744  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1744

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

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Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1745  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1745  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

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gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1746  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1746

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80



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Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1747

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1747

caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat    | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac  | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgtac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc  | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 660  |
| aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct  | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg    | 780  |
| atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag  | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggtgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc  | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc  | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt  | 1380 |
| ggcggatccg aggtacaact ggtggaatca ggtggaggtt tggtgcagcc ggggagatcg  | 1440 |
| ctcaggctta gctgtgcggc atcgggggtt actttcgatg attatgcgat gcattgggtc  | 1500 |
| cggaaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac  | 1560 |

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atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac 1620  
 agcctgtacc ttcatgatgaa ctacttcgc gcggaagata ccgccgtata ctactgcgcc 1680  
 aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtcaagg aacgttggtc 1740  
 accgtctcta gtactgtggc tgcacatct gtcttcatct tcccgccatc tgatgagcag 1800  
 ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860  
 aaagtacagt ggaagggtgga taacgccctc caatcgggta actcccagga gagtgtcaca 1920  
 gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980  
 gactacgaga aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040  
 gtcacaaaaga gcttcaacag gggagagtgt 2070

<210> 1748  
 <211> 690  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1748

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

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Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

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Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

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Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685

Glu Cys  
690

<210> 1749  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1749  
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 1750  
<211> 211

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1750

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160



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Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1751  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1751  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

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<210> 1752  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1752

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 145 150 155 160

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Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1753  
<211> 2052  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1753  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtgggtat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540  
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600  
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aagaaagttag agcccaaatac ttgtgacaaa actcacacat gcccaccgtg cccagcacct | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg   | 780  |
| atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag   | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt   | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac   | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc    | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc   | 1080 |
| ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc  | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg   | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt   | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct   | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg   | 1500 |
| cgcaagatgc ccgggaaaagg cctggagtgg atggggatca tctatcttgg tgactcagat  | 1560 |
| accagatata gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt   | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg    | 1680 |
| agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtcag   | 1740 |
| cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac   | 1800 |
| aaggccacac tagtgtgtct gatcagtgac ttctacccgg gagctgtgac agtggcctgg   | 1860 |
| aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc   | 1920 |
| aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtcccac   | 1980 |
| agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct   | 2040 |
| acagaatggt ca                                                       | 2052 |

<210> 1754  
 <211> 684  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1754

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

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Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

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Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro  
580 585 590

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
595 600 605

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly  
610 615 620

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser  
625 630 635 640

Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln  
645 650 655

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser  
660 665 670

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

<210> 1755

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide



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<400> 1755

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag      120
tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc      360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg      420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt                      645

```

<210> 1756

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1756

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
          35          40          45

```

```

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

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Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1757

<211> 2064

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1757

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt  | 60   |
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaaagcg | 120  |
| cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct | 360  |
| agtacggtgg ctgcaccatc tgtcttcac tccccgcat ctgatgagca gttgaaatct     | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc   | 780  |
| tccccgaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc   | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag   | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tccccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc   | 1380 |

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```

ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg      1440
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc      1500
aagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac      1560
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc      1620
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga      1680
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc      1740
tcctcaactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa      1800
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta      1860
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag      1920
gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac      1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca      2040
aagagcttca acaggggaga gtgt                                             2064

```

<210> 1758  
 <211> 688  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1758

```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1           5           10           15

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20           25           30

```

```

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45

```

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Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

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Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

A-1937-W0-PCT\_ST25

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1759  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1759  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633



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<210> 1760  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1760

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

A-1937-W0-PCT\_ST25

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1761  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1761  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga cctgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttcag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1762  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1762

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1763  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1763  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggaagcgg 120  
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttggtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc   | 780  |
| tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc  | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat  | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg   | 1440 |
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg  | 1500 |
| aagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa    | 1560 |
| tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc    | 1620 |
| tccctgaagc tgagctctgt gaccgtgcg gacacggccg tgtattactg tgcgagagaa    | 1680 |
| actgggagct actacggctt tgactactgg ggccaggga ccttggtcac cgtctcctca    | 1740 |
| actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga   | 1800 |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 1860 |
| aagggtgata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc   | 1920 |
| aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 1980 |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc   | 2040 |

ttcaacaggg gagagtgt

2058

&lt;210&gt; 1764

&lt;211&gt; 686

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1764

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
 130 135 140

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Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

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Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525



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Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1765

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1765

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagtga gccc aaatct tgt                                633

```

<210> 1766

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1766

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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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1767  
<211> 633  
<212> DNA  
<213> Artificial Sequence

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 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 1767

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| gatatccaaa  | tgacacaatc  | accatcgtcg  | ctttcagcgt | ctgttggcga  | ccgtgtgacg | 60  |
| attacctgtc  | gcgcgtccca  | gggaatccgg  | aattacctcg | catggtatca  | ggaaaaaccc | 120 |
| ggaaaagcac  | cgaagctcct  | gatctatgcc  | gcctcgactc | ttcagagtgg  | tgtgccgtcg | 180 |
| aggttttagcg | ggtccgggtc  | aggtacggac  | tttactctca | caattttcag  | cctgcagccc | 240 |
| gaagatgtag  | ctacctatta  | ctgccagaga  | tacaaccgag | cgccttacac  | attcggacaa | 300 |
| gggacaaaag  | tcgagatcaa  | gcgtgcctcc  | accaagggcc | catcgggtctt | ccccctggca | 360 |
| ccctcctcca  | agagcacctc  | tgggggcaca  | gcggccctgg | gctgcctggg  | caaggactac | 420 |
| ttccccgaac  | cgggtgacgg  | gtcgtggaac  | tcaggcgccc | tgaccagcgg  | cgtgcacacc | 480 |
| ttcccggctg  | tcctacagtc  | ctcaggactc  | tactccctcg | aaagcgtggg  | gaccgtgccc | 540 |
| tccagcagct  | tgggcaccca  | gacctacatc  | tgcaacgtga | atcacaagcc  | cagcaacacc | 600 |
| aaggtgggaca | agaaaagttga | gccccaaatct | tgt        |             |            | 633 |

<210> 1768

$\langle 211 \rangle$  211

&lt;212&gt; PRT

## <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 1768

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

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Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1769

<211> 2079

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1769

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt  | 60   |
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaagcg  | 120  |
| cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct  | 360  |
| agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct    | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac    | 780  |
| tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc   | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag   | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgaggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |

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aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320  
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380  
ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 1440  
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 1500  
attaggaagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 1560  
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 1620  
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 1680  
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 1740  
accacggtca ccgtctcctc aactgtggct gcaccatctg tcttcatctt cccgccatct 1800  
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 1860  
agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 1920  
agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg 1980  
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 2040  
agctcgcccc tcacaaagag cttcaacagg ggagagtgt 2079

<210> 1770  
<211> 693  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1770

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

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Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220



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Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

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Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

A-1937-W0-PCT\_ST25

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

<210> 1771  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1771  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360  
tcgggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcttggtca aggactactt ccccgaaacc gtgacggtgt cgtggaactc aggcgcctg 480

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accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
 agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1772  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1772

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 115 120 125

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Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1773  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1773  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

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```

ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gccc aaatct tgt 633

```

<210> 1774  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1774

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20           25           30

```

```

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr
85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys
100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1775  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1775  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tgggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aacccccactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc   | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tcgggaggtg gcggatccca ggtgcagtta  | 1380 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc   | 1440 |
| catggtgggt ctttcagtgg ttactactgg aactggattc gcaagccacc aggggaagggg | 1500 |
| ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag  | 1560 |
| agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct  | 1620 |
| gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc  | 1680 |
| tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcaac tgtggctgca  | 1740 |
| ccatctgtct tcactttccc gccatctgat gagcagttga aatctggaac tgcctctgtt  | 1800 |



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gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 1860  
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 1920  
tacagcctcg aaagcacctt gacgctgagc aaagcagact acgagaaaca caaagtctac 1980  
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 2040  
gagtgt 2046

<210> 1776  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1776

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

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Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Lys Pro  
485 490 495

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Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
580 585 590

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
595 600 605

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
610 615 620

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
625 630 635 640

Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
645 650 655

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
660 665 670

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

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<210> 1777  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1777  
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 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1778  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1778

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Gly | Thr | Leu | Ser | Leu | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1779  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1779  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1780  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1780

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205



Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1781  
 <211> 2040  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1781  
 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc 360  
 aacccactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
 ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
 ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540  
 tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac 600  
 agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660  
 tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900  
 taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
 aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020

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aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc      1080
aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct atcccagcga catcgccgtg      1140
gagtgggaga gcaatgggca gccgggagaac aactacaaga ccacgcctcc cgtgctggac      1200
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag      1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1320
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caggagtctg gccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc      1440
tctggtggct ccatcagtag ttacttctgg agctggattc ggaagcccc aggtaaggga      1500
ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag      1560
agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct      1620
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc      1680
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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc      1860
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      1920
ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      1980
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      2040

```

<210> 1782  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1782

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

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Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Lys Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

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Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1783

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1783

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300

gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccctggca 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

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```

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                  633

```

<210> 1784  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1784

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys
          100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1785  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1785  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360



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```

ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg      420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt                      645

```

<210> 1786  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1786

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
          20          25          30

```

```

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
          35          40          45

```

```

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
          50          55          60

```

```

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65          70          75          80

```

```

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
          85          90          95

```

```

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
          100         105         110

```

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1787  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1787  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120  
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaggcc    | 360  |
| aacccccactg tcaactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat   | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag   | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac   | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcgga tcgggaggtg gcggatccca ggtacagttg  | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc   | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggaa gccccagg     | 1500 |
| aaaggccttg agtggatagg aaggacatac tacaggtcca agtggataa tgattatgca    | 1560 |
| gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg   | 1620 |
| aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg    | 1680 |
| gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc   | 1740 |

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tcaactgtgg ctgcaccatc tgtcttcac tttcccgccat ctgatgagca gttgaaatct 1800  
 ggaactgcct ctgttggtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 1860  
 tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 1920  
 agcaaggaca gcacctacag cctcgaaagc accctgacgc tgagcaaagc agactacgag 1980  
 aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 2040  
 agcttcaaca ggggagagtg t 2061

<210> 1788  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1788

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

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Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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

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Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

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Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510

Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
580 585 590

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
595 600 605

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
610 615 620

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
625 630 635 640

Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys  
645 650 655

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
660 665 670

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Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1789  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1789  
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaggcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t 651

<210> 1790  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1790

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15



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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1791  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1791  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1792  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1792

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

## A-1937-W0-PCT\_ST25

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 195 200 205

Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1793  
 <211> 2064  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1793  
 cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgcaagcca 120  
 ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggaacac gctgtgtatt actgtgagag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
 aagggtggata acgcccctca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
 aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
 ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720  
 ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780  
 cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840  
 ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag 900  
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa  | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc   | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg  | 1200 |
| cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag  | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga | 1380 |
| tccgaggtac aactgggtga atcaggtgga ggtttgggtgc agccggggag atcgctcagg | 1440 |
| cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggaaa  | 1500 |
| gcgcctggaa aagggctcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat  | 1560 |
| tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg  | 1620 |
| taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc  | 1680 |
| tcctacttgt ctacagcttc gtcgctcgac tattgggggtc aaggaacgtt ggtcaccgtc | 1740 |
| tctagtactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa   | 1800 |
| tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta  | 1860 |
| cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag  | 1920 |
| gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac  | 1980 |
| gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca  | 2040 |
| aagagcttca acaggggaga gtgt                                         | 2064 |

<210> 1794

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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&lt;400&gt; 1794

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
 115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
 130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
 145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
 165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
 180 185 190

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Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

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Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575



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Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1795  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1795  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

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gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gccc aaatct tgt 633

```

<210> 1796  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1796

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1797  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1797  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

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cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacacctac cttcggccaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1798  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1798

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

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Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1799  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1799  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat tcgcaagcca 120  
ccagggaagg ggctagagtg gattgggggaa atcaatcatg ctggaaacac caactacaac 180

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg   | 240  |
| acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt   | 300  |
| agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca   | 360  |
| acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 420  |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 480  |
| aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc   | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 720  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgagggtcaag  | 840  |
| ttcaactggg acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag   | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag    | 1260 |
| agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac  | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |
| tccgagggtgc agctgggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag | 1440 |
| atctcctgta agacttctga atacagcttt accagctact ggatcggtg ggtgcgcaag    | 1500 |
| atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga   | 1560 |
| tacagcccgt ccttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc   | 1620 |

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tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt 1680  
aactgggggtc ttgactactg gggccagggga accctgggtca ccgctctctag tcagcccaag 1740  
gccaaccccca ctgtcactct gttcccgccc tcctctgagg agctccaagc caacaaggcc 1800  
acactagtgt gtctgatcag tgactttctac ccgggagctg tgacagtggc ctggaaggca 1860  
gatggcagcc ccgtaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac 1920  
aagtacgcgg ccgagagcta cctgagcctg acgcccgagc agtggaagtc ccacagaagc 1980  
tacagctgcc aggtcacgca tgaaggggagc accgtggaga agacagtggc ccctacagaa 2040  
tgttca 2046

<210> 1800  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1800

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

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Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270



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Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

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Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
485 490 495

Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser  
580 585 590

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp  
595 600 605

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro  
610 615 620

Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn  
625 630 635 640

Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys  
645 650 655

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Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val  
660 665 670

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

<210> 1801  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1801  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaa at cttgt 645

<210> 1802  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1802

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 180 185 190

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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 195 200 205

Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1803  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1803  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1804  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>

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&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1804

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
 165 170 175

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1805  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1805  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggaagccc 120  
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360  
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 420  
tctgttgtgt gcctgctgaa taacttctat ccagagagg ccaaagtaca gtggaagggtg 480  
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600  
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660  
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780  
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag  | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc  | 1440 |
| tgtgcggcat cgggggtttac tttcgatgat tatgcgatgc attgggtccg gaaagcgctt | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca  | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt  | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac   | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtcaaggaa cgttgggtcac cgtctctagt | 1740 |
| actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 1800 |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg  | 1860 |
| aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 1920 |
| aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa  | 1980 |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc  | 2040 |
| ttcaacaggg gagagtgt                                                | 2058 |

<210> 1806

<211> 686

<212> PRT

<213> Artificial Sequence



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<220>

<223> Synthetic polypeptide

<400> 1806

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

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Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
485 490 495

Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560

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Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1807  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1807  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc ggcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

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aggttttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 1808  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1808

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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

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Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1809  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1809  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

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```

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca    180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct    240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa    300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga    360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac    420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc    480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc    540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc    600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1810  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1810

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln 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

