

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

<210> 1

<211> 324

<212> DNA

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aggttttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240

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<212> PRT

<213> Homo sapiens

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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
100 105

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cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

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 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
 115 120

<210> 5
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gggaaagccc ctaagcgctt gatctatgat gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttactctca caatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa      300
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<210> 6
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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 Thr Ser Gln Asp Ile Arg Asp Asp
          20           25          30

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

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Tyr Asp 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 Glu 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 Leu Gln His Asn Ser Tyr Pro Pro
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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acagactccg tgaagggccg attcaccatc tccagagacg attccaagag cacgctgtat 240
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gtctcctca 369

<210> 8
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<213> Homo sapiens

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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
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 aggttcagtg gcagtggatc tgggacagat ttctctctca ccatcagcag tctgcaacct 240
 gaagattttg caacttactt ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagg tggagatcaa acga 324

<210> 10
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 10

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

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ccaggggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaattggg 300
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<210> 12
<211> 118
<212> PRT
<213> Homo sapiens

<400> 12

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 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
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<210> 13
<211> 324
<212> DNA
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<400> 13
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gggaccaagc tggaaatcaa acga 324

<210> 14
<211> 107
<212> PRT
<213> Homo sapiens

<400> 14

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
100 105

<210> 15
<211> 354
<212> DNA
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ccaggtaagg gactggagtg gattggctat atctattaca gtgggaacac caaatacaac 180
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<210> 16
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<212> PRT
<213> Homo sapiens

<400> 16

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 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
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<210> 17
<211> 342
<212> DNA
<213> Homo sapiens

<400> 17
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cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga 342

<210> 18
<211> 113

<212> PRT
<213> Homo sapiens

<400> 18

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

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

Lys

<210> 19
<211> 375
<212> DNA
<213> Homo sapiens

<400> 19

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aatgattatg cagtttctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240

cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca	300
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gtcaccgtct cctca	375

<210> 20
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 20

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

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
 <211> 324
 <212> DNA

<213> Homo sapiens

<400> 21

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gtcacctac cttcggccaa      300
gggacacgac tggagattaa acga                                           324
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<210> 22

<211> 107

<212> PRT

<213> Homo sapiens

<400> 22

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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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
100          105
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<210> 23
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<212> DNA
<213> Homo sapiens

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ccagggaagg ggctggagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
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<210> 24
<211> 120
<212> PRT
<213> Homo sapiens

<400> 24

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
 115 120

<210> 25
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 25
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 tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180
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 cctctcactt tcggcggagg gaccaagggtg gagatcaaac ga 342

<210> 26
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 26

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

<210> 27
<211> 375
<212> DNA
<213> Homo sapiens

<400> 27
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gtcaccgtct cctca 375

<210> 28
<211> 125
<212> PRT
<213> Homo sapiens

<400> 28

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> 29
 <211> 342
 <212> DNA
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<210> 30
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 <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

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

<400> 31

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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

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
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 <212> DNA
 <213> Homo sapiens

<400> 33
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gggaaagccc ctaagcgcct gatctatgct gcgtccagtt tgcaaagtgg ggtcccatca 180
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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

<400> 35
caggtgcagt tgggtggagtc tgggggaggc gtgggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagagggtc 300
cgtagtgga 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

<400> 37
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcagggttatg 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 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

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
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccggaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgctcct tccaaggcca ggatcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
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
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
<213> Homo sapiens

<400> 41
gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca 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 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

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
 gaggttcagc tggtcgagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60
 tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120
 ccgggaaagg gcctggaatg gatgggttgg attaatactt acattggaga gcctatttat 180
 gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240
 ctccaaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300
 agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctca 354

<210> 44
 <211> 118
 <212> PRT
 <213> Homo sapiens

<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
115

<210> 45
<211> 708
<212> DNA
<213> Homo sapiens

<400> 45
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgata tccaaatgac acaatcacca tcgtcgcttt cagcgtctgt tggcgaccgt 120
gtgacgatta cctgtcgcgc gtcccaggga atccggaatt acctcgcatt gtatcagcaa 180
aaacccggaa aagcaccgaa gtcctgatc tatgccgcct cgactcttca gagggtgtg 240
ccgtcgaggt ttagcgggtc cgggtcaggt acggacttta ctctcacaat ttccagcctg 300
cagcccgaag atgtagctac ctattactgc cagagatata accgagcgcc ttacacattc 360

ggacaaggga caaaagtcga gatcaagcgt 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 gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 46
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 46

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

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

<400> 47

atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgagg tacaactggt ggaatcagggt ggaggtttgg tgcagccggg gagatcgctc 120

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 tggcaccctc ctccaagagc 480

acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 540

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
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

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 Lys
450

<210> 49
<211> 708
<212> DNA
<213> Homo sapiens

<400> 49
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 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 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> 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

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 ggccctgctgc tgctgtggct gagaggcgcc	60
agatgccagg tgcagctggt 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 agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg	840
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	900
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg	960
gaggagcagt acggcagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac	1020
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agccccatc	1080
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta 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> 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
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
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
 atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
 agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120
 gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
 aaaccaggga tagcccctaa gtcctgatc 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 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 gctcgcccggt 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		

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

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

<400> 55
 atgaaacatc tgtggttctt cctgctgctg gtggcggcgc cgcgctgggt gctgagccag 60
 gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
 tgcactgtct ctggtggctc catcagtagt tacttctgga gctggatccg gcagccccc 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
 aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 540
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720

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
	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
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

<210> 57
<211> 708
<212> DNA
<213> Homo sapiens

<400> 57
atggacatga gaggatgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
agaccaggga aagcccctaa gctcctgac tatgctgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 300
caacctggag attttgcaac ttactactgt caacagagtt acagtacccc tcggacgttc 360
ggccaaggga ccaagctgga aatcaaacga 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> 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	
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
ccaggtgaagg gactggagtg gattggctat atctattaca gtgggaacac 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 ccccttgga cctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctgg caaggactac ttccccgaac cggtagcggg gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtaggaca agaaagtga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc	780
acatgcgtgg tggtagcgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta cggcagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctggc aaaggcttct atcccagcga catcgccgtg	1140
gagtgaggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct cttcttctct 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
	20		
Thr	Cys	Thr	Val
			25
Ser	Gly	Gly	Ser
Ile	Ser	Ser	Tyr
	30		
Phe	Trp	Ser	Trp
	35		
Ile	Arg	Gln	Pro
			40
Pro	Gly	Lys	Gly
Leu	Glu	Trp	Ile
	45		
Gly	Tyr	Ile	Tyr
	50		
Tyr	Ser	Gly	Asn
			55
Thr	Lys	Tyr	Asn
			60
Pro	Ser	Leu	Lys
Ser	Arg	Val	Thr
Ile	Ser	Ile	Asp
			70
Thr	Ser	Lys	Asn
			75
Gln	Phe	Ser	Leu
			80
Lys	Leu	Ser	Ser
Val	Thr	Ala	Ala
			85
Asp	Thr	Ala	Val
			90
Tyr	Tyr	Cys	Ala
			95
Arg	Glu	Thr	Gly
			100
Ser	Tyr	Tyr	Gly
Phe	Asp	Tyr	Trp
			105
Gly	Gln	Gly	Thr
			110
Leu	Val	Thr	Val
			115
Ser	Ser	Ala	Ser
Thr	Lys	Gly	Pro
			120
Ser	Val	Phe	Pro
			125
Leu	Ala	Pro	Ser
Ser	Lys	Ser	Thr
			130
Ser	Gly	Gly	Thr
			135
Ala	Ala	Leu	Gly
			140
Cys	Leu	Val	Lys
Asp	Tyr	Phe	Pro
			145
Glu	Pro	Val	Thr
			150
Val	Thr	Val	Ser
Trp	Asn		
	155		160
Ser	Gly	Ala	Leu
Thr	Ser	Gly	Val
			165
His	Thr	Phe	Pro
			170
Ala	Val	Leu	Gln
			175
Ser	Ser	Gly	Leu
			180
Tyr	Ser	Leu	Ser
Ser	Val	Val	Thr
			185
Val	Pro	Ser	Ser
			190
Ser	Leu	Gly	Thr
Gln	Thr	Tyr	Ile
			195
Cys	Asn	Val	Asn
His	Lys	Pro	Ser
			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
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

<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 tttactgggc atctacccgg 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 aacacaaaagt ctacgcctgc 660
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaaga 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

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

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

<210> 63
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<400> 63
 atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60
 agatgccagg tacagttgca gcagtcaggt ccaggactgg tgaagccctc gcagaccctc 120
 tcactcacct gtgtcatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
 atcaggcagt ccccatcgag aggccttgag tggctgggaa ggacatacta caggtccaag 240
 tggataatg attatgcagt ttctgtgaaa agtcgaataa ccatcaaccc agacacatcc 300
 aagaaccagt tctccctgca gctgaactct gtgactcccg aggacacggc tgtgtattac 360
 tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420
 accacggtca cgtctctc agcctccacc aagggcccat cgtcttccc cctggcacc 480
 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540
 cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600
 ccggctgtcc tacagtcctc aggactctac tcctcagca gcgtggtgac cgtgccctcc 660
 agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720
 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca 780
 gcacctgaac tcctgggggg accgtcagtc ttctcttcc cccaaaacc caaggacacc 840
 ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900
 cctgaggtca agttcaactg gtacgtggac ggctggagg tgcataatgc caagacaaag 960
 ccgcgggagg agcagtacgg cagcacgtac cgtgtgggtc 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 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

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

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
<213> Homo sapiens

<400> 65	
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtggt gtctggggaca gacttcactc tcaccatcag cagactggag	240

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa	300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc	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

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 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
 caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagccc 120
 ccagggaagg ggctggagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
 ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
 acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
 agaagtacca cctgctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
 ggacacgcgg ccctgggctg cctggtcaag 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 cacatgcccc ccggtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggc	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc 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 tccgggtaaa	1350

<210> 68
 <211> 450
 <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

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

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
ttagtttggg 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 tcactttccc gccatctgat gagcagttga aatctggaac tgcctctggt 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> 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

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
cagggtacagt 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
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg 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 aaagccgcgg 900
gaggagcagt acggcagcac gtaccgtgtg 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

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			
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

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

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 ccgtgggtgcc 60
 cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120
 gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180
 ttagtttggt accagcagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240
 acccggggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
 ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360
 aagactcctc tcacttttcgg cggaggggacc 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 gcagcaccct gacgctgagc aaagcagact acgagaaaaca caaagtctac 660
 gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720
 gagtgt 726

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

<400> 74

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

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 gagtgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60
 agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120
 cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
 atcaggcagg cccaggggaa aggccttgag tgggtgagca ggacatacta caggtccaag 240
 tggataatg attatgcagt ttctgtgaaa ggtcgattca ccatcagccc agacacatcc 300
 aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc 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
 ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 660

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agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag      720
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca      780
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc      840
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac      900
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag      960
ccgcgggagg agcagtacgg cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac     1020
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc     1080
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc     1140
ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa     1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac     1260
tacaagacca cgcctcccg tctggactcc gacggctcct tcttcctcta tagcaagctc     1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag     1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a              1431

```

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