```

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1811

<211> 2040

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1811

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc

60



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggaagccc   | 120  |
| ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaataacaac  | 180  |
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg   | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg   | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg   | 360  |
| gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc   | 420  |
| tctgttgtgt gcctgctgaa taacttctat ccagagagg ccaaagtaca gtggaagggtg   | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac   | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa   | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac   | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc    | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac   | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaagggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccagggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag   | 1380 |
| gtgcagctgg tgcagtctgg agcagagggtg aaaaagcccg gggagtctct gaagatctcc  | 1440 |
| tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg caagatgccc   | 1500 |

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gggaaaggcc tggagtggat ggggatcatc tatcttgggtg actcagatac cagatacagc 1560  
 ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg 1620  
 cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg 1680  
 ggtcttgact actggggcca gggaaccctg gtcaccgtct ctagtcagcc caaggccaac 1740  
 cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta 1800  
 gtgtgtctga tcagtgactt ctacccggga gctgtgacag tggcctggaa ggcagatggc 1860  
 agccccgtca aggcgggagt ggagaccacc aaaccctcca aacagagcaa caacaagtac 1920  
 gcggccgaga gctacctgag cctgacgccc gagcagtgga agtcccacag aagctacagc 1980  
 tgccagggtca cgcataaagg gagcaccgtg gagaagacag tggcccctac agaattgtca 2040

<210> 1812  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1812

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

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Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gln  
565 570 575

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
580 585 590

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
595 600 605

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys  
610 615 620

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
625 630 635 640

Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
645 650 655

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Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
 660 665 670

Thr Val Ala Pro Thr Glu Cys Ser  
 675 680

<210> 1813  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1813  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
 tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1814  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1814

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 165 170 175

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Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1815  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1815  
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1816  
<211> 211  
<212> PRT  
<213> Artificial Sequence



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<220>

<223> Synthetic polypeptide

<400> 1816

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Glu | Arg | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Glu | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1817  
<211> 2079  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1817  
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtgggaagggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540  
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac 780

## A-1937-W0-PCT\_ST25

accctcatga tctccccggac ccctgaggtc acatgcgtgg tggaggacgt gagccacgaa 840  
 gaccttgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900  
 aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960  
 caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1020  
 gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080  
 accctgcccc catccccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1140  
 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200  
 aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag 1260  
 ctcaccgtgg acaagagcag gtggcagcag gggaacgtct ttcctatgctc cgtgatgcat 1320  
 gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga 1380  
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 gggagatcgc tcaggcttag ctgtgcggca tcgggggtta ctttcgatga ttatgcgatg 1500  
 cattgggtcc ggaaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat 1560  
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 acgttgggtca ccgtctctag tactgtggct gcaccatctg tcttcatctt cccgccatct 1800  
 gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 1860  
 agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag 1920  
 agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg 1980  
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 2040  
 agctcgcccc tcacaaagag cttcaacagg ggagagtgt 2079

&lt;210&gt; 1818

&lt;211&gt; 693

A-1937-WO-PCT\_ST25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1818

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

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Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

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Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

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Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

<210> 1819

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

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<400> 1819  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtcg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattc tgt 633

<210> 1820  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1820

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Gly | Ile | Arg | Asn | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Trp | Tyr | Gln | Glu | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Thr | Leu | Gln | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |



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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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1821

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1821

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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca      360
tcgggtcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      420
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa      540
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651