```

```
<400> 76
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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 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
 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

<400> 77
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcg 60
cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
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
ggcggaggga ccaaggtgga gatcaaactg 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> 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

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

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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 cgggtgtcgt gaactcaggc gccctgacca gcggcgtgca caccttcccc	600
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc	660
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gagggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg	960
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aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	1428

<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
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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 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
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 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
 caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
 gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
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acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta	600
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	660
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa	720
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ttcaactggt acgtggacgg cgtggaggtg cataatgcc aagacaaagcc 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 tgggtcaaagg cttctatccc	1200
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cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga	1440
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ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag	1860
tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt	1920
cagagcatta acaactatth aaattggtat cagcagagac cagggaagc ccctaagctc	1980
ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga	2040

tctgggacag atttcactct caccatcagc agtctgcaac ctgaagatt tgcaacttac	2100
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aaacga	2166

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

<220>
<223> Synthetic polynucleotide

<400> 82

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 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
 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
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

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 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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60

cgctgtcagt ctgtgctgac 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
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ggttcgggtgt tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc	420
tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactgggtg	480
tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc	540
cccgtaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg	600
gccagcagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc	660
caggtcacgc atgaaggagg 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
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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aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgctgc	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 ccccttgga cctcctcca 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 tctcccgac ccctgaggtc	840
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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 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		
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

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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 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 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
 ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<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

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

<400> 89
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 agattgtcct gtgctgcatc 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 ggccagggtta 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 gtcttctctt tcccccaaa acccaaggac 840
 accctcatga tctcccggac ccctgagggtc acatgcgtgg tgggtggacgt gagccacgaa 900
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 960
 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020
 caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1080
 gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1140
 accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1200
 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag 1320

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1434

<400> 90

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

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

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

<400> 91
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33

<210> 92
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 92

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

<210> 93
<211> 21
<212> DNA
<213> Homo sapiens

<400> 93
gccgcctcga ctcttcagag t 21

<210> 94
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 94
agggccagtc agagtgttag aagcagttac ttagcc 36

<210> 95
<211> 27
<212> DNA
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<400> 95
cagagataca accgagcgcc ttacaca 27

<210> 96
<211> 9
<212> PRT
<213> Homo sapiens

<400> 96

Gln Arg Tyr Asn Arg Ala Pro Tyr Thr
1 5

<210> 97
<211> 33
<212> DNA
<213> Homo sapiens

<400> 97
cggacaagtc aggacattag agatgattta ggc 33

<210> 98
<211> 11
<212> PRT
<213> Homo sapiens

<400> 98

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

<210> 99
<211> 21
<212> DNA
<213> Homo sapiens

<400> 99

gatgcatcca gtttgcaaag t

21

<210> 100
<211> 7
<212> PRT
<213> Homo sapiens

<400> 100

Asp Ala Ser Ser Leu Gln Ser
1 5

<210> 101
<211> 27
<212> DNA
<213> Homo sapiens

<400> 101

ctacagcata atagttaccc tccgacg

27

<210> 102
<211> 9
<212> PRT
<213> Homo sapiens

<400> 102

Leu Gln His Asn Ser Tyr Pro Pro Thr
1 5

<210> 103
<211> 33
<212> DNA
<213> Homo sapiens

<400> 103
cgggcaagtc agagcattaa caactattta aat 33

<210> 104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 104
cagcagtatg gtagctcacc tacc 24

<210> 105
<211> 21
<212> DNA
<213> Homo sapiens

<400> 105
gctacatcca gtttgcaaag t 21

<210> 106
<211> 7
<212> PRT
<213> Homo sapiens

<400> 106

Ala Thr Ser Ser Leu Gln Ser
1 5

<210> 107
<211> 27
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<213> Homo sapiens

<400> 107
caacagagtt acagtacccc tcggacg 27

<210> 108
<211> 9
<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
1 5 10

<210> 111
<211> 21
<212> DNA
<213> Homo sapiens

<400> 111
gctgcatcca gtttgcaaag t

21

<210> 112
<211> 7
<212> PRT
<213> Homo sapiens

<400> 112

Ala Ala Ser Ser Leu Gln Ser

1

5

<210> 113
<211> 27
<212> DNA
<213> Homo sapiens

<400> 113
caacagagtt acagtacccc tcggacg

27

<210> 114
<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>
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<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>
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<222> (6)..(7)
<223> Xaa may independently be M, G, A, V, I, or L

<220>
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<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

<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
<213> Homo sapiens

<400> 123
ggtgcatcca gcagggccac t

21

<210> 124
<211> 7
<212> PRT
<213> Homo sapiens

<400> 124

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 125
<211> 24
<212> DNA
<213> Homo sapiens

<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
aggtccagcc agagtgtggtt 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

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

<220>

<223> Synthetic polynucleotide

<400> 129

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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca	120
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt	300
agaagtacca cctgctactt tgactactgg ggccaggga ccttagtcac 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 aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc	900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag	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

<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
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

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

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

<220>
 <223> Synthetic polynucleotide

<400> 131
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 atcacttgta aagccagtca gaacgtaggt actaacgtag cctggtatca gcaaaaacca 120
 ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180
 aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240
 gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300

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gg tactaa ag 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

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<220>
<223> Synthetic polypeptide

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<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

```

```

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

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```

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

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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

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

<220>
<223> Synthetic polynucleotide

<400> 133
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctggggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gtcacctac cttcggccaa	300
gggacacgac tggagattaa acgaacgggtg gctgcaccat 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

<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
			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

<400> 135
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 agattgtcct gtgctgcacg tgggttacgctc ttcacagact atggaatgaa ttgggttaga 180

caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct	240
atttatgctg acagcgtcaa gggcagattc acgttctctc tagacacatc caagtcaaca	300
gcataacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga	360
ggatacagat cttatgccat ggactactgg ggccagggta 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 cgtggtgacc 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 gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaagggtctc 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
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtaaa	1410

<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
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
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

<400>	137						
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acctgcactg	tctctggtgg	ctccatcagt	agttacttct	ggagctggat	ccggcagccc		120
ccaggggaagg	gactggagtg	gattgggtat	atctattaca	gtggggagcac	caactacaac		180
ccctccctca	agagtcgagt	caccatgtca	atagacacgt	ccaagaacca	gttctccctg		240
aagctgagct	ctgtgaccgc	tgcggacacg	gccgtgtatt	actgtgcgag	agaaattggg		300
agctactacg	gctttgacta	ctggggccag	ggaaccctgg	tcaccgtctc	cagtgccctc		360
accaagggcc	catcggctctt	ccccctggca	ccctcctcca	agagcacctc	tgggggcaca		420
gcggccctgg	gctgcctggt	caaggactac	ttccccgaac	cggtgacggt	gtcgtggaac		480
tcaggcgccc	tgaccagcgg	cgtgcacacc	ttcccggtctg	tcctacagtc	ctcaggactc		540

tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaaagttga gcccaaattct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttctctt tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc	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 ctttcttctt 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
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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

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

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

<210> 139
<211> 33
<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
<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 atcggccctc a

21

<210> 148
<211> 7

<212> PRT
<213> Homo sapiens

<400> 148

Gly Asn Ser Asn Arg Pro Ser
1 5

<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
<213> Homo sapiens

<400> 153
agtcctctt tcctctatag t

21

<210> 154
<211> 7
<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 tgcac

15

<210> 158
<211> 5

<212> PRT
<213> Homo sapiens

<400> 158

Asp Tyr Ala Met His
1 5

<210> 159
<211> 51
<212> DNA
<213> Homo sapiens

<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

<210> 163
<211> 15
<212> DNA
<213> Homo sapiens

<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
gtcatatcat atgatggaaa taataaactc tatacagact ccgtgaaggg c 51

<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

<212> PRT

<213> Homo sapiens

<400> 172

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

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

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 aacccctccc 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

<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

<400> 185
gaggatggggg atagctacta ccgctacggt atggacgtc 39

<210> 186
<211> 13
<212> PRT
<213> Homo sapiens

<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 aacccgtccc 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
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

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> 195

<211> 54

<212> DNA

<213> Homo sapiens

<400> 195

aggacatact acaggtccaa gtggtataat gattatgcag tttctctgaa aagt

<210> 196
<211> 18
<212> PRT
<213> Homo sapiens

<400> 196

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

Lys Ser

<210> 197
<211> 39
<212> DNA
<213> Homo sapiens

<400> 197

gaggatgggg atagctacta ccgctacggt atggacgtc

39

<210> 198
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

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
<213> Homo sapiens

<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
<213> Homo sapiens

<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)
<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

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

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

<400> 213
atcatctatc ttggtgactc agataccaga tacagcccggt ccttccaagg 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

<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

<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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 236
atggacatga gagtgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
aaaccaggga aagcccctaa 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 aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 237
<211> 9
<212> 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

<400> 238

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

<210> 239
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

<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>
<223> Synthetic polynucleotide

<400> 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 ctgggggcac 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
aagaaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg	780
atctcccgga 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
gagaaaacca tctcaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc	1080
ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc	1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1200
accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg	1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa	1365

<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

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

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

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

Ser Tyr Tyr Trp Ser
1 5

<210> 257
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 257
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agatgcgaca tccagatgac ccagctctcca agctccctgt ctgcgtctgt gggcgatagg 120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180
ttagtttggg accagcagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240
acccgggaat cgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360
aagactcctc tcactttcgg cggagggacc aagggtggaga tcaaacgaac ggtggctgca 420
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggaac tgcctctggt 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

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

<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

<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
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<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

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

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

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
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cgctgtgagg tacaactggg ggaatcagggt ggaggtttgg tgcagccggg gagatcgctc 120
aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180
caagcgctg 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 agacaaaagcc 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 tggctaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1260
cctcccgtag tggactccga cggctcctt cttctctata gcaagctcac cgtggacaag	1320
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga	1440
tcccaggtag agttgcagga gtcagggtcca ggactgggtga agccctcgga gaccctctca	1500
ctcacctgta ccatctccgg ggacagtgtc tctaccaaca gtgttgcttg gaactggatt	1560
aggcagcccc cagggaagg ccttgagtgg ataggaagga catactacag gtccaagtgg	1620
tataatgatt atgcagtttc tctgaaaagt cgagtaacca tcagcccaga cacatccaag	1680
aaccagttct ccctgaagct gagctctgtg actgccgcgg acacggctgt gtattactgt	1740
gcaagagagg atggggatag ctactaccgc tacggatatg acgtctgggg ccaagggacc	1800
acggtcaccg tctcctcagg aggcggagga tctgggtggcg gtggttcttg cggcggaggc	1860
tccgacatcc agatgaccca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc	1920
accatcactt gcagggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta	1980
gtttggtagc agcagaaaacc aggaaagggt cctaaactgc tcatttactg ggcatctacc	2040
cgggaatccg ggggtccctag tcgattcagt ggcagcgggt ctgggacaga tttcactctc	2100
accatcagca gcctgcagcc tgaagatgtg gcaacttatt actgtcagca atattataag	2160
actcctctca ctttcggcgg agggaccaag gtggagatca aacga	2205

<210> 284

<211> 713

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 284

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
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

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

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
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
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
cgctgtgagg tacaactggt ggaatcaggt ggaggtttgg tgcagccggg gagatcgctc 120

aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg	180
caagcgccctg 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 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 acaccaaggt ggacaagaaa	720
gttgagccca aatcttgtga caaaactcac acatgccac cgtgcccagc acctgaactc	780
ctggggggac cgtcagtctt cctcttcccc caaaaacca aggacaccct catgatctcc	840
cggacccctg aggtcacatg cgtgggtggtg 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 tgggtcaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1260
cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag	1320
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga	1440
tcccaggtgc agctgcagga gtcgggcca ggactgggtga agccttcgga gaccctgtcc	1500
ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag	1560
ccccaggta agtgtctgga gtggattggc tataatctatt acagtgggca gaccaaatac	1620

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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 acaactatth aaattggtat cagcagagac cagggaagc ccctaagctc 1980
ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga 2040
tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2100
tactgtcaac agagttacag taccctcgg acgttcggct gtgggaccaa gctggaaatc 2160
aaacga 2166

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<210> 286
<211> 700
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polynucleotide

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<400> 286

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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

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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 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

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

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> 287

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 287

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagggttaga agcagttact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacagggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtta 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

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

<400> 289
cagggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtagca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctccagt 360

<210> 290
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 290

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	
gacatccaga tgacccagtc tccatcctcc ctatctgcat ctgtaggaga cagagtcacc	60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgct acatccagtt tgcaaagtgg ggtcccatca	180
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

caggtgcagc	tgcaggagtc	gggcccagga	ctggtgaagc	cttcggagac	cctgtccctc	60
acctgcactg	tctctggtgg	ctccatcagt	agttacttct	ggagctggat	ccggcagccc	120
ccagggaaagg	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

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaagggtg 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

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

caggtagctg tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaaccagtg 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

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

<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 ttactgggc atctaccgg 180

gaatccggggg 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
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> 301

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 301
gaggtacagt tgctggagtc aggtggagga ctggtgcagc ccggggggag cctccgactc 60
agctgtgcca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120
caggccccag ggaaaggcct tgagtgggtg agcaggacat actacaggtc caagtggtat 180
aatgattatg cagtttctgt gaaaggtcga ttcaccatca gccagacac 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

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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc ggacaagtca ggacattaga gatgatttag gctggatatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttactctca 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
cagggtgcagc tgggtggagtc tggggggaggc 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> 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

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> 307
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 307

gacatccaga	tgacccagtc	tccatcctcc	ctgtctgcat	ctgtaggaga	cagagtcacc	60
atcacttgcc	ggacaagtca	ggacattaga	gatgatttag	gctggtatca	gcagaaacca	120
gggaaagccc	ctaagcgcct	gatctatgat	gcatccagtt	tgcaaagtgg	gtcccatca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	caatcagcag	cctgcagcct	240
gaagattttg	caacttatta	ctgtctacag	cataatagtt	accctccgac	gttcggccaa	300
gggaccaagg	tggaatcaa	acga				324

<210>	308
<211>	107
<212>	PRT
<213>	Artificial Sequence

<400> 308

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

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

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

<210> 309
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 309
caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc 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
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 311
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
cgctgtgagg tacaactggg ggaatcaggg ggaggtttgg tgcagccggg gagatcgctc 120
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 gttgggtcacc 420
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 480
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 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 cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	840
cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagaccc tgagggtcaag	900
ttcaactgggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
aatggcaagg agtacaagtg caagggtctcc aacaaagccc tcccagcccc catcgagaaa	1080
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1140
cgggaggaga tgaccaagaa ccagggtcagc 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
tcccagggtac 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 tacggtatgg acgtctgggg ccaagggacc	1800
acggtcaccg tctcctcagg aggcggagga tctgggtggcg gtggttcttg cggcggaggc	1860
tccgacatcc agatgaccca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc	1920
accatcactt gcagggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta	1980
gtttgggtacc 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
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
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
 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
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 gagagggtgcg	60
cgctgtgagg tgcagctggg gcagctctgga gcagagggtga aaaagcccgg ggagtctctg	120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc	180
cagatgcccc ggaaaggcct 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 catcggctct cccctggca 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 ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccctgagggtc	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 acagggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctgggt aaaggcttct atcccagcga catcgccgtg	1200
gagtgggaga gcaatgggca gccggagaa aactacaaga ccacgcctcc cgtgctggac	1260
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtctccggg tgggtggcga tcgggagggt gcggatccca ggtgcagctg	1440
caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc	1500

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	
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

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			
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> 315
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 315
atggacatga gagtgcctgc acagctgctg ggccctgctgc tgctgtggct gagaggcgcc 60
agatgcgagg ttcagctggg cgagtcagga ggccggtctcg 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 agggccccatc 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 cacatgcca ccgtgcccag cacctgaact cctgggggga 780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 960

```

agcacgtacc gttgcgtcag 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 acgacaccac gcctcccgtg      1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg      1320
cagcagggga 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

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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 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 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
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
 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

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
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 319
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggcg 60
cgctgtgagg tgcagctggg gcagtctgga gcagagggtga aaaagcccgg ggagtctctg 120
aagatctcct gtaagacttc tgaatacagc ttaccagct actggatcgg ctgggtgctgc 180
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctgagatacc 240
agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc 300
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgctctc 420
accaagggcc catcggtctt cccctggca cctcctcca agagcacctc tgggggcaca 480
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac 540
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctgaggactc 600

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagttga gcccaaattct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttctctt 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 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 ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtctccggg tgggtggcggga tcgggagggtg gcggatccca ggtacagttg	1440
caggagtca gtcaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1500
tccggggaca gtgtctctac caacagtgtt gcttggaaact ggattaggca gccccaggg	1560
aaaggccttg agtggatagg aaggacatac tacaggcca agtgggtataa tgattatgca	1620
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg	1680
aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg	1740
gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggc caccgtctcc	1800
tcaggaggcg gaggatctgg tggcgggtgg tctggcggcg gaggctccga catccagatg	1860
accagtctc caagctccct gtctgcgtct gtgggcgata gggtcaccat cacttgagg	1920
tccagccaga gtgtgttata cagctccaac aataagaact acttagtttg gtaccagcag	1980
aaaccaggaa aggttcctaa actgctcatt tactgggcat ctaccggga atccggggtc	2040
cctagtcgat tcagtggcag cgggtctggg acagatttca ctctcacat 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

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

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

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

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
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 tgcagctggt gcagtctgga gcagagggtga aaaagcccgg ggagtctctg	120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc	180
cagatgcccc ggaaaaggcct ggagtggatg gggatcatct atcttgggtga ctcagatacc	240
agatacagcc cgtccttcca aggccagggtc 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 agaaagttga gccc aaatct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttctct 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
aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc	1080
aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctggtc 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

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agcctctccc tgtctccggg tgggtggcggg tcgggagggtg gcggatccca ggtgcagctg      1440
caggagtcgg gccaggact 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
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc      1740
tttgactact ggggccaggg aaccctgggt accgtctcct caggaggcgg aggatctggt      1800
ggcgggtggtt ctggcggcgg aggctccgac atccagatga ccagtcctcc 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 cggctgtggg accaagctgg aaatcaaacg a              2151

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<210> 322
<211> 695
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polynucleotide

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<400> 322

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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 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

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

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
 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

<210> 323
<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

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 gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120

cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg	180
atcaggcagg ccccagggaa aggccttgag tgggtgagca ggacatacta caggtccaag	240
tgggtataatg attatgcagt ttctgtgaaa ggctcgattca ccatcagccc agacacatcc	300
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac	360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg	420
accacgggtca ccgtctccag tgcctccacc aaggggcccat cggctcttccc cctggcaccc	480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	540
cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	600
ccggctgtcc tacagtctc aggactctac tccctcgaga 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
cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	960
ccgtgagagg agcagtagcg cagcacgtac cgttgctgca gcgtcctcac cgtcctgcac	1020
caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc	1080
cccatcgaga aaacctctc 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

<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 Trp
1 5 10 15

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

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

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
 atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtggtgcc 60
 cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120
 gtcaccatca cttgcaggtc cagccagagt gtgttatata gtcaccaaaa taagaactac 180
 ttagtttggg accagcagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240
 acccggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
 ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360
 aagactcctc tcactttcgg cggaggggacc aaggtggaga 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> 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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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 ggcctgctgc 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 cttccccggct	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 ttccccccaa aaccaagga caccctcatg	840
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	900
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc	960
gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac	1020
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agccccatc	1080
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

<210> 329
 <211> 475
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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
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
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 gaggcctgc 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
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360
ggccaaggga ccaaggtgga aatcaaacga acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg 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> 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
			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

<210> 332

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 332

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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 ccagtgctc caccaagggc ccatcgggtct tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggct	600
gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc	660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	720
aagaaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa 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 agccccatc	1080
gagaaaacca 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

<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

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> 334
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 334
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agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180
aaaccaggga aagcccctaa gcgcctgatc tatgatgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360
ggccaaggga ccaaggtgga aatcaaacga acgggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg 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> 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
 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
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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
gggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360
ggttcggtgt 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 cagtggaaagt cccacagaag ctacagctgc 660
caggtcacgc atgaagggag 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
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	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
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
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 cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120
 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 cagatgcccc ggaaaaggcct ggagtggatg gggatcatct atcttgggtga ctcagatacc 240
 agatacagcc cgtccttcca aggccaggct 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
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 600
 tactccctca agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 720
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
 gtcttctct tcccccaaaa acccaaggac accctcatga tctcccgga 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 gcccccatcg agaaaaccat ctccaaagcc	1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctgggtc 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

<210> 339
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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
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
 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

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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga      120
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag      180
aaaccaggga aagcccctaa gcgctgatc tatgctgcgt ccagtttgca aagtggggtc      240
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg      300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc      360
ggcggaggga ccaaggtgga gatcaaacgt 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 gctcgcccgt cacaaagagc ttcaacaggg gagagtgt      708
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<210> 341

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 341

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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 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
 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

<210> 342
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 342
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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 cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840
atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct 900
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tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1080
atcgagaaaa ccatctcaa 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

<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

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

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

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

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60

cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg	120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc	180
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttgggtga 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 ccctcctcca agagcacctc tgggggcaca	480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc	600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttcctct tcccccaaaa 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 agaaaaccat ctccaaagcc	1080
aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggga ggagatgacc	1140
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1200
gagtgggaga gcaatgggca gccggagaa aactacaaga ccacgcctcc cgtgctggac	1260
tccgacggct ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtacagttg	1440
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1500
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg	1560


```

aaatgccttg agtggatagg aaggacatac tacagggtcca agtgggtataa tgattatgca      1620
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg      1680
aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg      1740
gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc      1800
tcaggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctccga catccagatg      1860
acccagtctc caagctccct gtctgcgtct gtgggcgata gggtcaccat cacttgagg      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

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<210> 345
<211> 708
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polynucleotide

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<400> 345

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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 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				
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

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 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
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
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agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180
caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240
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acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480
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ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt	2100
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<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 347

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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

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

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

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

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acatccaaga accagttctc cctgaagctg agctctgtga ctgccgcgga cacggctgtg	1740

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
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
 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

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

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agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc      180
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 <212> PRT
 <213> Artificial Sequence

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 <223> Synthetic polynucleotide

 <400> 351

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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

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

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 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

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

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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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
 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

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

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

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

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tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240
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tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 960
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gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga	1560
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aagcgt	2166

<210> 355
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 355

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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 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

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

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
 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

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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggtg	1440
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ggtaacagca atcgccctc aggggtccct gaccgattct ctggctccaa gtctggcacc	2040
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<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
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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 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

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

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 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 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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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1260
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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atcccaggtg	1440
cagttgggtg agtctggggg aggcgtgggtc cagcctggga ggtccctgag actctcctgt	1500

gcagcctctg gattcacctt cagtagctat gacatgcact ggggccgcca 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 tgggtggcggg ggttctggcg gcggaggctc cgacatccag 1860
atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 1920
cgggcaagtc aggacatcag aaatgattta ggctggtatc agcagaaacc agggaaagcc 1980
cctaagcgcc tgatctatgc tgcgtccagt ttgcaaagtg gggccccatc aaggttcagc 2040
ggcagtggtat ctggggccaga attcactctc acaatcagca gcctgcagcc tgaagatttt 2100
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
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
 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
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

<210> 360
 <211> 2166
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 360
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120
 tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
 cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240
 tacaaccct 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
 ggacagcgg 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
 aaatcttggt acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 780
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840
 gaggtcacat gcgtgggtggg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc	960
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggctctc 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 gagcagggtg	1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtggt ggcggtatcg gaggtggcgg atccgaggta	1440
caactggtgg aatcagggtg aggtttggtg cagccgggga gatcgctcag gcttagctgt	1500
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgccctgga	1560
aaatgtctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1620
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1680
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctctacttg	1740
tctacagctt cgtcgtcga ctattgggggt caaggaacgt tggtcaccgt ctctagtgga	1800
ggcggaggat ctggtggcgg tggttctggc ggcgagggt ccgatatcca aatgacacaa	1860
tcaccatcgt cgctttcagc gtctgttggc gaccgtgtga cgattacctg tcgcgcgtcc	1920
cagggaatcc ggaattacct cgcattggtat cagcaaaaac ccggaaaagc accgaagctc	1980
ctgatctatg ccgcctcgac tcttcagagt ggtgtgccgt cgaggtttag cgggtccggg	2040
tcaggtagcg actttactct cacaatttcc agcctgcagc ccgaagatgt agctacctat	2100
tactgccaga gatacaaccg agcgcccttac 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

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

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

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

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
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 cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg 120
 tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
 cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240
 tacaaccct 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 ccgaaccggg gacgggtgtcg	540
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg aaaaaactca cacatgccc cgtgcccag cacctgaact cctgggggga	780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	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 tgccccatc ccgggaggag	1140
atgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1260
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cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg	1440
cagctgggtgc agtctggagc agagggtgaaa aagccccggg agtctctgaa gatctcctgt	1500
aagacttctg aatacagctt taccagctac tggatcggct gggcgcgcca gatgccccggg	1560
aaatgcctgg agtggatggg gatcatctat cttgggtgact cagataccag atacagcccg	1620
tccttccaag gccagggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgag	1680
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt	1740
cttgactact ggggccaggg aaccctgggt accgtctcta gtggaggcgg aggatctggt	1800

ggcggtggtt	ctggcggcgg	aggctcccag	tctgtgctga	cgcagccgcc	ctcagtgtct	1860
ggggccccag	ggcagagggt	caccatctcc	tgcactggga	gcagttccaa	catcggggca	1920
ggttatgatg	tacactggta	ccagcagttt	ccaggaacag	ccccaaact	cctcatccaa	1980
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tcagcctccc	tggccatcac	tgggctccag	gctgaggatg	aggctgatta	ttactgccag	2100
tcctatgaca	gcagcctgag	tggttcggtg	ttcggctgtg	ggaccaagct	gaccgtccta	2160
ggt						2163

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

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

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

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
 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
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 gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact ccctcagcag cgtggtgacc 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 gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
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agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccac cggggaggag 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 tccgggtggt ggcggatcgg gaggtggcgg atcccaggtg	1440
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gcagcctctg gattcacctt cagtagctat gacatgcact ggggccgcca ggctccaggc	1560
aagtgtctgg agtgggtggc agttatatca tatgatggaa gtattaaata ctatgcagac	1620
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gtgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ggtccgtagt	1740
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tctagtggag gcggaggatc tgggtggcggg ggttctggcg gcggaggctc cgacatccag	1860
atgaccaggt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc	1920
cgggcaagtc aggacatcag aaatgattta ggctggtatc agcagaaaacc agggaaaagcc	1980
cctaagcgcc tgatctatgc tgcgtccagt ttgcaaagtg gggccccatc aaggttcagc	2040
ggcagtggat ctgggccaga attcactctc acaatcagca gcctgcagcc tgaagatttt	2100
gcaacttatt actgtctaca acataatagt tatccgctca ctttcggctg tgggaccaag	2160
gtggagatca aacgt	2175

<210> 365
 <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

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

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

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

<400> 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 cgtctctc agcctccacc aagggcccat cggctttccc cctggcaccc 480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600

ccggctgtcc tacagtccctc aggactctac tccctcagca gcgtggtgac 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 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 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 gatccgaggt acaactgggtg gaatcagggtg 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
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
cccggaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg	2040
tcgaggttta gcgggtccgg gtcagggtacg gactttactc tcacaatttc cagcctgcag	2100

cccgaaagatg 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
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
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
 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
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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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 cggctcttccc 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 ggctggagg 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
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac	1260
tacaagacca cgctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc	1320
accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380

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

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

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

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

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

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
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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
 tggataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 300
 aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 360
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 accacggtca cgtctcctc agcctccacc aagggcccat cggctcttccc cctggcaccc 480
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agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	720
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc	780
gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc	840
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ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac	1020
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cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc	1140
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accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
ggagggtggcg gatcccaggt gcagttgggt gagtctgggg gaggcgtgggt ccagcctggg	1500
agggtccctga gactctcctg tgcagcctct ggattcacct tcagtagcta tgacatgcac	1560
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agtattaaat actatgcaga ctccgtgaag ggccgattca ccatctccag agacaattcc	1680
aagaacacgc tgtatctgca agtgaacagc ctgagagctg aggacacggc tgtgtattac	1740
tgtgcgagag aggtccgtag tgggagctac tactattact acagtatgga cgtctggggc	1800
caagggacca cggtcaccgt ctctagtgga ggcgaggat ctggtggcgg tggttctggc	1860
ggcggagggt ccgacatcca gatgaccag tctccatcct ccctgtctgc atctgtagga	1920
gacagagtca ccatcacttg ccgggcaagt caggacatca gaaatgattt aggctggtat	1980
cagcagaaac cagggaaagc ccctaagcgc ctgatctatg ctgcgtccag tttgcaaagt	2040
ggggtcccat caagggtcag 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
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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			
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

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
530 535 540

Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

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

<213> Artificial Sequence

<223> Synthetic polynucleotide

<400> 372

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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
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 cccaaaacc 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 tgcaaggctt 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 agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440