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&lt;210&gt; 1822

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1822

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

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```

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30

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```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys
35           40           45

```

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Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1823

<211> 2061

<212> DNA

<213> Artificial Sequence

## A-1937-W0-PCT\_ST25

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1823

|                                                                    |      |
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| acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg   | 120  |
| aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtgggtat  | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac   | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgtac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag  | 420  |
| cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag  | 480  |
| gccaaagtac agtgggaagg ggataacgcc ctccaatcgg gtaactcca ggagagtgtc   | 540  |
| acagagcagg acagcaagga cagcacctac agcctcaaga gcacctgac gctgagcaaa   | 600  |
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg  | 660  |
| cccgtcaca agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc    | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac   | 780  |
| accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtaggacgt gagccacgaa | 840  |
| gacctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg  | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctcca    | 1020 |
| gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac    | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc  | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac  | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat  | 1320 |

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gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggcggcgga 1380  
tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc 1440  
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc 1500  
ggctgggtgc gcaagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggt 1560  
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag 1620  
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat 1680  
tactgtgcga gaagtaactg gggctttgac tactggggcc agggaaacct ggtcaccgtc 1740  
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc 1800  
caagccaaca aggccacact agtgtgtctg atcagtgact tctaccggg agctgtgaca 1860  
gtggcctgga aggcagatgg cagccccgtc aaggcgggag tggagaccac caaacctcc 1920  
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg 1980  
aagtcacaca gaagctacag ctgccaggtc acgcatgaag ggagcaccgt ggagaagaca 2040  
gtggccccta cagaatgttc a 2061

<210> 1824  
<211> 687  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1824

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu  
35 40 45

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Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

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Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu  
580 585 590

Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val  
595 600 605

Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys  
610 615 620



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Ala Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser  
625 630 635 640

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr  
645 650 655

Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His  
660 665 670

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680 685

<210> 1825  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1825  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 1826  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1826

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1827  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1827  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgctgtgtca aggactactt ccccgaaaccg gtgacgggtg cgtggaactc aggcgcctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

651

<210> 1828

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1828

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Glu Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

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Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1829  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1829  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1830

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1830

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1831  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1831  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1832  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1832

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125



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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1833  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1833  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg  | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 540  |
| tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcacccag | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag  | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc   | 780  |
| cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc   | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcgtgtcc atggtgggtc cttcagtggt tactactgga actggattcg ccagccacca   | 1500 |
| gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaaccg   | 1560 |
| tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg  | 1620 |
| ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga  | 1680 |
| agtaccacct gctactttga ctactggggc aagggaaccc tagtcaccgt ctctcagcc   | 1740 |
| tccaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc   | 1800 |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg  | 1860 |

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aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 1920  
 ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 1980  
 atctgcaacg tgaatcacao gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 2040  
 tcttgt 2046

<210> 1834  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1834

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

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Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

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Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560

Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

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<210> 1835  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1835  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
 gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1836  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1836

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210



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<210> 1837  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1837  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
 gggaaagagc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
 gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcga 360  
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1838  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1838

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1839  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1839  
gaggtagaac tggtagaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360  
agtgcccca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcacccag 600  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660  
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca cctcatgat ctcccgacc 780  
cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840  
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac 900  
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960  
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020  
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag 1080

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gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1140  
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200  
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260  
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320  
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380  
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 1440  
tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagccccc 1500  
ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc 1560  
tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620  
ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680  
tactacggct ttgactactg gggcaaggga accctgggtca ccgtctcctc agcctccacc 1740  
aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800  
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860  
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1840  
<211> 680  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1840

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

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Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

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Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

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Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1841  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1841  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480



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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1842  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1842

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1843  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1843  
gacatccaga tgaccagtc tccaagctcc ctgtctgct ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggagcct aaactgctca tttactgggc atctacccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
 ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1844  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1844

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1845  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1845  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| agtcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct   | 420  |
| gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc   | 540  |
| tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcaccag   | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag   | 660  |
| cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc     | 780  |
| cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtag  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc   | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc    | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac  | 1140 |
| atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg   | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac   | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag   | 1380 |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc    | 1440 |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag   | 1500 |
| ccccaggga aaggccttga gtggatagga aggacatact acagggtccaa gtggtataat   | 1560 |
| gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag   | 1620 |
| ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga   | 1680 |
| gaggatgggg atagctacta ccgctacgggt atggacgtct ggggcaaagg gaccacggtc  | 1740 |
| accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag    | 1800 |

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agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaaccg 1860  
 gtgacgggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920  
 ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg 1980  
 ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040  
 aaagttgagc ccaaattcttg t 2061

<210> 1846  
 <211> 687  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1846

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495



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Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

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<210> 1847  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1847  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1848  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1848

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

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Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1849  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1849  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcga 360  
tctgatgagc agttgaaatc tggtagcgcc tctgtttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1850  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1850

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1851  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1851  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600  
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac 660  
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780  
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840  
gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt 900  
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960  
aaggctctcca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg  | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac  | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtgca gttacagcag | 1380 |
| tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt  | 1440 |
| gggtccttca gtggttacta ctggaactgg attcgccagc caccagggaa ggggctagag  | 1500 |
| tggattgggg aaatcaatca tgctggaaac accaactaca acccgccct caagagtcga   | 1560 |
| gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc  | 1620 |
| gccgcggaca cggctgtgta ttactgtgcg agaggatatt gtagaagtac cacctgctac  | 1680 |
| tttgactact ggggcaaggg aaccctagtc accgtctcct cagcctccac caagggccca  | 1740 |
| tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc   | 1800 |
| tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg   | 1860 |
| accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag  | 1920 |
| agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat | 1980 |
| cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t           | 2031 |

<210> 1852

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1852

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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



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Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

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Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1853  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1853  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

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ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1854  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1854

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

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Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1855  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1855  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagagc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360

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|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| tctgatgagc | agttgaaatc | tggtaccgcc  | tctgtttgtgt | gcctgctgaa | taacttctat | 420 |
| cccagagagg | ccaaagtaca | gtggaagggtg | gataacgccc  | tccaatcggg | taactcccag | 480 |
| gagagtgtca | cagagcagga | cagcaaggac  | agcacctaca  | gcctcaagag | caccctgacg | 540 |
| ctgagcaaag | cagactacga | gaaacacaaa  | gtctacgcct  | gcgaagtcac | ccatcagggc | 600 |
| ctgagctcgc | ccgtcacaaa | gagcttcaac  | aggggagagt  | gt         |            | 642 |

|       |                     |
|-------|---------------------|
| <210> | 1856                |
| <211> | 214                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1856

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1857  
<211> 2025  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1857  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tggggtcttg actactgggg ccaggggaacc ctggtcaccg tctctagtgc ctccaccaag  | 360  |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc   | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc   | 540  |
| ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac   | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac  | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc  | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc     | 780  |
| gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt   | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc   | 960  |
| aaggctctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg    | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg     | 1140 |
| gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac   | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc   | 1320 |
| tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtgca gctgcaggag   | 1380 |
| tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt   | 1440 |
| ggctccatca gtagttactt ctggagctgg attcggcagc cccaggtaa gggactggag    | 1500 |
| tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga   | 1560 |
| gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc   | 1620 |
| gctgcggaca cggccgtgta ttactgtgag agagaaactg ggagctacta cggctttgac   | 1680 |
| tactggggca agggaaacct ggtcaccgtc tcctcagcct ccaccaaggg cccatcggtc   | 1740 |



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ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 1800  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 1860  
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgagagcgtg 1920  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 1980  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 2025

<210> 1858  
 <211> 675  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1858

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val  
290 295 300

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Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
305 310 315 320

Lys 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 Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

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Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
660 665 670

Lys Ser Cys  
675

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<210> 1859  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1859  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540  
 agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1860  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1860

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

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Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1861  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1861  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggagcct aaactgctca ttacttgggc atctaccg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1862  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1862

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205



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Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

<210> 1863  
 <211> 2046  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1863  
 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
 cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
 agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
 tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540  
 ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600  
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac 660  
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720  
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780  
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840  
 gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt 900  
 tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960  
 aaggctctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg  | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac  | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac  | 1260 |
| gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag | 1380 |
| tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg  | 1440 |
| gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc   | 1500 |
| cttgagtgga taggaaggac atactacagg tccaagtggg ataagtatta tgcagtttct  | 1560 |
| ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg  | 1620 |
| agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc  | 1680 |
| tactaccgct acggtatgga cgtctggggc aaagggacca cggtcaccgt ctctcagcc   | 1740 |
| tccaccaagg gcccatcggg cttccccctg gcaccctcct ccaagagcac ctctgggggc  | 1800 |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg  | 1860 |
| aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga  | 1920 |
| ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac  | 1980 |
| atctgcaacg tgaatcaca gcccagcaac accaaggtgg acaagaaagt tgagcccaaa   | 2040 |
| tcttgt                                                             | 2046 |

<210> 1864  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1864

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu  
180 185 190

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Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

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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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr  
565 570 575

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Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1865  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1865  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gtcacctac cttcggcgag 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360

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|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| tctgatgagc | agttgaaatc | tggtaccgcc  | tctgtttgtgt | gcctgctgaa | taacttctat | 420 |
| cccagagagg | ccaaagtaca | gtggaagggtg | gataacgcc   | tccaatcggg | taactcccag | 480 |
| gagagtgtca | cagagcagga | cagcaaggac  | agcacctaca  | gcctcgagag | caccctgacg | 540 |
| ctgagcaaag | cagactacga | gaaacacaaa  | gtctacgcct  | gcgaagtcac | ccatcagggc | 600 |
| ctgagctcgc | ccgtcacaaa | gagcttcaac  | aggggagagt  | gt         |            | 642 |

|       |                     |
|-------|---------------------|
| <210> | 1866                |
| <211> | 214                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1866

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1867  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1867  
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300



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gggacaaaag tcgagatcaa gcgtacgggtg gctgcacccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

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<210> 1868  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1868

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1869  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1869  
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acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgccagcca 120  
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgcgag aggatattgt    | 300  |
| agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca   | 360  |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 420  |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 480  |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 540  |
| ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 660  |
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga  | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    | 780  |
| gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc   | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   | 960  |
| gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag    | 1080 |
| atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtg   | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg   | 1320 |
| cagaagagcc tctccctgtc tccgggtggg ggcgatcgg gaggtggcgg atccgaggta    | 1380 |
| caactgggtg aatcagggtg aggtttgggtg cagccgggga gatcgctcag gcttagctgt  | 1440 |
| gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcttga    | 1500 |
| aaagggtctg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac   | 1560 |
| agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag   | 1620 |
| atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg   | 1680 |

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tctacagctt cgtcgtcga ctattggggt aaaggaacgt tggtcaccgt ctctagtgcc 1740  
tccaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 1800  
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860  
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 1920  
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 1980  
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tcttgt 2046

<210> 1870  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1870

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

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Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

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Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

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Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1871  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1871  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgag 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgccca 360  
tctgatgagc agttgaaatc tggtaaccgcc tctgtttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1872  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1872



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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1873  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1873  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggacca gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1874  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1874

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 180 185 190

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His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1875  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1875  
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgccagcca 120  
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900

# A-1937-W0-PCT\_ST25

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agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc      1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag      1080
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc      1140
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cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgagggt      1380
cagctgggtg agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt      1440
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tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt      1680
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tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg      1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag      1920
agcgtgggtg ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t          2031

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<210> 1876

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1876

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
 180 185 190

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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

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Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575



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Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1877  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1877  
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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300

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gggaccaagc tggaaatcaa acgaacgggtg gctgcacccat ctgtcttcat cttcccgccca    360
tctgatgagc agttgaaatc tggtagccgcc tctgtttgtgt gcctgctgaa taactttctat    420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag    480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg    540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc    600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt    642

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<210> 1878  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1878

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

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Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1879  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1879  
gatatcaaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240

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gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgccca 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1880  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1880

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1881  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1881  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg  | 240  |
| aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg  | 300  |
| agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc  | 360  |
| accaagggcc catcggctct ccccttgga cctcctcca agagcacctc tgggggcaca    | 420  |
| gcggccctgg gctgcctgg caaggactac ttccccgaac cggtgacggg gtcgtggaac   | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc   | 540  |
| tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc  | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaactc  | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttctct tcccccaaa acccaaggac accctcatga tctcccgga ccctgaggtc     | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc      | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaa aactacaaga ccacgcctcc cgtgctggac   | 1200 |
| tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag   | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtacaactg  | 1380 |
| gtggaatcag gtggagggtt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca  | 1440 |
| tcggggttta ctttcgatga ttatgcgatg cattgggtcc ggcaagcgcc tggaaaagg   | 1500 |
| ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg   | 1560 |
| gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac  | 1620 |

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tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680  
gcttcgctgc tcgactattg gggtaaagga acgttgggtca ccgtctctag tgcctccacc 1740  
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800  
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860  
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980  
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1882  
<211> 680  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1882

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

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Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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



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Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
450 455 460

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

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Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

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Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1883  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1883  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1884  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1884

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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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1885  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1885  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggacca gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1886  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1886

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 180 185 190

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His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1887  
<211> 2025  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1887  
cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctacgcctcc 360  
accaagggcc catcggtctt ccccttgga cctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 660  
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaacat ctccaaagcc   | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tggtagcgga tcgggaggtg gcggatccga ggtgcagctg  | 1380 |
| gtgcagtctg gagcagaggt gaaaaagccc ggggagcttc tgaagatctc ctgtaagact  | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc  | 1500 |
| ctggagtgga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc  | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc  | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac | 1680 |
| tactggggca agggaaacct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc  | 1740 |
| ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg   | 1800 |
| gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc  | 1860 |
| ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactccct cgagagcgtg   | 1920 |
| gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag  | 1980 |
| cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt                  | 2025 |

<210> 1888

<211> 675

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide



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&lt;400&gt; 1888

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys Ser Val Val Thr Val Pro Ser Ser  
 180 185 190

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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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
565 570 575

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
580 585 590

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
595 600 605

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
610 615 620

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
625 630 635 640

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
645 650 655

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
660 665 670

Lys Ser Cys  
675

<210> 1889  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1889  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

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cctctcactt tcggcgaggg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1890

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1890

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

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Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1891  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1891  
gatatcaaaa tgacacaatc accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240

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gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1892  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1892

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1893  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1893  
caggtagct tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtgggtat 180



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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac  | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg  | 360  |
| gtcaccgtct cctcagcctc caccaagggc ccatcggctt tccccctggc accctcctcc  | 420  |
| aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa | 480  |
| ccggtgacgg tgctgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct  | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc  | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac  | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct  | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg  | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag   | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agccccatc   | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc  | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc  | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt  | 1380 |
| ggcggatccg aggtacaact ggtggaatca ggtggaggtt tggtgcagcc ggggagatcg  | 1440 |
| ctcaggctta gctgtgcggc atcggggttt actttcgatg attatgcgat gcattgggtc  | 1500 |
| cggcaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac  | 1560 |
| atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac  | 1620 |

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agcctgtacc ttcagatgaa ctcaacttcgc gcggaagata ccgccgtata ctactgcgcc 1680  
aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtaaagg aacgttggtc 1740  
accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 1800  
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg 1860  
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920  
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg 1980  
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040  
aaagttgagc ccaaattctg t 2061

<210> 1894  
<211> 687  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1894

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

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Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

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Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
580 585 590

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
595 600 605

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
610 615 620

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
625 630 635 640

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro  
645 650 655

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Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
660 665 670

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1895  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1895  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaggg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1896  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 1896

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 180 185 190

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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

<210> 1897  
 <211> 651  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1897  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1898  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>



&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1898

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 165 170 175

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Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1899  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1899  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540  
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600  
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660  
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 720  
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 780  
atctccccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt  | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc   | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc  | 1080 |
| ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt  | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct  | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg  | 1500 |
| cgccagatgc ccgggaaagg cctggagtggt atggggatca tctatcttgg tgactcagat | 1560 |
| accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt  | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg   | 1680 |
| agaagtaact ggggtcttga ctactggggc aagggaaccc tggtcaccgt ctctagtgcc  | 1740 |
| tccaccaagg gcccacggtt cttccccctg gcaccctcct ccaagagcac ctctgggggc  | 1800 |
| acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg  | 1860 |
| aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga  | 1920 |
| ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac | 1980 |
| atctgcaacg tgaatcacia gcccagcaac accaaggtgg acaagaaagt tgagcccaaa  | 2040 |
| tcttgt                                                             | 2046 |

<210> 1900

<211> 682

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1900

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

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Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

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Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

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Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro  
580 585 590

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val  
595 600 605

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala  
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1901  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1901  
gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1902  
<211> 214  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1902

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80



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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1903  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1903  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60

agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg 120

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggc caccgtctct  | 360  |
| agtacgggtg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct    | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac    | 780  |
| tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc   | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag   | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgaggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tgcaattaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg   | 1440 |
| tcctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc   | 1500 |
| cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac   | 1560 |

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|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| tacaaccggt  | ccctcaagag | tcgagtcacc | atatcattag | acacgtcaa   | gaaccagttc | 1620 |
| tccctgacgc  | tgacctctgt | gaccgccgcg | gacacggctg | tgtattactg  | tgcgagagga | 1680 |
| tattgtagaa  | gtaccacctg | ctactttgac | tactggggca | agggaaccct  | agtcaccgtc | 1740 |
| tcctcagcct  | ccaccaaggg | cccatcggtc | ttccccctgg | caccctcctc  | caagagcacc | 1800 |
| tctggggggca | cagcggccct | gggctgcctg | gtcaaggact | acttccccga  | accggtgacg | 1860 |
| gtgtcgtgga  | actcaggcgc | cctgaccagc | ggcgtgcaca | ccttcccggc  | tgtcctacag | 1920 |
| tcctcaggac  | tctactccct | cgagagcgtg | gtgaccgtgc | cctccagcag  | cttgggcacc | 1980 |
| cagacctaca  | tctgcaacgt | gaatcacaag | cccagcaaca | ccaagggtgga | caagaaagtt | 2040 |
| gagcccaa    | attgt      |            |            |             |            | 2055 |

|       |                     |
|-------|---------------------|
| <210> | 1904                |
| <211> | 685                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1904

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

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Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

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Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

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Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1905  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1905  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtagcggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1906  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>

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&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1906

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Gly | Ile | Arg | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Thr | Leu | Gln | 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 | Arg | Tyr | Asn | Arg | Ala | Pro | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Glu | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Glu | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |



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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1907  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1907  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagagc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 1908  
<211> 214  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1908

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Lys | Glu | Pro | Lys | Leu | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Val | Thr | Glu | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1909  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1909  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 660  
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc 780

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc   | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg   | 1440 |
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg  | 1500 |
| cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa    | 1560 |
| tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc    | 1620 |
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa   | 1680 |
| actgggagct actacggctt tgactactgg ggcaagggaa ccctgggtcac cgtctcctca  | 1740 |
| gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg   | 1800 |
| ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg | 1860 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca   | 1920 |
| ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc   | 1980 |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc   | 2040 |
| aaatcttgt                                                           | 2049 |

<210> 1910

<211> 683

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1910

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

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Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

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Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1911

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1911

gatatccaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120



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```

ggaaaaaacac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa      300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tggggaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 1912  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1912

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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

```

# A-1937-W0-PCT\_ST25

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1913  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1913  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

60

A-1937-W0-PCT\_ST25

```

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggagcct aaactgctca ttacttgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc      480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

```

<210> 1914  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1914

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
          20          25          30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
          35          40          45

```

```

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50          55          60

```

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Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1915

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

## A-1937-W0-PCT\_ST25

&lt;400&gt; 1915

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt  | 60   |
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcatgtgggt ccggcaagcg | 120  |
| cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat    | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac    | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc    | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct   | 360  |
| agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct     | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag    | 480  |
| tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac    | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag    | 600  |
| aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag  | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa    | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac     | 780  |
| ttccggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc    | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag    | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg    | 960  |
| ctgaatggca aggagtacaa gtgcaagggt tccaacaaag ccctcccagc ccccatcgag    | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca    | 1080 |
| tcccgggagg agatgaccaa gaaccagggt agcctgacct gcctgggtcaa aggcttctat   | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc    | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac    | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgtccg tgatgcatga ggctctgcac     | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc    | 1380 |
| ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc    | 1440 |

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|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| tcactcacct  | gtaccatctc | cggggacagt | gtctctacca | acagtgttgc  | ttggaactgg | 1500 |
| attaggcagc  | ccccagggaa | aggccttgag | tggataggaa | ggacatacta  | caggtccaag | 1560 |
| tgggtataatg | attatgcagt | ttctctgaaa | agtcgagtaa | ccatcagccc  | agacacatcc | 1620 |
| aagaaccagt  | tctccctgaa | gctgagctct | gtgactgccg | cggacacggc  | tgtgtattac | 1680 |
| tgtgcaagag  | aggatgggga | tagctactac | cgctacggta | tggacgtctg  | gggcaaaggg | 1740 |
| accacggtca  | ccgtctcctc | agcctccacc | aagggcccat | cggtcttccc  | cctggcaccc | 1800 |
| tcctccaaga  | gcacctcttg | gggcacagcg | gccctgggct | gcctgggtcaa | ggactacttc | 1860 |
| cccgaaccgg  | tgacggtgtc | gtggaactca | ggcgccctga | ccagcggcgt  | gcacaccttc | 1920 |
| ccggctgtcc  | tacagtcttc | aggactctac | tccctcgaga | gcgtgggtgac | cgtgccctcc | 1980 |
| agcagcttgg  | gcacccagac | ctacatctgc | aacgtgaatc | acaagcccag  | caacaccaag | 2040 |
| gtggacaaga  | aagttgagcc | caaatcttgt |            |             |            | 2070 |

|       |                     |
|-------|---------------------|
| <210> | 1916                |
| <211> | 690                 |
| <212> | PRT                 |
| <213> | Artificial Sequence |

<220>  
<223> Synthetic polypeptide

<400> 1916

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

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Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

A-1937-W0-PCT\_ST25

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445



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Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1917  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1917  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1918  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1918

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1919  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1919  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

642

&lt;210&gt; 1920

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1920

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1921  
<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1921  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360  
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac   | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt   | 660  |
| tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca    | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc     | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc     | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcga tcgggagggtg gcggatccca ggtgcagtta  | 1380 |
| cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc    | 1440 |
| catggtgggt ctttcagtgg ttactactgg aactggattc gccagccacc aggggaagggg  | 1500 |
| ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag   | 1560 |
| agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct   | 1620 |
| gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc   | 1680 |
| tgctactttg actactgggg caagggaacc ctagtcaccg tctcctcagc ctccaccaag   | 1740 |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc   | 1800 |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc | 1860 |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc   | 1920 |
| ctcgagagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 1980 |

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gtgaatcaca agcccagcaa caccaaggtg gacaagaaaag ttgagcccaa atcttgt 2037

<210> 1922  
 <211> 679  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1922

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
 115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
 130 135 140



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Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

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Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
580 585 590

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
595 600 605

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
610 615 620

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
625 630 635 640

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
645 650 655

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
660 665 670

Lys Val Glu Pro Lys Ser Cys  
675

<210> 1923

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic polynucleotide

<400> 1923

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc      360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg      420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt                      645
```