```

ggaggtggcg gatccgaggt acaactgggtg gaatcaggtg gaggtttggt gcagccgggg 1500
agatcgctca ggcttagctg tgcggcatcg gggtttactt tcgatgatta tgcgatgcat 1560
tgggtccggc aagcgcctgg aaaatgtctc gagtggggtt 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 aggcgggagga tctggtggcg gtggttcttg 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
cccgaagatg tagctaccta ttactgccag agatacaacc gagcgcctta cacattcgga 2160
tgtgggacaa aagtcgagat caagcgt 2187

```

```

<210> 373
<211> 707
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Synthetic polynucleotide

```

```

<400> 373

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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 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

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

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

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
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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
accacgggtca cagtctcctc agcctccacc aaggggccat cggctcttccc 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 ttcctcttcc ccccaaaacc caaggacacc	840
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg 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 aaccaggctc gcctgacctg cctggtcaaa	1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac	1260
tacaagacca cgctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc	1320
accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
ggagggtggcg gatccgaggt gcagctggtg cagtctggag cagaggtgaa aaagcccggg	1500
gagtctctga agatctcctg taagacttct gaatacagct ttaccagcta ctggatcggc	1560
tgggtgcgcc agatgcccgg gaaatgcctg gagtggatgg ggatcatcta tcttggtgac	1620
tcagatacca gatacagccc gtccttccaa ggccagggtc ccatctcagc cgacaagtcc	1680
atcagtaccg cctacctgca gtggagcagc ctgaaggcct cggacaccgc catgtattac	1740
tgtgcgagaa gtaactgggg tcttgactac tggggccagg gaaccctggt caccgtctct	1800
agtggaggcg gaggatctgg tggcgggtgt tctggcggcg gaggctcca gtctgtgctg	1860
acgcagccgc cctcagtgtc tggggcccca gggcagaggg tcaccatctc ctgcactggg	1920
agcagttcca acatcggggc aggttatgat gtacactggt accagcagtt tccaggaaca	1980
gccccaaac tcctcatcca aggtaacagc aatcggccct caggggtccc tgaccgattc	2040
tctggctcca agtctggcac ctcagcctcc ctggccatca ctgggctcca ggctgaggat	2100
gaggctgatt attactgcc a gtcctatgac agcagcctga gtggttcggg 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
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

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

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 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
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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tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg	180
attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag	240
tggтатаatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc	300
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac	360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg	420
accacggtca cagtctctc agcctccacc aagggcccat cggctctccc cctggcaccc	480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	540
cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	600
ccggctgtcc tacagtcctc aggactctac tcctcagca gcgtgggtgac cgtgccctcc	660
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	720
gtggacaaga aagttgagcc caaatcttgt gacaaaaactc acacatgccc accgtgccc	780
gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc	840
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac	900
cctgaggtca agttcaactg gtacgtggac ggctggagg 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 aaccaggtca gcctgacctg cctgggtcaaa	1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac	1260
tacaagacca cgctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc	1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
ggagggtggcg gatcccaggt gcagttggtg gagtctgggg gaggcgtggt ccagcctggg	1500

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agggtccctga gactctcctg tgcagcctct ggattcacct tcagtagcta tgacatgcac      1560
tgggtccgcc aggctccagg 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 ctctagtggg ggcgaggagg ctggtggcgg tggttctggc      1860
ggcggaggct ccgacatcca gatgaccagc tctccatcct ccctgtctgc atctgtagga      1920
gacagagtca ccatcacttg ccgggcaagt caggacatca gaaatgattt aggctggtat      1980
cagcagaaac cagggaaaag ccctaagcgc ctgatctatg ctgcgtccag tttgcaaagt      2040
ggggtcccat caagggttcag cggcagtggg tctggggccag aattcactct cacaatcagc      2100
agcctgcagc ctgaagattt tgcaacttat tactgtctac aacataatag ttatccgctc      2160
actttcggct gtgggaccaa ggtggagatc aaacgt                                2196

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<210> 377
<211> 710
<212> PRT
<213> Artificial Sequence

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```

<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

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

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

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

Lys Val Glu Ile Lys Arg
 705 710

<210> 378
 <211> 2172
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 378
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
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 aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180
 caagcgctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
 gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
 ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgcaaaa 360
 gtctcctact tgtctacagc ttcgtcgtc gactattggg gtcaaggaac gttggtcacc 420
 gtctctagt 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
 acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720
 gttgagccca aatcttgtga caaaactcac acatgccac cggtgccagc acctgaactc 780

ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	840
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgaggtcaag	900
ttcaactggg acgtggacgg cgtggagggtg cataatgcc aagacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa	1080
accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc	1140
cgggaggaga tgaccaagaa ccagggtcagc ctgacctgcc tgggtcaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1260
cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag	1320
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga	1440
tcccagggtgc agttacagca gtcgggcgca ggactgttga agccttcgga gaccctgtcc	1500
ctcacctgcg ctgtccatgg tgggtccttc agtggttact actggaactg gattcgccag	1560
ccaccaggga aggggctaga gtggattggg gaaatcaatc atgctggaaa caccaactac	1620
aaccgtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc	1680
ctgacgtga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat	1740
tgtagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc	1800
tcaggaggcg gaggatctgg tggcgggtgg tctggcggcg gaggctccga aattgtgttg	1860
acgcagtctc caggcacct gtctttgtct ccaggggaaa gagccaccct ctctgcagg	1920
gccagtcaga gtgttagaag cagttactta gcctggtacc agcagaaaacc tggccaggct	1980
cccaggctcc tcatctatgg tgcatccagc agggccactg gcatcccaga caggttcagt	2040
ggcagtgggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt	2100
gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggccaagg gacacgactg	2160
gagattaaac ga	2172

<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<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
 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
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

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

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60

cgctgtgagg tacaactggg ggaatcaggt ggagggttgg tgcagccggg gagatcgctc 120

aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180

caagcgctg gaaaagggt cagtggtt 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
gtctctagt 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
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaagggt ggacaagaaa	720
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc	780
ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	840
cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgaggtcaag	900
ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
aatggcaagg agtacaagtg caaggctctc 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
cctcccgtgc tggactccga cggctcctt ttcctctata gcaagctcac cgtggacaag	1320
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga	1440
tcccagggtgc agttacagca gtcgggcgca ggactgttga agccttcgga gaccctgtcc	1500
ctcacctgcg ctgtccatgg tgggtcctt agtggttact actggaactg gattcgccag	1560
ccaccaggga agtgtctaga gtggattggg gaaatcaatc atgctggaaa caccaactac	1620
aacccgtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc	1680

ctgacgctga cctctgtgac cgccgcggac acggctgtgt attactgtgc gagaggatat 1740
 tgtagaagta ccacctgcta ctttgactac tggggccagg gaaccctagt caccgtctcc 1800
 tcaggaggcg gaggatctgg tggcgggtgg tctggcggcg gaggctccga aattgtgttg 1860
 acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccacctt ctcctgcagg 1920
 gccagtcaga gtgttagaag cagttactta gcctgggtacc agcagaaacc tggccaggct 1980
 cccaggctcc tcatttatgg tgcattccagc agggccactg gcatcccaga caggttcagt 2040
 ggcaagtgggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt 2100
 gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggctgtgg gacacgactg 2160
 gagattaaac ga 2172

<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

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

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

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

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 gcagagggtga aaaagcccgg ggagtctctg 120
aagatctcct gtaagacttc tgaatacagc ttaccagct 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 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 gcccaaactc 720
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga 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

aaagggcagc	cccgagaacc	acaggtgtac	accctgcccc	catcccggga	ggagatgacc	1140
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	atcccagcga	catcgccgtg	1200
gagtgggaga	gcaatgggca	gccgggagaac	aactacaaga	ccacgcctcc	cgtgctggac	1260
tccgacggct	ccttcttcct	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1320
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1380
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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	caagggaacac	gactggagat	taaacga	2157

<210> 383

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 383

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

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

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

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

<210> 384
 <211> 2157
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 384
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120
 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 cagatgcccc ggaaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240
 agatacagcc cgtccttcca aggccaggct 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 gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg 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
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 ggtgcagtta	1440
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc	1500
catggtgggt ctttcagtgg ttactactgg aactggattc gccagccacc agggaaagtgt	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 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

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

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

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

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 gagagggtgcg	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 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 caaaaccaa 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 aaggctctca 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 ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcagggtgca gcagggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtg cggatcggga	1440
ggtggcggat cccagggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag	1500

accctgtccc tcacctgcgc tgtccatggg gggtccttca gtggttacta ctggaactgg	1560
attcgccagc caccagggaa ggggctagag tggattgggg aaatcaatca tgctggaaac	1620
accaactaca acccgtccct caagagtcga gtcaccatat cattagacac gtccaagaac	1680
cagttctccc tgacgctgac 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 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
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
 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
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
 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
 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 ggcaccctcc 480
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540
 gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600
 gctgtcctac agtcctcagg actctactcc ctgagcagcg 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 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 agccaaaagg cagccccgag aaccacaggt gtacaccctg	1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc	1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac	1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tcctgtctc cgggtggtgg cggatcggga	1440
ggtggcggat cccaggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag	1500
accctgtccc tcacctgcgc tgtccatggt gggtccttca gtggttacta ctggaactgg	1560
attcgccagc caccaggga 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 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

<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

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

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

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

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 390

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60

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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 agggaaacct agtcaccgtc	420
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tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
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gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	780
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accctgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgtg tgaggagcag	960
tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
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gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
cccgtgctgg actccgacgg ctcccttcttc ctctatagca agctcaccgt ggacaagagc	1320
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tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc	1440
gagggtacaac tgggtggaatc aggtggagggt ttggtgcagc cggggagatc gctcaggctt	1500
agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg	1560

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
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
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						
		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

<210> 392
<211> 2169
<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
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgcctacag 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 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 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
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg	1560
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	1620
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	1680
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	1740
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga	1800
tctgggtggcg gtggttcttg cggcggaggc tcccagtctg tgctgacgca gccgccctca	1860
gtgtctgggg ccccaggga gagggtcacc atctcctgca ctgggagcag ttccaacatc	1920
ggggcagggtt atgatgtaca ctggtaccag cagtttccag gaacagcccc caaactcctc	1980
atccaaggta acagcaatcg gccctcaggg gtccctgacc gattctcttg ctccaagtct	2040
ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac	2100
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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

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

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

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

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

<210> 394
<211> 2181
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 394
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tcctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
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tcctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360

tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaaccct 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 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
atctccaaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1140
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tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc	1440
cagggtcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	1500
tcctgtgcag cctctggatt caccttcagt agctatgaca tgcactgggt ccgccaggct	1560
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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	1680
ctgcaagtga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggtc	1740
cgtagtggga gctactacta ttactacagt atggacgtct ggggccaagg gaccacggtc	1800
accgtctcta gtggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgac	1860

atccagatga	cccagttctcc	atcctccctg	tctgcatctg	taggagacag	agtcaccatc	1920
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aaagccccta	agcgcctgat	ctatgctgcg	tccagtttgc	aaagtggggg	cccatcaagg	2040
ttcagcggga	gtggatctgg	gccagaattc	actctcacia	tcagcagcct	gcagcctgaa	2100
gattttgcaa	cttattactg	tctacaacat	aatagttatc	cgctcacttt	cggcggaggg	2160
accaaggtgg	agatcaaacg	t				2181

<210>	395
<211>	705
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 395

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

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			
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	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
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 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

<210> 396
 <211> 2172
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 396
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 tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180
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 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
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 gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 780
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aagctcctga tctatgccgc ctcgactctt cagagtgggt tgccgtcgag gtttagcggg	2040
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<210> 397
 <211> 702
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 397

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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

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
 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 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

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

tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300

tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360

tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc 420

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tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	660
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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag	960
tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
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gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc	1500
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg	1560
cccgggaaat gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	1620
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tggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga	1800
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ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac 2100
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 gtcctaggt 2169

<210> 399
 <211> 701
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 399

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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
 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
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 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

<210> 400

<211> 2181

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 400

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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 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
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	780
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctccgg	840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	900
aactggtacg tggacggcgt ggagggtgcat aatgccaaga caaagccgtg tgaggagcag	960
tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
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tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc	1440

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
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
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

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

<400> 402
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aact	gg	tac	g	tg	gac	gg	cgt	gg	ag	gt	gcat	aat	g	cca	aga	caa	ag	cc	gt	tg	ag	gag	cag	960					
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gag	gag	at	ga	cc	aa	ga	acca	gg	tc	ag	cct	g	ac	ct	gc	ct	gg	t	caa	ag	g	ctt	ct	at	ccc	cag	c	1200	
gac	at	cg	cc	g	tg	g	agt	gg	ga	gag	ca	at	gg	g	cag	cc	gg	aga	aca	act	aca	gac	ca	gc	cct	1260			
ccc	gt	g	ct	gg	act	cc	gac	gg	ct	c	tt	ct	ct	tc	ta	tag	ca	ag	ct	cac	gt	gg	aca	ag	ag	c	1320		
agg	tg	gc	cag	c	agg	g	ga	ac	gt	ct	ct	cat	gc	tcc	gt	gat	gc	at	gag	g	ct	ct	gc	aca	acc	ac	1380		
tac	ac	gc	aga	ag	ag	c	ct	ct	c	ct	gt	ct	cc	g	gg	tg	gg	gg	g	at	c	ggg	agg	tg	gc	gg	at	cc	1440
gag	gt	gc	cag	c	tg	gt	gc	ag	t	gg	ag	cag	ag	gt	g	aaaa	a	gc	cc	ggg	g	ag	tc	tct	ga	ag	at	c	1500
tc	ct	g	ta	agg	ctt	ct	gg	ata	cag	ctt	t	acc	ag	ct	act	gga	tc	gg	ct	gg	gt	gc	gcc	cag	at	g	1560		
ccc	ggg	aa	ag	gc	ct	gg	ag	tg	gat	ggg	gat	c	at	ct	at	ct	tg	gt	aat	caga	aa	cc	ag	ata	c	1620			
ag	ccc	gt	c	ct	tcca	agg	cca	gg	tc	acc	at	c	tcag	cc	gaca	ag	tcc	at	cag	tacc	gc	c	tac	1680					
ct	gc	agt	gga	gc	ag	c	ct	gaa	gg	c	ct	cg	gac	acc	g	ccat	gt	att	act	gt	gc	gaga	ag	ta	ac	1740			
tg	ggg	gt	ct	tg	act	act	ggg	g	cc	agg	ga	acc	ct	gg	tc	acc	g	tct	ct	ag	tg	gg	agg	cg	gag	ga	1800		
tct	gg	tg	gg	c	gt	gt	t	ct	gg	c	gg	cg	agg	c	tccc	ag	t	ct	g	tg	ct	gac	gca	gcc	g	cc	ct	ca	1860
gt	gt	ct	ggg	g	cccc	agg	gca	gag	gg	tc	acc	at	ct	c	ct	gca	ct	ggg	ag	cag	ttcca	ac	at	c	1920				
ggg	gc	agg	tt	at	gat	gt	taca	ct	gg	t	acc	ag	cag	ctt	cc	ag	ga	ac	ag	cccc	caa	act	c	ctc	1980				
at	ct	at	gg	ta	ac	ag	ca	at	cg	gcc	ct	cagg	g	gt	cc	t	gacc	gatt	ct	ct	gg	ctcca	ag	t	ct	2040			
gg	ca	ct	cag	c	ct	cc	ct	gg	c	at	ca	ct	gg	g	ctcc	agg	ct	g	ag	gag	gc	tgatt	att	ac	2100				
tg	cc	ag	tc	ct	at	gaa	ag	cag	c	ct	gag	tg	gt	tc	gg	t	gt	tc	g	cg	gag	gg	gac	caag	ct	gacc	2160		
gt	c	ct	ag	gt	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
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
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
 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
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
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga	360
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc	420
tcctcagcct ccaccaaggg cccatcgggtc 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 gcccagcacc tgaactcctg	780
gggggaccgt cagtcttcct cttcccccca aaaccaagg 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 ctcttcttc 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
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac	1620

```

agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac      1680
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac      1740
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgg aggcggagga      1800
tctggtggcg gtggttctgg cggcggaggc tcccagtctg tgctgacgca gccgccctca      1860
gtgtctgggg ccccaggga gagggtcacc atctcctgca ctgggagcag ttccaacatc      1920
ggggcaggtt 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

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<210> 405
<211> 701
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polynucleotide

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<400> 405

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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 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

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

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 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

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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cgctgtcagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg      120
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 ggccaggga cctgggtcac 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 cctggggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc      960
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020

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gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaaag ggcagcccccg 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 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 taactgggggt	1740
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ggcgggtggtt 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

<210> 407
 <211> 699
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <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
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
 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
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

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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 gcgcccctgac 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
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 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
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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 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

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

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 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

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

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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 agggaaacct agtcaccgtc	420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgccttacag	600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	660
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaagggtgga caagaaagtt	720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc 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
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gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1260
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc	1320

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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
cccgggaaat gcctggagtg gatggggatc atctatcttg gtgaatcaga aaccagatac      1620
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gtcctaggt                                         2169

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<210> 411
<211> 701
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polynucleotide

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<400> 411

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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

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Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

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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
 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
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
 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

<210> 412
<211> 2169
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 412
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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720

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<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
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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
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

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

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

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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cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac	240
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga	360
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cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	720
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	780
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caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	1500
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 ttcagcggca gtggatctgg gccagaattc actctcacia tcagcagcct gcagcctgaa 2100
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 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
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

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
 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
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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 tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180
 cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
 tacaaccgt cctcaagag 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
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgccttacag 600
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
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tacggcagca cgtaccgttg tgtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1020
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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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tacacgcaga agagcctctc cctgtctccg ggtgggtggcg gatcgggagg tggcggatcc	1440
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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 ggggcccaagg gaccttggtc	1800
accgtctcta gtggaggcgg aggatctggt ggcgggtggt ctggcggcgg aggctccgac	1860
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acttgccggg caagtcagga catcagaaat gatttaggct ggtatcagca gaaaccaggg	1980
aaagccccta agctcctgat ctatgctgcg tccagtttgc aaagtggggt cccatcaagg	2040
ttcagcggca gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa	2100
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accaaggtgg agatcaaacg t	2181

<210> 417
 <211> 705
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 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

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

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

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

<210> 418
 <211> 2187
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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 tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180

attaggcagc cccagggaa aggccttgag tggataggaa ggacatacta caggtccaag	240
tggataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc	300
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac	360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg	420
accacggtca ccgtctctc agcctccacc aaggggcccat cggctctccc 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 cccaaaacc caaggacacc	840
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac	900
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ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac	1020
caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcccagcc	1080
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gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
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ggacacatcg attatgcaga cgctgtggag ggcagattca caatctcacg agacaatgct	1680

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

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

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
 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

<210> 420
<211> 2187
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 420
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attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240
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tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420
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gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
ggagggtggcg gatccgaggt acaactgggtg gaatcagggtg gaggtttggt gcagccgggg	1500
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ggacacatcg attatgcaga aagtgtggag 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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cccgaagatt tcgctacctt ttactgccag agatacaacc gagcgcctta cacattcgga	2160
caagggacaa aagtcgagat caagcgt	2187

<210> 421

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<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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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

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
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 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

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

<210> 422
<211> 2187
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 422
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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 ccgtctcctc agcctccacc aaggggcccat cggctcttccc cctggcaccc	480
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gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
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cccgaagatt	tcgctaccta	ttactgccag	agatacaacc	gagcgcctta	cacattcgga	2160
tgtgggacaa	aagtcgagat	caagcgt				2187

<220>
<223> Synthetic polynucleotide

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

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 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 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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<210> 425

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 425

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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

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

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

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

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

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<210> 427
 <211> 695
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 427

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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 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

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
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

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
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 428
atggacatga gggtgcccg tcagctcctg gggctcctgc tgctgtggct gagaggcg 60
cgctgtgagg tgcagctggt gcagtctgga gcagaggatga aaaagcccg ggagtctctg 120
aagatctcct gtaaggcttc tgaatacagc ttaccagct actggatcgg ctgggtgcgc 180
cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga atcagaaacc 240
agatacagcc cgtccttcca aggccaggct 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 gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 660
tgcaacgtga atcacaagcc cagcaacacc aagggtgaca agaaagtga gccc aaatct 720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac 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 agccctcca gccccatcg agaaaaccat ctcaaagcc 1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1140
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1200
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260

tccgacggct ctttcttctt ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccca ggtgcagctg	1440
caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc	1500
tctggtggct ccatcagtag ttacttctgg agctggatcc ggagcccc 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
ggcggtggtt 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
actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt	2100
tacagtaccc ctcggacgtt cggccaaggg accaagctgg aaatcaaacg a	2151

<210> 429
 <211> 695
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 429

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	Ala	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 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

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

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

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> 430
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 430
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 caccttcccc 600
gctgtcctac agtcctcagg actctactcc ctgagcagcg 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 ggacccctga ggtcacatgc gtgggtgggtgg acgtgagcca cgaagaccct	900
gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgccaa 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 cagggtcagcc tgacctgcct ggtcaaaggc	1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac	1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtgg cggatcggga	1440
ggtggcggtat 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 aagggaacctt ggtcaccgtc	1800
tcctcaggag gcggaggatc tgggtggcgg gtctctggcg gcggaggctc cgacatccag	1860
atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc	1920
cgggcaagtc agagcattaa caactattta aattgggtatc agcagagacc agggaaagcc	1980
cctaagctcc tgatctatgc tgcattcagt ttgcaaagtg gggccccatc aaggttcagt	2040
ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt	2100
gcaacttact actgtcaaca gagttacagt acccctcgga cggttcggcca agggaccaag	2160
ctggaaatca aacga	2175

<210> 431
<211> 703
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 431

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

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

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

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> 432
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 432
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
ttggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc	480
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc	540
gaaccggtga cgggtgtcgtg 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
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 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 cgggtgggtgg cggatcggga	1440
ggtggcggat cccagggtgca gctgcaggag tcgggcccag gactggtgaa gccttcggag	1500
accctgtccc tcacctgcac tgtctctggg ggctccatca gtagttactt ctggagctgg	1560
atccggcagc ccccaggtaa gtgtctggag tggattggct atatctatta cagtgggcag	1620

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

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

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

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
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 cgctgtcagg tgcagttggg ggagtcctgg 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 ggcccacg tcttccccct ggcaccctcc 480
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 540
 gaaccggtga cgggtgtcgt gaactcaggc gccctgacca gcggcgtgca caccttcccc 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 caaaaccaa ggacaccctc 840
 atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 900
 gaggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcaa gacaaagccg 960
 tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag 1020

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc	1080
atcgagaaaa ccatctccaa agccaaaagg 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 cgggtgggtgg cggatcggga	1440
ggtggcggat cccaggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag	1500
accctgtccc tcacctgcgc tgtccatggg gggtccttca gtggttacta ctggaactgg	1560
attcgccagc caccagggaa ggggctagag tggattgggg aaatcaatca tgctggaaac	1620
accaactaca acccgctcct caagagtcga gtcaccatat cattagacac gtccaagaac	1680
cagttctccc tgacgtgac ctctgtgacc gccgcggaca cggctgtgta ttactgtgcg	1740
agaggatatt gtagaagtac cacctgctac tttgactact ggggccaggg aaccctagtc	1800
accgtctcct caggaggcgg aggatctggg gccgggtgggt 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 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

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

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
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
 <211> 2181
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 436
 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
ttgggtcaccg 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 caccaagggtg	720
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca	780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc	840
atgatctccc ggacccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct	900
gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcaa gacaaagccg	960
tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag	1020
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagcccc	1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacagggt gtacaccctg	1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc	1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac	1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtgggtg cggtatcgga	1440
gggtggcggtat cccagggtgca gttacagcag tcgggcgcag gactgttgaa gccttcggag	1500
accctgtccc tcacctgcgc tgtccatgggt 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 aggatctggt ggcggtgggt ctggcggcgg aggctccgaa 1860
attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaaag 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

<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

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

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

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

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
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aggcttagct gtgcggcatc ggggtttact ttcagtgatt atgcgatgca ttgggtccgg 180
caagcgcttg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
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gtctcctact tgtctacagc ttcgtcgctc gactattggg gtcaaggaac gttgggtcacc 420
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 480
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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 cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840
cggacccttg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgagggtcaag 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 gcccccatcc	1140
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1260
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cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga	1440
tcccagggtgc agctgcagga gtcgggcccc ggactgggtga agccttcgga gaccctgtcc	1500
ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag	1560
ccccaggta agggactgga gtggattggc tatatctatt acagtgggca gaccaaatac	1620
aaccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc	1680
ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact	1740
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ggcggaggat ctggtggcgg tggttctggc ggcgagggt cgcacatcca gatgaccag	1860
tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt	1920
cagagcatta acaactatit aaattggtat cagcagagac cagggaagc ccctaagctc	1980
ctgatctatg ctgcatccag ttgcaaaagt ggggtcccat caaggttcag tggcagtgga	2040
tctgggacag atttactct 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
	20		
Ser	Cys	Ala	Ala
		25	
Ser	Gly	Phe	Thr
			Phe
Ser	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	Ala	Val
Glu	Gly	Arg	Phe
	65		
Thr	Ile	Ser	Arg
	70		
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	His	
Pro	Ser	Ser	Ser
			195
Leu	Gly	Thr	Gln
			200
Thr	Tyr	Ile	Cys
Asn	Val	Asn	His
			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

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

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 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
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caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	660
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tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt	1920
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ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga	2040
tctgggacag atttcactct 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
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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

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

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

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

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 442

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aggcttagct gtgcggcatc ggggtttact ttcagtgatt atgcgatgca ttgggtccgg	180
caagcgcctg gaaaagggt 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
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acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccggtg	540
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta	600
cagtcctcag gactctactc cctcagcagc gtgggtgaccg tgccctccag cagcttgggc	660
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaagggt ggacaagaaa	720
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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
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
 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
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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aggcttagct gtgcggcatc ggggtttact ttcagtgatt atgcgatgca ttgggtccgg      180
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc      660
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa      720
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc      780

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ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	840
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<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 445

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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
 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
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 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

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 gctcctgatc tatgctgcat ccagtttgca aagtggggtc 240

ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagcagtctg 300

caacctgaag attttgcaac ttactactgt caacagagtt acagtacccc tcggacgttc	360
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<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
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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	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					80	

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
 145 150 155 160

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 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

<210> 448
 <211> 717
 <212> DNA
 <213> Homo sapiens

<400> 448
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtcagt ctgtgctgac gcagccgccc tcagtgtctg gggccccagg gcagagggtc 120
 accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aactggtac 180
 cagcagcttc caggaacagc ccccaaactc ctcatctatg gtaacagcaa tcggccctca 240
 ggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300
 gggctccagg ctgaggatga ggctgattat tactgccagt cctatgaaag cagcctgagt 360

gggttcggtgt tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420
 tcggtcactc tgttcccgcc ctctctgag gagcttcaag ccaacaaggc cacactggtg 480
 tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540
 cccgtcaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600
 gccagcagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660
 caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca 717

<210> 449
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 449

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

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

atggacatga ggggtgccccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60

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

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> 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
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	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 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> 452
 <211> 708
 <212> DNA
 <213> Homo sapiens

<400> 452
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtgata tccaaatgac acaatcacca tcgtcgcttt cagcgtctgt tggcgaccgt 120
 gtgacgatta cctgtcgcgc gtcccaggga atccggaatt acctcgcatt gtatcagcaa 180
 aaacccggaa aagcaccgaa gctcctgatc 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

<210> 453
<211> 214
<212> PRT
<213> Homo sapiens

<400> 453

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 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

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 ttgcagtgta ttactgtcag cagtatggta gctctcctac cttcggccaa 300

gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt 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

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

<210> 456

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 456

cagggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgatg tctatgggtg 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 ggccagggaa ccctgggtcac cgtctcctca 360

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttggt acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780

gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aacctcttcc 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
cagcaggggga 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

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

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 tttgctgcat ccagtttgca aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300

cagcctgaag attttgcaac ttattactgt ctccagcata atagttaccc tcccactttc 360