<210> 1924

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1924

```
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1           5           10          15
```

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20          25          30
```

```
Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35          40          45
```

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1925

<211> 642

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 1925

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagagc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc      360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

<210> 1926

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1926

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile
          35           40           45

```

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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1927

<211> 2031

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1927

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| cccggaaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac  | 180  |
| agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc  | 360  |
| aacccactg tcactctgtt ccgcccctcc tctgaggagc tccaagccaa caaggccaca   | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |



A-1937-W0-PCT\_ST25

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
 agcctctccc tgtctccggg tggtagcgga tcgggaggtg gcggatccca ggtgcagctg 1380  
 caggagtcgg gccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc 1440  
 tctggtggct ccatcagtag ttacttctgg agctggattc ggcagcccc aggtaaggga 1500  
 ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag 1560  
 agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct 1620  
 gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc 1680  
 ttgtactact ggggcaaggg aaccctggtc accgtctcct cagcctccac caagggccca 1740  
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 1800  
 tgcctggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgccctg 1860  
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag 1920  
 agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1980  
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 2031

<210> 1928

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1928

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

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Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly  
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560

Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser  
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr  
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro  
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
610 615 620

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His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu  
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile  
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val  
660 665 670

Glu Pro Lys Ser Cys  
675

<210> 1929  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1929  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 1930  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1930

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1931  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1931  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggagcct aaactgctca tttactgggc atctaccg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

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gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1932  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1932

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140



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Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 1933  
<211> 2052  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1933  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc 360  
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc   | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tcgggagggtg gcggatccca ggtacagttg | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc  | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg   | 1500 |
| aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca    | 1560 |
| gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg  | 1620 |
| aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg   | 1680 |
| gatagctact accgctacgg tatggacgtc tggggcaaag ggaccacggc caccgtctcc  | 1740 |
| tcagcctcca ccaaggggcc atcggctctc cccctggcac cctcctccaa gagcacctct  | 1800 |
| gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggg   | 1860 |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc  | 1920 |
| tcaggactct actccctcga gagcgtgggtg accgtgccct ccagcagctt gggcacccag | 1980 |

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acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 2040

cccaaattctt gt 2052

<210> 1934

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1934

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

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Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

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Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510

A-1937-W0-PCT\_ST25

Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
580 585 590

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
595 600 605

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
610 615 620

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
625 630 635 640

Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser  
645 650 655

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn  
660 665 670

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1935

<211> 645

<212> DNA

<213> Artificial Sequence

A-1937-W0-PCT\_ST25

<220>

<223> Synthetic polynucleotide

<400> 1935

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc | 60  |
| tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag | 120 |
| tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc | 180 |
| cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc | 240 |
| caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg | 300 |
| gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc | 360 |
| ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg  | 420 |
| gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc | 480 |
| ggcgtgcaca ccttcccggc tgcctacag tcctcaggac tctactccct cgaaagcgtg  | 540 |
| gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag | 600 |
| cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt               | 645 |

<210> 1936

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1936

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Val | Ser | Gly | Ala | Pro | Gly | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Thr | Ile | Ser | Cys | Thr | Gly | Ser | Ser | Ser | Asn | Ile | Gly | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asp | Val | His | Trp | Tyr | Gln | Gln | Phe | Pro | Gly | Thr | Ala | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1937

<211> 642



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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1937

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg  | 60  |
| attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc  | 120 |
| ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg  | 180 |
| aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc  | 240 |
| gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa  | 300 |
| gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc  | 360 |
| tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat  | 420 |
| cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag | 480 |
| gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg  | 540 |
| ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc  | 600 |
| ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                     | 642 |

<210> 1938

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1938

|                                                                    |  |
|--------------------------------------------------------------------|--|
| 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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr    |  |
| 20                    25                    30                     |  |

A-1937-W0-PCT\_ST25

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

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<210> 1939  
 <211> 2055  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1939  
 cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120  
 ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtcccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
 aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
 aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
 ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720  
 ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780  
 cggaccccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgagggtcaag 840  
 ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag 900  
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960  
 aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020  
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080  
 cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140  
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

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cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260  
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 cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga 1380  
 tccgaggtac aactgggtga atcaggtgga ggtttgggtg agccggggag atcgctcagg 1440  
 cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa 1500  
 gcgcctggaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat 1560  
 tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg 1620  
 taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc 1680  
 tcctacttgt ctacagcttc gtcgctcgac tattggggta aaggaacgtt ggtcaccgtc 1740  
 tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 1800  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 1860  
 gtgtcgtgga actcaggcgc cctgaccagc ggctgcaca cttcccggc tgcctacag 1920  
 tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980  
 cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt 2040  
 gagcccaa at cttgt 2055

<210> 1940  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1940

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

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Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

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Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

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Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

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Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1941  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1941  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540



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tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1942

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1942

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1943  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1943  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

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aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1944  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1944

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

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Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1945  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1945  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtgg gtccttcagt gggtactact ggaactggat tcgccagcca 120  
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg   | 480  |
| aaggtggata acgcccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa   | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc   | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc   | 720  |
| ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccttg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgaggtcaag   | 840  |
| ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg   | 960  |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa   | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc    | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc  | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg   | 1200 |
| cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag    | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac  | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga  | 1380 |
| tccgaggtgc agctgggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag  | 1440 |
| atctcctgta agacttctga atacagcttt accagctact ggatcggctg ggtgcgccag   | 1500 |
| atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga   | 1560 |
| tacagcccgt ccttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc   | 1620 |
| tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt   | 1680 |
| aactggggtc ttgactactg gggcaaggga accctgggtc ccgtctctag tgcctccacc   | 1740 |
| aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg     | 1800 |
| gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca | 1860 |

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ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920  
 tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980  
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1946  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1946

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
 115 120 125

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Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

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Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
485 490 495

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
500 505 510



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Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
595 600 605

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
610 615 620

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
625 630 635 640

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1947

<211> 633

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1947

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

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<210> 1948

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1948

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10          15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
          20          25          30

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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 Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
 195 200 205

Lys Ser Cys  
 210

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<210> 1949  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1949  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1950  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1950

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1951  
 <211> 2049  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1951  
 cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
 acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
 ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
 cctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacgggtg 360  
 gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 420  
 tctgtttgtg gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480  
 gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
 agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600  
 gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660  
 aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 780  
 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840  
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac 900  
 ggagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960  
 aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020  
 tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgagg 1080  
 gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag  | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc  | 1440 |
| tgtgcggcat cgggggtttac tttcgatgat tatgcatgac attgggtccg gcaagcgcct | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca  | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt  | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac   | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtaaaggaa cgttggtcac cgtctctagt  | 1740 |
| gcctccacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg  | 1800 |
| ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggg gacggtgtcg  | 1860 |
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 1920 |
| ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc   | 1980 |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc  | 2040 |
| aaatcttgt                                                          | 2049 |

<210> 1952  
 <211> 683  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1952

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205



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Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

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Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560

Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
580 585 590

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Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu  
595 600 605

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly  
610 615 620

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser  
625 630 635 640

Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu  
645 650 655

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr  
660 665 670

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680

<210> 1953

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1953

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc  | 60  |
| atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca  | 120 |
| gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca  | 180 |
| aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct  | 240 |
| gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa  | 300 |
| gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca | 360 |
| ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggc caaggactac  | 420 |
| ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc | 480 |

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ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 1954  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1954

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1955  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1955  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

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ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540  
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600  
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1956  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1956

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

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Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1957  
<211> 2034  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1957  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360

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|                                                                      |      |
|----------------------------------------------------------------------|------|
| gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc    | 420  |
| tctgtttgtgt gcctgctgaa taactttctat cccagagagg ccaaagtaca gtggaagggtg | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac    | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa    | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac    | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg    | 720  |
| ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc      | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac   | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac    | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc    | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgagg      | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac   | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg    | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac    | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag    | 1380 |
| gtgcagctgg tgcagtctgg agcagagggtg aaaaagcccg gggagtctct gaagatctcc   | 1440 |
| tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg ccagatgccc    | 1500 |
| gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc    | 1560 |
| ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg    | 1620 |
| cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgcgag aagtaactgg    | 1680 |
| ggtcttgact actggggcaa gggaaccctg gtcaccgtct ctagtgcctc caccaagggc    | 1740 |
| ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg    | 1800 |



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ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 1860  
 ctgaccagcg gcgtgcacac cttccccggct gtcctacagt cctcaggact ctactccctc 1920  
 gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1980  
 aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaadc ttgt 2034

<210> 1958  
 <211> 678  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1958

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

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Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

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Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala  
565 570 575

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser  
580 585 590

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe  
595 600 605

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
610 615 620

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
625 630 635 640

Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr  
645 650 655

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys  
660 665 670

Val Glu Pro Lys Ser Cys  
675

A-1937-WO-PCT\_ST25

<210> 1959  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1959  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 300  
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1960  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1960

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

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Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

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<210> 1961  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1961  
 gatatccaaa tgacacaatc accatcgctc gtttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1962  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1962

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205



Phe Asn Arg Gly Glu Cys  
210

<210> 1963  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1963  
caggtagct tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540  
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780  
accctcatga tctcccgga cctgagggtc acatgcgtgg tggaggacgt gagccacgaa 840  
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900  
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960  
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1020  
gccccatcg agaaaacat ctcaaagcc aaagggcagc ccgagaacc acaggtgtac 1080

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| accctgcccc catccccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc  | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac   | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat   | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggtagcgga   | 1380 |
| tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg   | 1440 |
| gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg   | 1500 |
| cattgggtcc ggcaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat    | 1560 |
| agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat   | 1620 |
| gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac   | 1680 |
| tactgcgcca aagtctccta cttgtctaca gcttcgtcgc tcgactattg gggtaaagga   | 1740 |
| acgttgggtca ccgtctctag tgcctccacc aaggggcccat cggctttccc cctggcaccc | 1800 |
| tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc  | 1860 |
| cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc   | 1920 |
| ccggctgtcc tacagtctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc   | 1980 |
| agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag   | 2040 |
| gtggacaaga aagttgagcc caaatcttgt                                    | 2070 |

<210> 1964  
 <211> 690  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1964

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

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Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

A-1937-W0-PCT\_ST25

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575

Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
580 585 590

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Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
595 600 605

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
610 615 620

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
625 630 635 640

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val  
645 650 655

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
675 680 685

Ser Cys  
690

<210> 1965  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1965  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

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cctctcactt tcggcgaagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctggtca aggactactt ccccgaaacc gtgacggtgt cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 1966  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1966

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

A-1937-W0-PCT\_ST25

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1967  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide"

<400> 1967  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagagcccaa actcctcatc caaggaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240



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caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480  
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag 540  
 agctatctga gcctgacgcc tgagcagtgg aagtcaccaca gaagctacag ctgccaggtc 600  
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1968  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1968

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

A-1937-W0-PCT\_ST25

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1969  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1969  
caggtagct tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtgggtat 180

## A-1937-W0-PCT\_ST25

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac   | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca   | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg   | 360  |
| gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag   | 420  |
| cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag  | 480  |
| gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc    | 540  |
| acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa   | 600  |
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg   | 660  |
| cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc   | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac    | 780  |
| accctcatga tctcccggac ccctgagggtc acatgcgtgg tgggtggacgt gagccacgaa | 840  |
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca   | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttggtg tcagcgtcct caccgtcctg  | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctcca     | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac   | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc   | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac   | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat   | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcgga  | 1380 |
| tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc   | 1440 |
| ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc   | 1500 |
| ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggt   | 1560 |
| gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag   | 1620 |