```

ggcggaggga ccaaggtgga gatcaaacga 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 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
          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> 460
 <211> 1425
 <212> DNA
 <213> Homo sapiens

<400> 460
 atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
 agatgccagg tgcagctggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120
 agactctcct gtgcagcctc tggattcacc ctgagtagct atggcatgca ctgggtccgc 180
 caggctccag gcaaggggct ggagtgggtg gcagttatgt catatgatgg aaataataaa 240
 ttatatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaaaacg 300
 ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360
 gacgaaactg aaaccctcta ctactactac ggtattgacg tctggggcca agggaccacg 420
 gtcaccgtct cctcagcctc caccaagggc ccatcggtct 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
aagaaagtgt agcccaaatac ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg	840
atctcccggg 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 cacaggtgta caccctgccc	1140
ccatcccggg 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> 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	

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

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

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
atggacatga gagtgctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt 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 ttactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta 540
ctgtcagcaa tattataaga ctctctcac ttctggcgga gggaccaaca aggacagcac 600
ctacagcctc aagagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta 660
cgcctgcgaa 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
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
 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
gacattcaaa tgacccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc 60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca 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 cttcccgcga 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

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

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 agagtgtgtaag aagcagctac ttagcc 36

<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

<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

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

<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

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

24

<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

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

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

<400> 476
ctccagcata atagttaccc tcccact

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

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

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

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
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

<210> 481
 <211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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 atagtggaaat taccaactac aaccggtccc 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

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
				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
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

<210> 488

<211> 42

<212> DNA

<213> Homo sapiens

<400> 488

gacgaaactg aaaccctcta ctactactac ggtattgacg tc

42

<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 gaggtaaga agcagctact tagcctggta ccagcagaga 120
gctggccagg ctcccaggct cctcatctat ggtgcatcca gccgggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtta 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

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 tgacccagtc 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
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
 100 105

<210> 494
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 494
 caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgatg 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

<210> 495
 <211> 120
 <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
 caggtgcagc tgggtggagtc tgggggaggc gtgggtccagc ctgggaggct cctgagactc 60
 tcctgtgcag cctctggatt caccctcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atgtcatatg atggaaataa taaattatat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa aacgctgtat 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagacgaa 300
 actgaaaccc tctactacta ctacgggtatt gacgtctggg gccaaaggac 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

<210> 498

<211> 57

<212> DNA

<213> Homo sapiens

<400> 498

atgaaacatc tgtggttctt cctgctgctg gtggcggcgc cgcgctgggt gctgagc

57

<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 Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 502
<211> 66
<212> DNA
<213> Homo sapiens

<400> 502
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcc 60

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 Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 505
<211> 19
<212> PRT
<213> Homo sapiens

<400> 505

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
atgaaacatc tgtggttctt cctgctgctg gtggcggcgc cgcgctgggt gctgagccag 60
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 gcccatcggg cttccccctg gcaccctcct ccaagagcac ctctgggggc 480
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 540
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 600
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 660
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tgagcccaaa 720
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg 780
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 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 ccagcccca tcgagaaaac catctccaaa 1080
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg gaaggagatg 1140

accaagaacc	aggtcagcct	gacctgcctg	gtcaaaggct	tctatcccag	cgacatcgcc	1200
gtggagtggg	agagcaatgg	gcagccggag	aacaactaca	agaccacgcc	tcccgtgctg	1260
aagtccgacg	gctccttctt	cctctatagc	aagctcaccg	tggacaagag	caggtggcag	1320
caggggaacg	tcttctcatg	ctccgtgatg	catgaggctc	tgcacaacca	ctacacgcag	1380
aagagcctct	ccctgtctcc	gggtaaa				1407

<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

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

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

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

atggacatga ggggtgccccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcc 60

agatgtgaca ttcaaagtac ccagagccca tccagcctga gcgcatctgt aggagaccgg 120

gtcacatca cttgtaaagc cagtcagaac gtaggtacta acgtagcctg gtatcaggaa 180
 aaaccaggta aagccccaaa agccctcatc tacagtgcct ctttcctcta tagtggtgta 240
 ccatacaggt tcagcggatc cggtagtggt 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

<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
 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

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

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
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagaagaaa 180
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 360
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 420
tctgatgagc agttgaaatc tggtaaccgcc tctgttgtgt gcctgctgaa taacttctat 480
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