A-1937-W0-PCT\_ST25

tccatcagta cgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat 1680  
tactgtgcga gaagtaactg gggctcttgac tactggggca aggggaaccct ggtcaccgtc 1740  
tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 1800  
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 1860  
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 1920  
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980  
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2040  
gagcccaaat cttgt 2055

<210> 1970  
<211> 685  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1970

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

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Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
595 600 605

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
610 615 620

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser  
645 650 655

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Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
675 680 685

<210> 1971  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1971  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgcctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

<210> 1972  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide



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&lt;400&gt; 1972

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
 130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
 145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
 165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
 180 185 190

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Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215

<210> 1973  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1973  
 gatattcaaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
 gggacaaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360  
 tctgatgagc agttgaaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
 ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1974  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 1974

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
 165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
 195 200 205

Phe Asn Arg Gly Glu Cys  
 210

<210> 1975  
 <211> 2055  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 1975  
 gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
 agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
 cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
 agtgcctcca ccaaggggccc atcggctctt cccctggcac cctcctccaa gagcacctct 420  
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480  
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
 tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccacg 600  
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660  
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
 ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc 780  
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc  | 1440 |
| tgcgctgtcc atggtgggtc cttcagtggt tactactgga actggattcg ccagccacca  | 1500 |
| gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg  | 1560 |
| tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg  | 1620 |
| ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga  | 1680 |
| agtaccacct gctactttga ctactggggc aagggaaccc tagtcaccgt ctctcaact   | 1740 |
| gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact  | 1800 |
| gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag  | 1860 |
| gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag  | 1920 |
| gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac  | 1980 |
| aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc   | 2040 |
| aacaggggag agtgt                                                   | 2055 |

<210> 1976  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1976

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

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Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His  
500 505 510

Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg  
545 550 555 560



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Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 1977  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1977  
gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg aacccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

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gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 1978  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 1978

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1979  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1979  
gatatccaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

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```

ggaaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa      300
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642

```

<210> 1980  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1980

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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

```

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Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1981  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1981  
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt

60

## A-1937-W0-PCT\_ST25

|                                                                      |      |
|----------------------------------------------------------------------|------|
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg  | 120  |
| cctggaaaaa agctcgagtg gggtttccgcc attacgtgga atagcggaca catcgattat   | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac    | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc    | 300  |
| tacttgtcta cagcttcgtc gtcgactat tgggggtcaag gaacgttgggt caccgtctct   | 360  |
| agtgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct  | 420  |
| gggggacacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg | 480  |
| tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc    | 540  |
| tcaggactct actccctcaa aagcgtgggtg accgtgccct ccagcagctt gggcacccag   | 600  |
| acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag    | 660  |
| cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg   | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc     | 780  |
| cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac  | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac    | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc    | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag     | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtc aaggcttcta tcccagcgac    | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg    | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac    | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag    | 1380 |
| gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc    | 1440 |
| tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagcccca     | 1500 |

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ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc 1560  
 tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620  
 ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680  
 tactacggct ttgactactg gggcaaggga accctgggtca ccgtctcctc aactgtggct 1740  
 gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1800  
 gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 1860  
 aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 1920  
 acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 1980  
 tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 2040  
 ggagagtgt 2049

<210> 1982  
 <211> 683  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1982

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

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Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255



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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

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Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile  
485 490 495

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr  
500 505 510

Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile  
515 520 525

Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val  
530 535 540

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser  
545 550 555 560

Tyr Tyr Gly Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
595 600 605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
610 615 620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

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Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1983  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1983  
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gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1984  
<211> 211  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 1984

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Ser | Ile | Asn | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Arg | Pro | Gly | Lys | Glu | Pro | Lys | Leu | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Ser | Leu | Gln | 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 | Ser | Tyr | Ser | Thr | Pro | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Ser | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Lys | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1985  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1985  
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1986  
<211> 214

A-1937-WO-PCT\_ST25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1986

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Gly | Ile | Arg | Asn | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Ala | Ser | Thr | Leu | Gln | 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 | Arg | Tyr | Asn | Arg | Ala | Pro | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Glu | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Thr | Val | Ala | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Ser | Val | Val | Cys | Leu | Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Trp | Lys | Val | Asp | Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 1987  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1987  
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agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg gggttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtcctcca ccaagggtccc atcgggtcttc cccctggcac ctcctccaa gagcacctct 420  
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480  
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540  
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccag 600  
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660  
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc  | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac | 840  |
| tggtagctgg acggcgtgga ggtgcataat gccaaagaca agccgtgtga ggagcagtag  | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc  | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc   | 1020 |
| tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag   | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag  | 1380 |
| gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc   | 1440 |
| tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag  | 1500 |
| ccccaggga aaggccttga gtggatagga aggacatact acagggtcaa gtggtataat   | 1560 |
| gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag  | 1620 |
| ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga  | 1680 |
| gaggatgggg atagctacta ccgctacgggt atggacgtct ggggcaaagg gaccacggtc | 1740 |
| accgtctcct caactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag  | 1800 |
| ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc  | 1860 |
| aaagtacagt ggaagggtgga taacgccctc caatcgggtg actcccagga gagtgtcaca | 1920 |
| gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca  | 1980 |
| gactacgaga aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc | 2040 |
| gtcacaaaaga gcttcaacag gggagagtgt                                  | 2070 |



A-1937-W0-PCT\_ST25

<210> 1988  
 <211> 690  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1988

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160

A-1937-W0-PCT\_ST25

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val  
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

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Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln  
450 455 460

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
465 470 475 480

Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn  
485 490 495

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr  
500 505 510

Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser  
515 520 525

Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys  
530 535 540

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Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
545 550 555 560

Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys  
565 570 575

Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685

Glu Cys  
690

<210> 1989

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

A-1937-W0-PCT\_ST25

<223> Synthetic polynucleotide

<400> 1989

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggaacct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca      360
tcgggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      420
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa      540
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651

```

<210> 1990

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1990

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35           40           45

```

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Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 1991  
<211> 651  
<212> DNA  
<213> Artificial Sequence

A-1937-W0-PCT\_ST25

<220>

<223> Synthetic polynucleotide

<400> 1991

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg aagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa      540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

```

<210> 1992

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1992

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1              5              10              15

```

```

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20              25              30

```

```

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35              40              45

```

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1993

<211> 2040



&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 1993

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc  | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg   | 120  |
| cccggaaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac   | 180  |
| agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac   | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag  | 360  |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc   | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc   | 540  |
| ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac   | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc   | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc     | 780  |
| gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggaggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt    | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc   | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg     | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg    | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac   | 1260 |

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gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320  
 tccctgtctc cgggtgggtgg cggatcggga ggtggcggat cccaggtgca gttacagcag 1380  
 tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt 1440  
 gggtccttca gtggttacta ctggaactgg attcgccagc caccagggaa ggggctagag 1500  
 tggattgggg aaatcaatca tgctggaaac accaactaca acccgctccct caagagtcga 1560  
 gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc 1620  
 gccgcggaca cggctgtgta ttactgtgcg agaggatatt gtagaagtac cacctgctac 1680  
 tttgactact ggggcaaggg aaccctagtc accgtctcct caactgtggc tgcaccatct 1740  
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 1800  
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 1860  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 1920  
 ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc 1980  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 2040

<210> 1994  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1994

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

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Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
225 230 235 240

A-1937-W0-PCT\_ST25

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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly  
435 440 445

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Gly  
450 455 460

Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val His Gly  
465 470 475 480

Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn Thr Asn  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser  
515 520 525

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr  
545 550 555 560

Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

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Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 1995  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1995  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg aacccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480  
ttccccgctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1996  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1996

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 1997  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1997  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360  
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420  
ataagtgact tctacccggg agccgtgaca gtggcctgga aggagatag cagccccgtc 480  
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540  
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600



A-1937-W0-PCT\_ST25

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a

651

<210> 1998  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 1998

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 130 135 140

A-1937-W0-PCT\_ST25

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 1999  
<211> 2034  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 1999  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360  
ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420  
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480  
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctcaaaagcg tggtagaccgt gccctccagc agcttgggca cccagaccta catctgcaac | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc    | 780  |
| gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggagggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc  | 960  |
| aaggctctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg  | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac   | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg   | 1140 |
| gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac | 1260 |
| gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc  | 1320 |
| tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gctgcaggag | 1380 |
| tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt  | 1440 |
| ggctccatca gtagttactt ctggagctgg attcggcagc cccaggtaa gggactggag   | 1500 |
| tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga  | 1560 |
| gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc  | 1620 |
| gctgcggaca cggccgtgta ttactgtgcg agagaaactg ggagctacta cggctttgac  | 1680 |
| tactggggca aggggaaccct ggtcaccgtc tcctcaactg tggctgcacc atctgtcttc | 1740 |
| atcttccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg   | 1800 |
| aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg  | 1860 |
| ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcgaa  | 1920 |
| agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc  | 1980 |

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acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt

2034

<210> 2000

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2000

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
325 330 335

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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
340 345 350

Ser Arg Glu Glu Met 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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
465 470 475 480

Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly  
485 490 495

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys  
500 505 510

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser  
515 520 525

A-1937-W0-PCT\_ST25

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp  
545 550 555 560

Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala  
565 570 575

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
580 585 590

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
595 600 605

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
610 615 620

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
625 630 635 640

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
645 650 655

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
660 665 670

Phe Asn Arg Gly Glu Cys  
675

<210> 2001

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 2001

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca      120
gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagtga gcccaaattct tgt                                     633

```

&lt;210&gt; 2002

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 2002

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile
35           40           45

```



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Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2003  
<211> 651  
<212> DNA  
<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 2003

```

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc      360
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa      540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

```

<210> 2004

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2004

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1              5              10             15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
                20             25             30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35              40             45

```

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser  
210 215

<210> 2005

<211> 2055

A-1937-WO-PCT\_ST25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2005

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc  | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg   | 120  |
| cccggaaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac   | 180  |
| agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac  | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac   | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag  | 360  |
| ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc   | 420  |
| ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc | 480  |
| gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc   | 540  |
| ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac  | 600  |
| gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac   | 660  |
| aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc   | 720  |
| ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc    | 780  |
| gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc  | 840  |
| gtggaggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt    | 900  |
| tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc   | 960  |
| aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg     | 1020 |
| cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac    | 1080 |
| caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg    | 1140 |
| gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   | 1200 |
| ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac   | 1260 |

A-1937-W0-PCT\_ST25

```

gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag 1380
tcagggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaggc 1500
cttgagtgga taggaaggac atactacagg tccaagtggg ataagtatta tgcagtttct 1560
ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg 1620
agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc 1680
tactaccgct acggtatgga cgtctggggc aaagggacca cggtcaccgt ctctcaact 1740
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980
aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc 2040
aacaggggag agtgt 2055

```

<210> 2006  
 <211> 685  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2006

```

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1           5           10          15

```