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

atggacatga gagtgcctgc acagctgctg ggccctgctgc tgctgtggct gagaggcgcc	60
agatgcgagg ttcagctggg cgagtcagga ggcggtctcg tgcagcctgg cggatcactg	120
agattgtcct gtgctgcatc tggttacgtc 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
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 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
gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaaag ggagccccg agaaccacag gtgtacaccc tgccccatc 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

<210> 514
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 514

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 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

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

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 ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120
agattgtcct gtgctgcatc tggttacacc ttcacagact atggaatgaa ttgggttaga 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 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 cgtggtgacc 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 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

<210> 516
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 516

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 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

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

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 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> 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

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 gtgctgcatc tggttacacc ttacagact atggaatgaa ttgggttaga 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 ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
 aaatcttgtg acaaaactca cacatgcccc cctgtgcccag cacctgaact cctggggggga 780
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 960
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
 gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
 aaagccaaaag ggcagccccg 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

<210> 520
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 520

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

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
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc	420
acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc	480
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc	540
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttccccg	600
gctgtcctac agtcctcagg actctactcc ctcaagagcg 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 ggacccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct	900
gaggtcaagt 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 ggagccgga gaacaactac	1260
gacaccacgc ctcccgctgt ggactccgac ggctccttct tcctctatag cgacctcacc	1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380

ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa

1428

<210> 522

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 522

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

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

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

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

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 Ser 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> 524
<211> 642
<212> DNA
<213> Homo sapiens

<400> 524
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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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc 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> 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 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 aaggtggaga tcaaacgaac ggtggctgca 420

ccatctgtct tcattttccc gccatctgat gagcagttga aatctggtac cgcctctgtt	480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac	540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc	600
tacagcctca gcagcacctt gacgctgagc aaagcagact acgagaaaca 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
atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaaacca	120
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 cttcccgcc	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

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 gcctcaagag caccctgaag	540
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 gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc	60
agatgcgagg ttcagctggg cgagtcagga ggcgggtctcg 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 ggccagggtg ccctagtcac cgtctctagt	420

gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	480
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 gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc 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 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

<210> 529

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 529

cagggtcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatgggtg gtccttcagt ggttactact 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 cgtctctagt	360
gcctccacca agggcccatc ggtcttcccc ctggcacctt 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 acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc	900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccggaaggag	1080
atgaccaaga accaggtcag cctgacctgc ctggtcaaag 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

<210> 530

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 530

gaaattgtgt 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 acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca	360
tctgatgagc agttgaaatc tggaactgcc aaagttgtgt 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> 531
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 531	
gacattcaaa tgacccagag cccatccagc ctgagcgcat 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 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> 532
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 532	
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agatgcgagg ttacgtgggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg	120
agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga	180
caggccccgg gaaagggcct ggaatggatg ggttggatta 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 cctggtcaag gactacttcc ccgaaccggt gacgggtgtcg	540
tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	600
ggactctact ccctcaagag cgtggtgacc 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 gcgtggaggt 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 accaggtcag cctgacctgc ctggtcaaag 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> 533
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial polynucleotide

<400> 533	
gacattcaaa tgaccagag cccatccagc ctgagcgcac ctgtaggaga ccgggtcacc	60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca	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 cttcccgcga	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

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gacattcaaa tgacccagag cccatccagc ctgagcgcat ctgtaggaga ccgggtcacc      60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca gcaaaaacca      120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc      180
aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca      240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtcag      300
ggtagtaaa tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcc      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
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<210> 535

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 535

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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
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 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
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
<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

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

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

<210> 538

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 538

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 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

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
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

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

<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
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

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
 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

<210> 544
 <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

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
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

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

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
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

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

<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
 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

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
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

<210> 552
<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

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
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120
 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 aagatgcccc 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 ccccttgcca cctcctcca agagcacctc tgggggcaca 480

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc	600
tactccctca agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgagggtc	840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	900
gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg	960
taccgttgcg 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 gccggagaa aactacgaca ccacgcctcc cgtgctggac	1260
tccgacggct ctttcttcct ctatagcgac ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
agcctctccc tgtctccggg taaa	1404

<210> 554
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 554	
cagggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcgagac cctgtccctc	60
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgcgagcca	120
ccagggaaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240

aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt	300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt	360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg	480
tggaactcag gcgccctgac 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 ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagga gcagtacggc	900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccggaaggag	1080
atgaccaaga accaggctcag 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

<210> 555

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 555

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

1	5	10	15
Thr	Leu	Ser	Leu
	20		
Thr	Cys	Ala	Val
			25
Gly	Gly	Ser	Phe
			30
Ser	Gly	Tyr	
Tyr	Trp	Asn	Trp
	35		
Ile	Arg	Glu	Pro
			40
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Ile
Gly	Glu	Ile	Asn
	50		
His	Ala	Gly	Ile
			55
Thr	Asn	Tyr	Asn
			60
Pro	Ser	Leu	Lys
Ser	Arg	Val	Thr
Ile	Ser	Leu	Asp
	70		
Thr	Ser	Lys	Asn
			75
Gln	Phe	Ser	Leu
			80
Lys	Leu	Thr	Ser
Val	Thr	Ala	Ala
	85		
Asp	Thr	Ala	Val
			90
Tyr	Tyr	Cys	Ala
			95
Arg	Gly	Tyr	Cys
Arg	Ser	Thr	Thr
Cys	Tyr	Phe	Asp
Tyr	Trp	Gly	Gln
			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	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

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

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 gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
 agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120
 gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagaag 180
 aaaccaggga aagcccctaa gtcctgatc 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
cagggtgcagc 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 actgtgagag agaaattggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 360
accaagggcc catcggctct cccctggca 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 agaaagtga gccc aaatct 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttctctt tcccccaaaa acccaaggac accctcatga tctcccgga cctgaggtc 780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgag agggagcagta cggcagcacg 900
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag 1200
tccgacggct ccttcttct 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

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

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 gggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtgggtgcc 60

cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120

gtcaccatca cttgcaggtc cagccagagt gtgttatata 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 tcacttttcgg cggaggggacc aaggtggaga tcaaacgaac ggtggctgca 420

ccatctgtct tcattttccc gccatctgat gagcagttga aatctggtac cgcctctgtt	480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac	540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc	600
tacagcctca agagcacctt 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 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 cttcccgcc	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> 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 gatcaggagg	180
cccccaggga aaggccttga 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 ccccgaaccg	540
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	600
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg	660
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	720
aaagttgagc ccaaactctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa	780
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac	840
tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc	900
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgagag	960
gagcagtacg gcagcacgta ccgttgctgc agcgtcctca ccgtcctgca ccaggactgg	1020
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaaag ccctcccagc ccccatcgag	1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca	1140
tcccgaagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggccttctat	1200
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1260
acgcctcccg tgctgaagtc cgacggctcc ttcttcctct 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

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		
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

<210> 563
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 563
atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtgggtgcc 60
cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcacaacaa taagaactac 180
ttagtttggg accagaagaa accaggaaaag gttcctaaac tgctcattta ctgggcatct 240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360

aagactcctc tcactttcgg cggaggggacc aaggtggaga 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> 564
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 564	
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agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc	120
cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg	180
atcaggaggagg ccccagggaagg aggccttgag tgggtgagca ggacatacta caggtccaag	240
tggtataatg attatgcagt ttctgtgaaa ggtcgattca ctatcagccc agacacatcc	300
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac	360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg	420
accacgggtca ccgtctctag tgcctccacc aaggggccat cggctttccc cctggcaccc	480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	600
ccggctgtcc tacagtctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc	660
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	720
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcca	780

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gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc      840
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg 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 aaccaggtca gcctgacctg cctgggtcaaa     1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac     1260
tacaagacca cgcctcccgt gctgaagtcc gacggctcct tcttcctcta tagcaagctc     1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag     1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a              1431

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<210> 565
<211> 455
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polypeptide

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<400> 565

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

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```

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

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```

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

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Val Ser Val Lys Gly Arg Phe Thr Ile Ser Pro Asp Thr Ser Lys Asn

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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	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
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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agatgacgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagaag 180
aaaccaggga aagcccctaa gctcctgac tatgatgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360
ggccaaggga ccaaggtgga aatcaaacga acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctggt accgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct caagagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 567
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 567
atggacatga gaggcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc 60
agatgccagg tgacgtggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120
agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180
gaggctccag 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 ccatcgggtct 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
aagaaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg	840
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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

<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
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 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
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
 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 ccaaggtgga aatcaaacga 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> 570
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 570
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accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aacttggtac 180
caggagtttc 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 cacactgggtg 480
tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540
cccgtaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600
gccgagagct atctgagcct gacgcctgag cagtggaaagt 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

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

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

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> 572

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 572

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agatgcgagg ttacagctggc cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg      120
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
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 acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga      780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020

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gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
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 atgaccaaga accaggtcag 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

<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

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

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

<400> 574

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcaaa	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> 575
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 575	
cagggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatgggtg gtccttcagt gggtactact ggaactggat ccgccagcca	120
ccagggaagg agctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt	300
agaagtacca cctgctactt tgactactgg ggccaggga ccttagtcac cgtctctagt	360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctggtcaag 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
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt 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
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccggaaggag	1080
atgaccaaga accaggctcag cctgacctgc ctggtcaaag 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

<210> 576

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 576

gacattcaaa tgacccagag cccatccagc ctgagcgcat ctgtaggaga ccgggtcacc	60
atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca	120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac	180
aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca	240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtag	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> 577
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 577	
atggacatga gagtgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc	60
agatgcgagg ttacgttgtt cgagtcagga ggcggtctcg 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 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 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
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgagagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccac cggggaggag	1140
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc	1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccggtg	1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg	1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtaaa	1410

<210> 578
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 578

Glu	Val	Gln	Leu	Val	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	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			

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

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

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
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
 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
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agatgcgaca tccagatgac ccagtctcca tcctccctat ctgcatctgt aggagacaga 120
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 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

<210> 581
<211> 1344
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 581

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc	60
acctgcactg tctctggtgg 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 catcggctct cccctggca 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 agaaagtga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttctct tcccccaaa 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 ctccaaagcc	1020
aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggaa ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag	1200
tccgacggct ctttcttct 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
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						
	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

<210> 583
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 583
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 cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg 120
 gtcaccatca cttgcaggtc cagccagagt gtgttatata gctccaacaa taagaactac 180
 ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240
 acccggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
 ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360
 aagactcctc tcactttcgg caaagggacc aaggtggaga 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> 584
 <211> 1422
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 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 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 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
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	720
aaagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa	780
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc	840
tcccggaacc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc	900

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgcgag 960
gagcagtacg gcagcacgta ccgttgcgtc agcgtcctca ccgtcctgca ccaggactgg 1020
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1140
tcccggaagg agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat 1200
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1260
acgcctcccg tgctgaagtc cgacggctcc ttcttcctct atagcaagct caccgtggac 1320
aagagcagggt 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
 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
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

atggacatga	gagtgccctgc	acagctgctg	ggcctgctgc	tgctgtggct	gagaggcgcc	60
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cgactcagct	gtgccatctc	cggggacagt	gtctctacca	acagtgttgc	ttggaactgg	180
atcaggcagg	ccccagggaa	agagcttgag	tgggtgagca	ggacatacta	caggtccaag	240
tgggtataatg	attatgcagt	ttctgtgaaa	ggctcgattca	ctatcagccc	agacacatcc	300
aagaacacgt	tctacctgca	gatgaactct	ctgagagccg	aggacacggc	tgtgtattac	360
tgtgcaagag	aggatgggga	tagctactac	cgctacggta	tggacgtctg	gggccaaggg	420
accacggtca	ccgtctctag	tgccctccacc	aagggcccat	cggtcttccc	cctggcaccc	480
tcctccaaga	gcacctctgg	gggcacagcg	gccctgggct	gcctgggtcaa	ggactacttc	540
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agcagcttgg	gcacccagac	ctacatctgc	aacgtgaatc	acaagcccag	caacaccaag	720
gtggacaaga	aagttgagcc	caaatcttgt	gacaaaactc	acacatgccc	accgtgccc	780
gcacctgaac	tcctgggggg	accgtcagtc	ttcctcttcc	ccccaaaacc	caaggacacc	840
ctcatgatct	cccggacccc	tgaggtcaca	tgctgtgggg	tggacgtgag	ccacgaagac	900
cctgagggtca	agttcaactg	gtacgtggac	ggcgtggagg	tgacataatgc	caagacaaag	960
ccgtgcgagg	agcagtacgg	cagcacgtac	cgttgctgca	gcgtcctcac	cgtcctgcac	1020
caggactggc	tgaatggcaa	ggagtacaag	tgcaagggtct	ccaacaaaagc	cctcccagcc	1080
cccatcgaga	aaaccatctc	caaagccaaa	gggcagcccc	gagaaccaca	ggtgtacacc	1140
ctgcccccat	cccggaagga	gatgaccaag	aaccagggtca	gcctgacctg	cctgggtcaaa	1200
ggcttctatc	ccagcgacat	cgccgtggag	tgggagagca	atgggcagcc	ggagaacaac	1260
tacaagacca	cgctcccgt	gctgaagtcc	gacggctcct	tcttcctcta	tagcaagctc	1320
accgtggaca	agagcagggtg	gcagcagggg	aacgtcttct	catgctccgt	gatgcatgag	1380