```

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr
20          25          30

```

A-1937-W0-PCT\_ST25

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr 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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 210 215 220

A-1937-W0-PCT\_ST25

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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

Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly  
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly  
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys  
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser  
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr  
530 535 540

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser  
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605



A-1937-W0-PCT\_ST25

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2007  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2007  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggaacct aaactgctca ttactgggc atctaccg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgctgtgtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgcctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

651

<210> 2008

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2008

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

A-1937-W0-PCT\_ST25

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2009  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2009  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgag 300  
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtaaccgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540

A-1937-W0-PCT\_ST25

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 2010

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2010

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 Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

A-1937-W0-PCT\_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 2011  
<211> 2055  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2011  
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acctgcgctg tccatgggtg gtccttcagt gggttactact ggaactggat ccgccagcca 120  
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca  | 540  |
| ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc  | 600  |
| tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc  | 660  |
| aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga | 720  |
| ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct  | 780  |
| gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg  | 840  |
| tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc  | 900  |
| agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag  | 960  |
| gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc  | 1020 |
| aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag  | 1080 |
| atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc | 1140 |
| gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg  | 1200 |
| ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg  | 1260 |
| cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg  | 1320 |
| cagaagagcc tctccctgtc tccgggtgtt ggccggtcgg gaggtggcgg atccgaggta  | 1380 |
| caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt  | 1440 |
| gcggcatcgg ggtttacttt cgatgattat gcgatgcatt gggtcgggca agcgcttga   | 1500 |
| aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac  | 1560 |
| agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag  | 1620 |
| atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctctacttg   | 1680 |
| tctacagctt cgtcgtcga ctattgggggt aaaggaacgt tggtcaccgt ctctagtact  | 1740 |
| gtggctgcac catctgtctt catcttcccc ccactctgatg agcagttgaa atctggaact | 1800 |
| gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag  | 1860 |
| gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag  | 1920 |

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gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980  
aaagtctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 2040  
aacaggggag agtgt 2055

<210> 2012  
<211> 685  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2012

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320



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Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
450 455 460

Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys  
465 470 475 480

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg  
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn  
500 505 510

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Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu  
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu  
545 550 555 560

Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser  
580 585 590

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn  
595 600 605

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala  
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp  
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu  
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2013

<211> 633

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2013

|                                                                    |     |
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| gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg  | 60  |
| attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc  | 120 |
| ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg  | 180 |
| aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc  | 240 |
| gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa  | 300 |
| gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca | 360 |
| ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac  | 420 |
| ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc  | 480 |
| ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc  | 540 |
| tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc  | 600 |
| aaggtggaca agaaagttga gcccaaattct tgt                              | 633 |

<210> 2014

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2014

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ala | Ser | Gln | Gly | Ile | Arg | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

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<210> 2015  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2015  
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 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgag 300  
 gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 2016  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2016

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 Arg Ser Ser  
 20 25 30

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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 Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 2017  
 <211> 2037  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2017  
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 acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120  
 ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420  
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 480  
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540  
 ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600  
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660  
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720  
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780  
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840  
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900  
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960  
 gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020  
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080  
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140

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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg      1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg      1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg      1320
cagaagagcc tctccctgtc tccgggtggt ggcgatcgg gaggtggcgg atccgaggtg      1380
cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt      1440
aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccggg      1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg      1560
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag      1620
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt      1680
cttgactact ggggcaaggg aaccctggtc accgtctcta gtcagcccaa ggccaacccc      1740
actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagtg      1800
tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc      1860
cccgtaagg cgggagtgga gaccaccaa cctccaac agagcaacaa cagtacgcg      1920
gccgagagct acctgagcct gacgcccag cagtggaagt cccacagaag ctacagctgc      1980
caggtcacgc atgaaggag caccgtggag aagacagtgg cccctacaga atgttca      2037

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<210> 2018  
 <211> 679  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2018

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
 20 25 30



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Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val  
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala  
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser  
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val  
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro  
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp  
210 215 220

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Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile  
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu  
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg  
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu  
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
405 410 415

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Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln  
450 455 460

Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys  
465 470 475 480

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg  
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly  
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile  
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu  
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly  
545 550 555 560

Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Gln Pro  
565 570 575

Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu  
580 585 590

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro  
595 600 605

A-1937-W0-PCT\_ST25

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala  
610 615 620

Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala  
625 630 635 640

Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg  
645 650 655

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr  
660 665 670

Val Ala Pro Thr Glu Cys Ser  
675

<210> 2019  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2019  
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tttccaggaa cagaacccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540

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gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt 645

<210> 2020

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2020

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2021  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2021  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300  
gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 2022  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2022

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 2023  
<211> 2049  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2023  
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acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420



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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac   | 480  |
| tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc  | 540  |
| tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc   | 600  |
| tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct | 660  |
| tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccttgaggtc     | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg  | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg   | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac   | 960  |
| aagtgaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc      | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 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 tgggtggcgga tcgggaggtg gcggatccga ggtacaactg  | 1380 |
| gtggaatcag gtggagggtt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca   | 1440 |
| tcggggttta ctttcgatga ttatgcgatg cattgggtcc ggcaagcgcc tggaaaaggg   | 1500 |
| ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg    | 1560 |
| gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac   | 1620 |
| tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca   | 1680 |
| gcttcgtcgc tcgactattg gggtaaagga acgttggtca ccgtctctag tactgtggct   | 1740 |
| gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct   | 1800 |
| gttgtgtgcc tgctgaataa cttctatccc agagaggcca agtacagtg gaagggtgat    | 1860 |

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aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 1920  
acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 1980  
tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 2040  
ggagagtgt 2049

<210> 2024  
<211> 683  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2024

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

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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 Lys 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 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly  
450 455 460

Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala  
465 470 475 480

Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala  
485 490 495

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Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly  
500 505 510

His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg  
515 520 525

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala  
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr  
545 550 555 560

Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
580 585 590

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
595 600 605

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
610 615 620

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
625 630 635 640

Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
645 650 655

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
660 665 670

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

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<210> 2025  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2025  
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
 ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaaagttga gcccaaattct tgt 633

<210> 2026  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2026

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

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<210> 2027  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2027  
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300  
 gggaccaagc tggaaatcaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360  
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420  
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480  
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540  
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 2028  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2028

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |



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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 2029  
<211> 2031  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2029  
cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctgggtg ctccatcagt agttacttct ggagctggat ccggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360  
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420  
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 480  
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540  
tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 660  
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720  
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780  
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840  
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900  
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960  
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020  
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |
| gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag  | 1320 |
| agcctctccc tgtctccggg tgggtggcgga tggggaggtg gcggatccga ggtgcagctg | 1380 |
| gtgcagtctg gagcagaggt gaaaaagccc ggggagcttc tgaagatctc ctgtaagact  | 1440 |
| tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc  | 1500 |
| ctggagtggA tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc  | 1560 |
| caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc  | 1620 |
| agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac | 1680 |
| tactggggca agggaaacct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc   | 1740 |
| actctgttcc cgccctctc tgaggagctc caagccaaca aggccacact agtgtgtctg   | 1800 |
| atcagtgact tctacccggg agctgtgaca gtggcctgga aggcagatgg cagccccgtc  | 1860 |
| aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccgag   | 1920 |
| agctacctga gcctgacgcc cgagcagtgA aagtcccaca gaagctacag ctgccaggtc  | 1980 |
| acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a           | 2031 |

<210> 2030

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2030

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly 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 Lys 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

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Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

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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 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly  
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr  
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser  
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala  
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala  
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp  
545 550 555 560

Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Gln Pro Lys Ala  
565 570 575

Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala  
580 585 590

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Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala  
595 600 605

Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val  
610 615 620

Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu  
625 630 635 640

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr  
645 650 655

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala  
660 665 670

Pro Thr Glu Cys Ser  
675

<210> 2031  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2031  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagaacccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

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ggcgtgcaca ctttcccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2032  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2032

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125



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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2033  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2033  
gacatccaga tgaccagtc tccaagctcc ctgtctgctg ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaggg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

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ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
 ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc 600  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 2034  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2034

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
 100 105 110

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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 2035  
<211> 2070  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2035  
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60  
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc  | 420  |
| aagagcacct ctggggggcac agcgggccctg ggctgcctgg tcaaggacta cttccccgaa | 480  |
| ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct   | 540  |
| gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc   | 600  |
| ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac   | 660  |
| aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct   | 720  |
| gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg     | 780  |
| atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agacctgag     | 840  |
| gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt   | 900  |
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac   | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc     | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc   | 1080 |
| ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc   | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag   | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg   | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg   | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt   | 1380 |
| ggcggatccg aggtacaact ggtggaatca ggtggaggtt tgggtgcagcc ggggagatcg  | 1440 |
| ctcaggctta gctgtgcggc atcgggggtt actttcgatg attatgcgat gcattgggtc   | 1500 |
| cggcaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac   | 1560 |
| atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac   | 1620 |
| agcctgtacc ttcagatgaa ctacttcgc gcggaagata ccgccgtata ctactgcgcc    | 1680 |
| aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtaaagg aacgttggtc   | 1740 |
| accgtctcta gtactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag   | 1800 |

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ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860  
aaagtacagt ggaagggtgga taacgccctc caatcgggta actcccagga gagtgtcaca 1920  
gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980  
gactacgaga aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040  
gtcacaaaaga gcttcaacag gggagagtgt 2070

<210> 2036  
<211> 690  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2036

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

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Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser  
465 470 475 480

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala  
485 490 495

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Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
500 505 510

Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu  
515 520 525

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu  
530 535 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
545 550 555 560

Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys  
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr  
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
675 680 685



Glu Cys  
690

<210> 2037  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2037  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaaccc 120  
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2038  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2038

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2039  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2039  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaggg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480  
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540  
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600  
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 2040  
<211> 220  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 2040

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
 130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
 145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
 165 170 175

Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
 180 185 190

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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
 195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

<210> 2041  
 <211> 2052  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2041  
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 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120  
 cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180  
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
 agagaggatg gggatagcta ctaccgtac ggtatggacg tctggggcca agggaccacg 360  
 gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420  
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540  
 gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600  
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660  
 aagaaagttg agcccaaatt ttgtgacaaa actcacacat gccaccgtg cccagcacct 720  
 gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 780  
 atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840  
 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt 900

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac  | 960  |
| tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc   | 1020 |
| gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc | 1080 |
| ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc | 1140 |
| tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag  | 1200 |
| accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg  | 1260 |
| gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg  | 1320 |
| cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtgggtggcgg atcgggaggc | 1380 |
| ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagctc  | 1440 |
| ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg  | 1500 |
| cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat  | 1560 |
| accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt  | 1620 |
| accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgccatgta ttactgtgcg  | 1680 |
| agaagtaact ggggtcttga ctactggggc aagggaaccc tggtcaccgt ctctagtcag  | 1740 |
| cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac  | 1800 |
| aaggccacac tagtgtgtct gatcagtgac ttctaccgg gagctgtgac agtggcctgg   | 1860 |
| aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc  | 1920 |
| aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtccac   | 1980 |
| agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggccccct | 2040 |
| acagaatggt ca                                                      | 2052 |

<210> 2042

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 2042

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
 20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
 35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
 50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
 115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
 130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu  
 145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
 165 170 175

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Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr  
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365



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Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
450 455 460

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser  
465 470 475 480

Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp  
485 490 495

Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly  
500 505 510

Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln  
515 520 525

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu  
530 535 540

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala  
545 550 555 560

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Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr  
565 570 575

Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro  
580 585 590

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
595 600 605

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly  
610 615 620

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser  
625 630 635 640

Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln  
645 650 655

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser  
660 665 670

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

<210> 2043  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2043  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagaacccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

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caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaagggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2044  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2044

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

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Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2045  
<211> 2064  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2045  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt cggcaagcg 120  
cctggaaaaa agctcgagtg gggtttccgcc attacgtgga atagcggaca catcgattat 180

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct  | 360  |
| agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct    | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac  | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac    | 780  |
| tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc   | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaagggt tccaacaaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac    | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac   | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg   | 1440 |
| tcctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc   | 1500 |
| cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgttg aaacaccaac    | 1560 |
| tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc   | 1620 |

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tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 1680  
tattgtagaa gtaccacctg ctactttgac tactggggca aggggaaccct agtcaccgtc 1740  
tcctcaactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa 1800  
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta 1860  
cagtgggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 1920  
gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac 1980  
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca 2040  
aagagcttca acaggggaga gtgt 2064

<210> 2046  
<211> 688  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2046

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

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Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
 290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
 450 455 460



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Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp  
485 490 495

Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu  
500 505 510

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu  
530 535 540

Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
545 550 555 560

Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

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Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2047  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2047  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg aaccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtcctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattct tgt 633

<210> 2048  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

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&lt;400&gt; 2048

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 180 185 190

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Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2049  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2049  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2050  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 2050

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
 165 170 175

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Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2051  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2051  
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60  
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120  
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180  
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240  
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300  
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360  
agtacggtgg ctgcaccatc tgtcttcac tccccgccat ctgatgagca gttgaaatct 420  
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480  
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540  
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600  
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660  
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac 780  
tcccggaacc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 840

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag  | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg  | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag  | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca  | 1080 |
| tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc  | 1200 |
| acgcctcccg tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac  | 1260 |
| aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc | 1380 |
| ggatcccagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg  | 1440 |
| tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg | 1500 |
| cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa   | 1560 |
| tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc  | 1620 |
| tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa  | 1680 |
| actgggagct actacggctt tgactactgg ggcaagggaa ccctgggtcac cgtctcctca | 1740 |
| actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 1800 |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg  | 1860 |
| aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 1920 |
| aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa  | 1980 |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc  | 2040 |
| ttcaacaggg gagagtgt                                                | 2058 |

<210> 2052

<211> 686

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 2052

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175



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Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

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Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp  
485 490 495

Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr  
500 505 510

Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg  
515 520 525

Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu  
530 535 540

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu  
545 550 555 560

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Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2053  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2053  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggc caaggactac 420  
ttccccgaac cggtgacggc gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtcgc tcctacagtc ctcaggactc tactccctca aaagcgtggc gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagtga gcccaaattc tgt 633

<210> 2054  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2054

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2055  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2055  
gatatccaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

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```

ggaaaaaacac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa      300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 2056  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2056

```

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Thr Leu Gln 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

```

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Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2057

<211> 2079

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2057

gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt

60

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg | 120  |
| cctggaaaaa agctcgagtg gggtttccgcc attacgtgga atagcggaca catcgattat  | 180  |
| gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac   | 240  |
| cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc   | 300  |
| tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct | 360  |
| agtacgggtg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct    | 420  |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag   | 480  |
| tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac   | 540  |
| agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag   | 600  |
| aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag   | 660  |
| agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa   | 720  |
| ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac    | 780  |
| tcccggaacc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc  | 840  |
| aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag   | 900  |
| gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg   | 960  |
| ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag   | 1020 |
| aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca   | 1080 |
| tcccgggagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat  | 1140 |
| cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc   | 1200 |
| acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac   | 1260 |
| aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac  | 1320 |
| aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc  | 1380 |
| ggatcccagg tacagttgca ggagtcaggc ccaggactgg tgaagccctc ggagaccctc   | 1440 |
| tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg   | 1500 |



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attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 1560  
 tgggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 1620  
 aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 1680  
 tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggcaaaggg 1740  
 accacgggtca ccgtctcctc aactgtggct gcaccatctg tcttcatctt cccgccatct 1800  
 gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 1860  
 agagaggcca aagtacagt gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 1920  
 agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg 1980  
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 2040  
 agctcgcccg tcacaaagag cttcaacagg ggagagtgt 2079

<210> 2058  
 <211> 693  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2058

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr  
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val  
 50 55 60

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Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val  
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu  
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

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Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly  
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

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Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
450 455 460

Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu  
465 470 475 480

Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val  
485 490 495

Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
500 505 510

Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser  
515 520 525

Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe  
530 535 540

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
545 550 555 560

Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val  
565 570 575

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

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Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

<210> 2059  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2059  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggaacct aaactgctca tttactgggc atctaccgg 180  
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctgggtca aggactactt ccccgaaccg gtgacgggtgt cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540  
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

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<210> 2060  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2060

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
 35 40 45

Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
 130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
 145 150 155 160

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Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2061  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2061  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
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ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttcag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 2062  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2062

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140



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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2063  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2063  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360  
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540  
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac 600

## A-1937-W0-PCT\_ST25

|            |            |             |             |            |             |      |
|------------|------------|-------------|-------------|------------|-------------|------|
| agctgccagg | tcacgcatga | agggagcacc  | gtggagaaga  | cagtggcccc | tacagaatgt  | 660  |
| tcagacaaaa | ctcacacatg | cccaccgtgc  | ccagcacctg  | aactcctggg | gggaccgtca  | 720  |
| gtcttctctt | tcccccaaaa | acccaaggac  | accctcatga  | tctcccggac | ccctgaggtc  | 780  |
| acatgcgtgg | tggtggacgt | gagccacgaa  | gaccctgagg  | tcaagttcaa | ctggtacgtg  | 840  |
| gacggcgtgg | aggtgcataa | tgccaagaca  | aagccgtgtg  | aggagcagta | cggcagcacg  | 900  |
| taccgttgtg | tcagcgtcct | caccgtcctg  | caccaggact  | ggctgaatgg | caaggagtac  | 960  |
| aagtgcaagg | tctccaacaa | agccctccca  | gcccccatcg  | agaaaaccat | ctccaaagcc  | 1020 |
| aaagggcagc | cccgagaacc | acaggtgtac  | accctgcccc  | catcccggga | ggagatgacc  | 1080 |
| aagaaccagg | tcagcctgac | ctgcctggtc  | aaaggcttct  | atcccagcga | catcgccgtg  | 1140 |
| gagtgggaga | gcaatgggca | gccgggagaac | aactacaaga  | ccacgcctcc | cgtgctggac  | 1200 |
| tccgacggct | ccttcttctt | ctatagcaag  | ctcaccgtgg  | acaagagcag | gtggcagcag  | 1260 |
| gggaacgtct | tctcatgctc | cgtgatgcat  | gaggctctgc  | acaaccacta | cacgcagaag  | 1320 |
| agcctctccc | tgtctccggg | tggtggcgga  | tcgggagggtg | gcggatccca | ggtgcagtta  | 1380 |
| cagcagtcgg | gcgcaggact | gttgaagcct  | tcggagaccc  | tgtccctcac | ctgcgctgtc  | 1440 |
| catggtgggt | ccttcagtgg | ttactactgg  | aactggattc  | gccagccacc | agggaagggg  | 1500 |
| ctagagtgga | ttggggaaat | caatcatgct  | ggaaacacca  | actacaaccc | gtccctcaag  | 1560 |
| agtcgagtca | ccatatcatt | agacacgtcc  | aagaaccagt  | tctccctgac | gctgacctct  | 1620 |
| gtgaccgccg | cggacacggc | tgtgtattac  | tgtgcgagag  | gatattgtag | aagtaccacc  | 1680 |
| tgctactttg | actactgggg | caagggaacc  | ctagtcaccg  | tctcctcaac | tgtggctgca  | 1740 |
| ccatctgtct | tcatcttccc | gccatctgat  | gagcagttga  | aatctggaac | tgccctctgtt | 1800 |
| gtgtgcctgc | tgaataactt | ctatcccaga  | gaggccaaag  | tacagtggaa | ggtggataac  | 1860 |
| gccctccaat | cgggtaactc | ccaggagagt  | gtcacagagc  | aggacagcaa | ggacagcacc  | 1920 |
| tacagcctcg | aaagcaccct | gacgctgagc  | aaagcagact  | acgagaaaca | caaagtctac  | 1980 |
| gcctgcgaag | tcacccatca | gggcctgagc  | tcgcccgtca  | caaagagctt | caacagggga  | 2040 |

gagtgt

2046

<210> 2064  
 <211> 682  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2064

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
 85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
 115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
 130 135 140

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Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
325 330 335

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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
340 345 350

Pro Pro Ser Arg Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly  
450 455 460

Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val  
465 470 475 480

His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ala Gly Asn  
500 505 510

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp  
515 520 525

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Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr  
545 550 555 560

Cys Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser  
565 570 575

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln  
580 585 590

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
595 600 605

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
610 615 620

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
625 630 635 640

Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
645 650 655

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
660 665 670

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 2065

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

A-1937-W0-PCT\_ST25

<223> Synthetic polynucleotide

<400> 2065

```

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg aaccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagtga gcccaaattct tgt                                     633

```

<210> 2066

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2066

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10          15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
20          25          30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu
35          40          45

```

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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2067  
<211> 645  
<212> DNA  
<213> Artificial Sequence



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 $\langle 220 \rangle$ 

<223> Synthetic polynucleotide

<400> 2067

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| cagtctgtgc | tgacgcagcc | gccctcagtg | tctggggccc  | cagggcagag | ggtcaccatc | 60  |
| tcctgcactg | ggagcagttc | caacatcggg | gcaggttatg  | atgtacactg | gtaccagcag | 120 |
| tttccaggaa | cagcccccaa | actcctcatc | caaggtaaca  | gcaatcggcc | ctcaggggtc | 180 |
| cctgaccgat | tctctggctc | caagtctggc | acctcagcct  | ccctggccat | cactgggctc | 240 |
| caggctgagg | atgaggctga | ttattactgc | cagtcctatg  | acagcagcct | gagtggttcg | 300 |
| gtgttcggcg | aagggaccaa | gctgaccgtc | ctaggtgcct  | ccaccaaggg | cccatcggtc | 360 |
| ttccccctgg | caccctcctc | caagagcacc | tctggggggca | cagcggccct | gggctgcctg | 420 |
| gtcaaggact | acttccccga | accggtgacg | gtgtcgtgga  | actcaggcgc | cctgaccagc | 480 |
| ggcgtgcaca | ccttcccggc | tgtcctacag | tcctcaggac  | tctactccct | cgaaagcgtg | 540 |
| gtgaccgtgc | cctccagcag | cttgggcacc | cagacctaca  | tctgcaacgt | gaatcacaag | 600 |
| cccagcaaca | ccaaggtgga | caagaaagtt | gagcccaa    | aatcttgt   |            | 645 |

<210> 2068

<211> 215

&lt;212&gt; PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 2068

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

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Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2069

<211> 2040

## A-1937-W0-PCT\_ST25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic polynucleotide

&lt;400&gt; 2069

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc | 60   |
| tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg  | 120  |
| cccggaaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac  | 180  |
| agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac | 240  |
| ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac  | 300  |
| tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc  | 360  |
| aacccactg tcactctgtt ccgcccctcc tctgaggagc tccaagccaa caaggccaca   | 420  |
| ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat  | 480  |
| ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag  | 540  |
| tacgcggcca agagctacct gagcctgacg ccgagcagt ggaagtcca cagaagctac    | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca  | 720  |
| gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc    | 1020 |
| aaagggcagc ccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc   | 1080 |
| aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg  | 1140 |
| gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac  | 1200 |
| tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag  | 1260 |

A-1937-W0-PCT\_ST25

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320  
 agcctctccc tgtctccggg tggtagcgga tcgggaggtg gcggatccca ggtgcagctg 1380  
 caggagtcgg gccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc 1440  
 tctggtggct ccatcagtag ttacttctgg agctggattc ggcagcccc aggtaaggga 1500  
 ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag 1560  
 agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct 1620  
 gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc 1680  
 tttgactact ggggcaaggg aaccctggtc accgtctcct caactgtggc tgcaccatct 1740  
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 1800  
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 1860  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 1920  
 ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 1980  
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 2040

<210> 2070

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2070

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
 35 40 45

A-1937-W0-PCT\_ST25

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
225 230 235 240

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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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys 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 Lys 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 Glu Glu Met 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

A-1937-W0-PCT\_ST25

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly  
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val  
465 470 475 480

Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp Ser Trp Ile Arg Gln Pro  
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gln  
500 505 510

Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp  
515 520 525

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala  
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly  
545 550 555 560

Phe Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Thr Val  
565 570 575

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
580 585 590

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
595 600 605

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
610 615 620

A-1937-W0-PCT\_ST25

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
625 630 635 640

Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
645 650 655

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
660 665 670

Lys Ser Phe Asn Arg Gly Glu Cys  
675 680

<210> 2071  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2071  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cggtgacggt gtcgtggaac tcaggcggcc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633



<210> 2072  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2072

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
 20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 130 135 140

A-1937-W0-PCT\_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2073  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2073  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
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gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt

645

<210> 2074

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2074

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2075  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2075  
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60  
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120  
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180  
agccccgtcct tccaaggcca gggtcaccatc tcagccgaca agtccatcag taccgcctac 240  
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300  
tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360  
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420  
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480  
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac  | 600  |
| agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt  | 660  |
| tcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca   | 720  |
| gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc    | 780  |
| acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg | 840  |
| gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg  | 900  |
| taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac  | 960  |
| aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc    | 1020 |
| aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc  | 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 tgggtggcga tcgggagggtg gcggatccca ggtacagttg | 1380 |
| caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc  | 1440 |
| tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg   | 1500 |
| aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca    | 1560 |
| gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg  | 1620 |
| aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg   | 1680 |
| gatagctact accgctacgg tatggacgtc tggggcaaag ggaccacggc caccgtctcc  | 1740 |
| tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct   | 1800 |
| ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag  | 1860 |
| tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac  | 1920 |
| agcaaggaca gcacctacag cctcgaaagc accctgacgc tgagcaaagc agactacgag  | 1980 |

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aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag 2040

agcttcaaca ggggagagtg t 2061

<210> 2076

<211> 687

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2076

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr  
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Lys Leu Glu Trp Met  
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro  
115 120 125

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Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu  
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp  
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln  
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu  
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly  
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr  
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 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 Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val  
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
305 310 315 320

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Lys Cys Lys 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 Glu Glu Met 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 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly  
450 455 460

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile  
465 470 475 480

Ser Gly Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg  
485 490 495

Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg  
500 505 510



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Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr  
515 520 525

Ile Ser Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser  
530 535 540

Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly  
545 550 555 560

Asp Ser Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly Lys Gly Thr Thr  
565 570 575

Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
580 585 590

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
595 600 605

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
610 615 620

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
625 630 635 640

Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys  
645 650 655

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
660 665 670

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2077

<211> 651

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic polynucleotide

<400> 2077

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggaacct aaactgctca tttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca      360
tcggctcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      420
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t              651

```

<210> 2078

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2078

```

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30

```

```

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35           40           45

```

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Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2079

<211> 645

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<212> DNA

## <213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic polynucleotide

<400> 2079

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggggttcg 300

gtgttcggcg aagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360

ttccccctgg caccctcttc caagagcacc tctggggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2080

<211> 215

<212> PRT

### <213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic polypeptide

<400> 2080

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

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Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

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<210> 2081  
 <211> 2064  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2081  
 caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120  
 ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
 ccgtcccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
 acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420  
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480  
 aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540  
 aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600  
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660  
 ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720  
 ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780  
 cggaccccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgaggtcaag 840  
 ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag 900  
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960  
 aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020  
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080  
 cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc 1140  
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200

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```

cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag      1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac      1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga      1380
tccgaggtag aactgggtga atcaggtgga ggtttgggtg agccggggag atcgctcagg      1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa      1500
gcgccctggaa aagggctcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat      1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg      1620
taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc      1680
tcctacttgt ctacagcttc gtcgctcgac tattggggta aaggaacgtt ggtcaccgtc      1740
tctagtactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa      1800
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta      1860
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag      1920
gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac      1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca      2040
aagagcttca acaggggaga gtgt                                             2064

```

<210> 2082  
 <211> 688  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2082

```

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
1           5           10           15

```

```

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
20           25           30

```

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Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220



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Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

A-1937-W0-PCT\_ST25

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg  
465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His  
485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile  
500 505 510

Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg  
515 520 525

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met  
530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val  
545 550 555 560

Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
595 600 605

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Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser  
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2083  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2083  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540

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tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2084

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2084

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2085  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2085  
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120  
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgaa 300  
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420  
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

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ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 2086  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2086

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 Arg Ser Ser  
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
 85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 115 120 125

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Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2087  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2087  
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60  
acctgcgctg tccatgggtgg gtccttcagt gggtactact ggaactggat tcgccagcca 120  
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180  
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240  
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300  
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360  
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420

## A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg  | 480  |
| aaggtggata acgcccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc | 540  |
| aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa  | 600  |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc  | 660  |
| ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc  | 720  |
| ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc | 780  |
| cggacccttg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgaggtcaag  | 840  |
| ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag  | 900  |
| cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg  | 960  |
| aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa  | 1020 |
| accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc   | 1080 |
| cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc   | 1140 |
| agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg  | 1200 |
| cctcccgtgc tggactccga cggctcctt cttctctata gcaagctcac cgtggacaag   | 1260 |
| agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac | 1320 |
| cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga  | 1380 |
| tccgaggtgc agctgggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag | 1440 |
| atctcctgta agacttctga atacagcttt accagctact ggatcggctg ggtgcgccag  | 1500 |
| atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga  | 1560 |
| tacagcccgt ccttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc  | 1620 |
| tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt  | 1680 |
| aactggggtc ttgactactg gggcaaggga accctgggtc ccgtctctag tcagcccaag  | 1740 |
| gccaacccca ctgtcactct gttcccgccc tcctctgagg agctccaagc caacaaggcc  | 1800 |
| acactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca  | 1860 |



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gatggcagcc ccgtaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac 1920  
aagtacgcgg ccgagagcta cctgagcctg acgcccgagc agtggaagtc ccacagaagc 1980  
tacagctgcc aggtcacgca tgaaggggagc accgtggaga agacagtggc ccctacagaa 2040  
tgttca 2046

<210> 2088  
<211> 682  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2088

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln  
100 105 110

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Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe  
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp  
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr  
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr  
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val  
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly  
210 215 220

Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser  
290 295 300

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Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln  
450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys  
465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly  
485 490 495

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Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile  
500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln  
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp  
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser  
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser  
565 570 575

Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser  
580 585 590

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp  
595 600 605

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro  
610 615 620

Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn  
625 630 635 640

Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys  
645 650 655

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val  
660 665 670

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680

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<210> 2089  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2089  
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagaacccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagt gagcccaa at cttgt 645

<210> 2090  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2090

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

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Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

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<210> 2091  
 <211> 633  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2091  
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60  
 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120  
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180  
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240  
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgaa 300  
 gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga 360  
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggtg tcctacagtc ctgaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 2092  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2092

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Gly | Thr | Leu | Ser | Leu | Ser | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser  
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu  
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro  
85 90 95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205



Lys Ser Cys  
210

<210> 2093  
<211> 2058  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2093  
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctgggtg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag agaaactggg 300  
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360  
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 420  
tctgttgtgt gcctgctgaa taacttctat ccagagagg ccaaagtaca gtggaagggtg 480  
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540  
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600  
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660  
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720  
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780  
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840  
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac 900  
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960  
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020  
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag 1080

A-1937-W0-PCT\_ST25

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc  | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg  | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac  | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag  | 1380 |
| gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc  | 1440 |
| tgtgcggcat cggggtttac tttcgatgat tatgcgatgc attgggtccg gcaagcgctt  | 1500 |
| ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca  | 1560 |
| gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt  | 1620 |
| cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcctac   | 1680 |
| ttgtctacag cttcgtcgct cgactattgg ggtaaaggaa cgttgggtcac cgtctctagt | 1740 |
| actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga  | 1800 |
| actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg  | 1860 |
| aagggtgata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc  | 1920 |
| aaggacagca cctacagcct cgaaaagcacc ctgacgctga gcaaagcaga ctacgagaaa | 1980 |
| cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc  | 2040 |
| ttcaacaggg gagagtgt                                                | 2058 |

<210> 2094  
 <211> 686  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2094

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys | Pro | Ser | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

A-1937-W0-PCT\_ST25

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

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Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
 290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 385 390 395 400

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Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val  
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp  
500 505 510

Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr  
515 520 525

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser  
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr  
545 550 555 560

Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val  
565 570 575

Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
580 585 590

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Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
595 600 605

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
610 615 620

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
625 630 635 640

Lys Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala  
645 650 655

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
660 665 670

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
675 680 685

<210> 2095  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2095  
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240  
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

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ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttccccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540  
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2096  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2096

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
 100 105 110

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2097  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2097  
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccctggca 360



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```

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                633

```

<210> 2098  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2098

```

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 Arg Ala Ser Gln Ser Ile Asn Asn Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg
          85           90           95

```

```

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys
          100          105          110

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2099  
<211> 2040  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2099  
cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60  
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120  
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180  
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240  
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300

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|                                                                      |      |
|----------------------------------------------------------------------|------|
| agctactacg gcttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg   | 360  |
| gctgcaccat ctgtcttcat cttcccgccca tctgatgagc agttgaaatc tggaactgcc   | 420  |
| tctgtttgtgt gcctgctgaa taactttctat cccagagagg ccaaagtaca gtggaagggtg | 480  |
| gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac    | 540  |
| agcacctaca gcctcaagag caccctgacg ctgagcaaaag cagactacga gaaacacaaa   | 600  |
| gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac    | 660  |
| aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg    | 720  |
| ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc    | 780  |
| cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac   | 840  |
| tgggtacgtgg acggcgtgga ggtgcataat gccaaagaca agccgtgtga ggagcagtac   | 900  |
| ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc    | 960  |
| aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     | 1020 |
| tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag    | 1080 |
| gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac   | 1140 |
| atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc    | 1200 |
| gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg    | 1260 |
| tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac    | 1320 |
| acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag    | 1380 |
| gtgcagctgg tgcagtctgg agcagagggtg aaaaagcccg gggagtctct gaagatctcc   | 1440 |
| tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg ccagatgccc    | 1500 |
| gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc    | 1560 |
| ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg    | 1620 |
| cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg    | 1680 |
| ggtcttgact actggggcaa gggaaccctg gtcaccgtct ctagtcagcc caaggccaac    | 1740 |

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cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta 1800  
 gtgtgtctga tcagtgactt ctacccggga gctgtgacag tggcctggaa ggcagatggc 1860  
 agccccgtca aggcgggagt ggagaccacc aaacctcca aacagagcaa caacaagtac 1920  
 gcggccgaga gctacctgag cctgacgccc gagcagtgga agtccacag aagctacagc 1980  
 tgccagggtca cgcataagg gagcaccgtg gagaagacag tggcccctac agaattgtca 2040

<210> 2100  
 <211> 680  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2100

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr  
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile  
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys  
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu  
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

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Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe  
115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys  
130 135 140

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
145 150 155 160

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln  
165 170 175

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser  
180 185 190

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His  
195 200 205

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr  
290 295 300

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Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val  
450 455 460

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser  
465 470 475 480

Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val  
485 490 495

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Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu  
500 505 510

Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr  
515 520 525

Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser  
530 535 540

Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp  
545 550 555 560

Gly Leu Asp Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Gln  
565 570 575

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
580 585 590

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr  
595 600 605

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys  
610 615 620

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr  
625 630 635 640

Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His  
645 650 655

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys  
660 665 670

Thr Val Ala Pro Thr Glu Cys Ser  
675 680

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<210> 2101  
 <211> 645  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polynucleotide

<400> 2101  
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 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
 tttccaggaa cagaacccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180  
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
 gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
 ggcgtgcaca ctttccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540  
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2102  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2102

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15



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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

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Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2103  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2103  
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60  
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120  
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180  
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240  
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 300  
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccttgga 360  
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540  
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2104  
<211> 211  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2104

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr  
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Ser Leu Gln 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 Ser Tyr Ser Thr Pro Arg  
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2105  
<211> 2079  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2105  
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120  
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180  
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240  
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300  
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360  
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420  
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480  
gccaaagtac agtgggaagg gataacgcc ctccaatcgg gtaactccca ggagagtgtc 540  
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600  
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660  
cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720  
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780  
accctcatga tctccggac ccctgagggtc acatgcgtgg tggaggacgt gagccacgaa 840  
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900  
aagccgtgtg aggagcagta cggcagcacg taccgttggtg tcagcgtcct caccgtcctg 960  
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1020

# A-1937-W0-PCT\_ST25

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gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac      1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc      1140
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac      1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag      1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat      1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggcggcgga      1380
tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggagggtt ggtgcagccg      1440
gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg      1500
cattgggtcc ggcaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat      1560
agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat      1620
gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac      1680
tactgcgcca aagtctccta cttgtctaca gttcgtcgc tcgactattg gggtaaagga      1740
acgttgggtca cgtctcttag tactgtggct gcaccatctg tcttcatctt cccgccatct      1800
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc      1860
agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag      1920
agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg      1980
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg      2040
agctcgcccc tcacaaagag cttcaacagg ggagagtgt                                2079

```

<210> 2106  
 <211> 693  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2106

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

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Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

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Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro  
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp  
485 490 495

Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp  
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser  
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr  
565 570 575



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Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro  
580 585 590

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
595 600 605

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
610 615 620

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
625 630 635 640

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu Ser  
645 650 655

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
660 665 670

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
675 680 685

Asn Arg Gly Glu Cys  
690

<210> 2107  
<211> 633  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2107  
gatatcaaaa tgacacaatc accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg 60  
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120  
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180  
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240

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gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300  
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360  
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420  
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480  
 ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540  
 tccagcagct tggggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600  
 aagggtggaca agaaagttga gcccaaattct tgt 633

<210> 2108  
 <211> 211  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic polypeptide

<400> 2108

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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile  
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln 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 Arg Tyr Asn Arg Ala Pro Tyr  
 85 90 95

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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys  
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val  
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro  
195 200 205

Lys Ser Cys  
210

<210> 2109  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2109  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180

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gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctgggtca aggactactt ccccgaaccg gtgacgggtg cgtggaactc aggcgccctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 2110  
<211> 217  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2110

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 Arg Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys  
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

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Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Glu Gly Thr Lys Val Glu Ile  
100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
165 170 175

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2111  
<211> 2061  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2111  
caggtagct tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggattagg 120

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat    | 180  |
| aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac  | 240  |
| cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca  | 300  |
| agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg  | 360  |
| gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag  | 420  |
| cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag  | 480  |
| gccaaagtac agtggaagggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc  | 540  |
| acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa  | 600  |
| gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg  | 660  |
| cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc  | 720  |
| ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac    | 780  |
| accctcatga tctcccggac ccctgagggtc acatgcgtgg tggaggacgt gagccacgaa | 840  |
| gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca  | 900  |
| aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg  | 960  |
| caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctcca    | 1020 |
| gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac  | 1080 |
| accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc  | 1140 |
| aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac  | 1200 |
| aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag   | 1260 |
| ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat  | 1320 |
| gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcgga | 1380 |
| tcgggagggt gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc  | 1440 |
| ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc  | 1500 |
| ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggt  | 1560 |

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gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag 1620  
tccatcagta cgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat 1680  
tactgtgcga gaagtaactg gggctcttgac tactggggca aggggaaccct ggtcaccgtc 1740  
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc 1800  
caagccaaca aggccacact agtgtgtctg atcagtgact tctaccggg agctgtgaca 1860  
gtggcctgga aggcagatgg cagccccgtc aaggcgggag tggagaccac caaacctcc 1920  
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg 1980  
aagtcccaca gaagctacag ctgccaggtc acgcatgaag ggagcaccgt ggagaagaca 2040  
gtggccccta cagaatgttc a 2061

<210> 2112  
<211> 687  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic polypeptide

<400> 2112

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn  
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu  
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala  
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn  
65 70 75 80

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Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
85 90 95

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met  
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr Val Ala  
115 120 125

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
130 135 140

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
180 185 190

Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
195 200 205

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
210 215 220

Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270



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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu  
290 295 300

Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu  
305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
355 360 365

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly  
450 455 460

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Gly Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro  
465 470 475 480

Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr  
485 490 495

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu  
500 505 510

Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro  
515 520 525

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr  
530 535 540

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr  
545 550 555 560

Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Lys Gly Thr  
565 570 575

Leu Val Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu  
580 585 590

Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val  
595 600 605

Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys  
610 615 620

Ala Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser  
625 630 635 640

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr  
645 650 655

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Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His  
660 665 670

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
675 680 685

<210> 2113  
<211> 645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2113  
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60  
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120  
tttccaggaa cagaacccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180  
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240  
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300  
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360  
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420  
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480  
ggcgtgcaca ctttccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540  
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600  
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2114  
<211> 215  
<212> PRT  
<213> Artificial Sequence

<220>

&lt;223&gt; Synthetic polypeptide

&lt;400&gt; 2114

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln  
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly  
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu  
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe  
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu  
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser  
 85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 165 170 175

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Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
195 200 205

Lys Val Glu Pro Lys Ser Cys  
210 215

<210> 2115  
<211> 651  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic polynucleotide

<400> 2115  
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60  
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120  
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttacttgggc atctaccg 180  
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300  
cctctcactt tcggcgaagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360  
tcgggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420  
tgcctgggtca aggactactt ccccgaaacc gtgacgggtg cgtggaactc aggcgcctg 480  
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540  
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600  
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 2116  
<211> 217  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> Synthetic polypeptide

<400> 2116

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 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 | Arg | Ser | Ser | Gln | Ser | Val | Leu | Tyr | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Asn | Lys | Asn | Tyr | Leu | Val | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Lys | Leu | Leu | Ile | Tyr | Trp | Ala | Ser | Thr | Arg | Glu | Ser | Gly | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Val | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Lys | Thr | Pro | Leu | Thr | Phe | Gly | Glu | Gly | Thr | Lys | Val | Glu | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

A-1937-W0-PCT\_ST25

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Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
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