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1431

<210> 587

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 587

atggacatga ggggtgccggc ccagctcctc ggtcttctgt tgctctggct ccgtgggtgcc	60
cgctgtgaca tccagatgac ccagtctcca agctccctgt ctgcgtctgt gggcgatagg	120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcceaaca taagaactac	180
ttagtttggg accagcagaa accaggaaa gttcctaaac tgctcattta ctgggcatct	240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact	300
ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat	360
aagactcctc tcactttcgg caaagggacc aaggtggaga tcaaacgaac ggtggctgca	420
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtag cgccctctgtt	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> 588

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 588

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

1	5	10	15
Ser	Leu	Arg	Leu
	20		
Ser	Cys	Ala	Ile
			25
Ser	Gly	Asp	Ser
			30
Ser	Val	Ser	Thr
			Asn
Ser	Val	Ala	Trp
	35		
Asn	Trp	Ile	Arg
			40
Gln	Ala	Pro	Gly
			45
Lys	Glu	Leu	Glu
Trp	Val	Ser	Arg
	50		
Thr	Tyr	Tyr	Arg
			55
Ser	Lys	Trp	Tyr
			60
Asn	Asp	Tyr	Ala
Val	Ser	Val	Lys
Gly	Arg	Phe	Thr
	70		
Ile	Ser	Pro	Asp
			75
Thr	Ser	Lys	Asn
			80
Thr	Phe	Tyr	Leu
Gln	Met	Asn	Ser
Leu	Arg	Ala	Glu
Asp	Thr	Ala	Val
			95
Tyr	Tyr	Cys	Ala
Arg	Glu	Asp	Gly
Asp	Ser	Tyr	Tyr
Arg	Tyr	Gly	Met
Asp	Val	Trp	Gly
Gln	Gly	Thr	Thr
Val	Thr	Val	Ser
Ser	Ser	Ala	Ser
Thr	Thr	Val	Trp
Val	Phe	Pro	Leu
Ala	Pro	Ser	Ser
Lys	Ser	Thr	Ser
Gly	Gly	Thr	Ala
Ala	Leu	Gly	Cys
Leu	Val	Lys	Asp
Tyr	Phe	Pro	Glu
Pro	Val	Thr	Val
Ser	Trp	Asn	Ser
Gly	Ala	Leu	Thr
Ser	Gly	Val	His
Thr	Phe	Pro	Ala
Val	Leu	Gln	Ser
Ser	Ser	Gly	Leu
Tyr	Ser	Leu	Glu
Ser	Val	Thr	Val
Pro	Ser	Ser	Ser
Leu	Gly	Thr	Gln
Thr	Tyr	Ile	Cys

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

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> 589
 <211> 1425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 589
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 agatgccagg tgcagctggg ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120
 agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180
 caggctccag gcaaggagct ggagtgggtg gcagtcatat catatgatgg aaataataaaa 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 ccatcgggtct 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 gccaccgtg cccagcacct 780

gaactcctgg ggggaccgtc agtcttcctc ttcccccaaa aaccaagga 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 agccccatc	1080
gagaaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta caccctgccc	1140
ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	1200
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1260
accacgcctc cctgtctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg	1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct cctgatgca tgaggctctg	1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa	1425

<210> 590

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 590

atggacatga gagtgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc	60
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga	120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag	180
aaaccaggga aagcccctaa gtcctgatc tatgatgcat ccagtttgca aagtggggtc	240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc	360
ggcaaaggga ccaagtgga aatcaaacga acggtggctg caccatctgt cttcatcttc	420
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

<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
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 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

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

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> 592
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 592
atggacatga gtagcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180
aaaccaggga aagcccctaa ggcctgatc tatgatgcat ccagtttgca aagtggggtc 240

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc	360
ggcaaaggga ccaaggtgga aatcaaacga acggtggctg caccatctgt cttcatcttc	420
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

<210> 593

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 593

atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagagggtgcg	60
cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga	120
gtcaccatca cttgccgggc aagtcaggac atcagaaaatg atttaggctg gtatcagcag	180
aaaccaggga aagcccctaa gcgcctgatc tatgctgcgt ccagtttgca aagtggggtc	240
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc	360
ggcgaaggga ccaaggtgga gatcaaacgt 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
atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
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 caccttcccg 600
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840
atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct 900
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 960
tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1080
atcgagaaaa ccatctcaa 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 gcagggtggca 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	

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

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

caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120

ccaggggaagg ggctagagtg gattgggggaa 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 ctggcacctt 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 acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc	900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccggaagaag	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

<210> 597
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 597

atggacatga gaggatgcctgc acagctgctg ggctgctgc tgctgtggct gagaggcgcc	60
agatgcgagg ttcagctggg cgagtcagga ggcggctctg tgcagcctgg cggatcactg	120
agattgtcct gtgctgcatc 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 ggccagggtta ccctagtcac cgtctctagt	420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtc	540
tggaactcag gcgcccctgac 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 gcgtgggtggg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	900
tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag	1140
atgaccaaga accaggctcag cctgacctgc ctggctgatg gcttctatcc cagcgacatc	1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg	1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcagggtgg	1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
cagaagagcc tctccctgtc tccgggtaaa	1410

<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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
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
 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

<210> 600

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 600

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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 tagtgcctcc	360
accaagggcc catcggctct cccctggca 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 agaaagtga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttctct tcccccaaa acccaaggac accctcatga tctcccgga cctgaggtc	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 ctccaaagcc	1020
aaagggcagc cccgagaacc acagggtgtac accctgcccc catcccggaa gaagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag	1200
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320

agcctctccc tgtctccggg taaa

1344

<210> 601

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 601

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
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

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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tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gatcaggcag 180
ccccaggga aaggccttga gtggatagga aggacatact acagggtcaa 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

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agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg      540
gtgacgggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc      600
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg      660
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag      720
aaagttgagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa      780
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgata      840
tcccggaccc ctgagggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgagggtc      900
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgagag      960
gagcagtacg gcagcacgta ccgttgctgc agcgtcctca ccgtcctgca ccaggactgg     1020
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag     1080
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca     1140
tcccggaaga agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat     1200
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc     1260
acgcctcccc tgctgaagtc cgacggctcc ttcttcctct atagcaagct caccgtggac     1320
aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac     1380
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<210> 603

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 603

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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

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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

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									
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		

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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cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
atcaggcagg cccaggggaa aggccttgag tgggtgagca ggacatacta caggtccaag 240
tggtataatg attatgcagt ttctgtgaaa ggtcgattca ctatcagccc agacacatcc 300
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420
accacggtca cgtctctag tgcctccacc aagggcccat 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 accgtgccca 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 cgttgctga gcgtcctcac cgtcctgcac 1020
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cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140
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accgtggaca agagcaggtg 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

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

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

<210> 606

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 606

atggacatga gagtgcctgc acagctgctg ggccctgctgc tgctgtggct gagaggcgcc	60
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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 ctagtgctc 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
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg	840
atctcccga 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 agccccatc	1080
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1140
ccatcccga agaagatgac 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

<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
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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
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
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 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

<400> 608
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 cgctgtgagg tgcagctggg gcagtctgga gcagaggtga aaaagcccgg ggagtctctg 120
 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctgagatacc 240
 agatacagcc cgtccttcca aggccagggt accatctcag ccgacaagtc catcagtacc 300
 gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360
 agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420

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

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

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

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agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga      180
caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct      240
atttatgctg acagcgtcaa gggcagattc acgatctctc tagacacatc caagtcaaca      300
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ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt      420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      480
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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      600
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gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgcgagga gcagtacggc      960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag     1020

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gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
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 atgaccaaga accaggtcag cctgacctgc ctggtcgatg 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> 611
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 611

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

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

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
atggacatga gaggcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgagg ttcagctggt cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg 120

agattgtcct gtgctgcatc 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
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 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
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga 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 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

<210> 613
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 613

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
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
 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

<210> 614
 <211> 1428
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 614
 atggacatga ggggtgccccgc 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 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

gacaagaaag	ttgagcccaa	atcttgtgac	aaaactcaca	catgcccacc	gtgcccagca	780
cctgaactcc	tgggggggacc	gtcagtcttc	ctcttcccc	caaaacccaa	ggacaccctc	840
atgatctccc	ggacccctga	ggtcacatgc	gtggtggtgg	acgtgagcca	cgaagaccct	900
gaggtcaagt	tcaactggta	cgtggacggc	gtggaggtgc	ataatgccaa	gacaaaagccg	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	ggtcgatggc	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

<210> 615

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<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

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 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

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
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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
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

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 ttcagctggg cgagtcagga ggcgggtctcg tgcagcctgg cggatcactg 120
 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180
 aaggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240
 atttatgctg acgccgtcaa gggcagattc acgttctctc 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 cgtggtgacc 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 gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc 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

<210> 618
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 618	
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatggtgg 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 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 aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc ccaaaaaccc 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 gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag 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 gagcagggtg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtaaa	1350

<210> 619
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 619	
atggacatga gtagtcctgc acagctgctg ggcttgctgc tgctgtggct gagaggcgcc	60
agatgcgagg ttcagctggt cgagtcagga ggcggtctcg 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 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 cctggggggga	780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	840
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga 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 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> 620

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

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
 atggacatga ggggtgccccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 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
 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 caccaaggtg 720

gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca	780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc	840
atgatctccc ggacccctga ggtcacatgc gtgggtgggtgg acgtgagcca cgaagaccct	900
gagggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg	960
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 ggagccgga gaacaactac	1260
gacaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag cgacctcacc	1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	1428

<210> 622

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 622

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cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga	120
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag	180
aaaccaggga aagcccctaa gctcctgac tatgctgcgt ccagtttgca aagtggggtc	240
ccatcaagggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc	360
ggcggaggga ccaaggtgga gatcaaacgt acggtggtg 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 gctcgcccgt 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
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
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
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 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
gagggtccgta 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 caccttccccg	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 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 aaggctctca acaaagccct cccagcccc	1080
atcgagaaaa ccatctcaa 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 gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	1428

<210> 625

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 625
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cgctgtgaca tccagatgac ccagtcctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag 180
aaaccaggga aagcccctaa gtcctgatc tatgctgcgt ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360
ggcggaggga ccaagggtga 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> 626
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

<210> 627
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 627
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 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagaagaaa 120
 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 cttcccgcc 360
 tctgatgagc agttgaaatc tggtagcgcc aaagtgtgtg 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> 628
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 628
 gacattcaaa tgacccagag cccatccagc ctgagcgcat ctgtaggaga ccgggtcacc 60
 atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca ggaaaaacca 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 cttcccgcc	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> 629

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 629

cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatggtgg gtccttcagt ggtagtact 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 ccgaaccggg gacgggtgtcg	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 cctggggggga	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	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

<210> 630

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 630

gacattcaaa	tgacccagag	cccatccagc	ctgagcgcat	ctgtaggaga	ccgggtcacc	60
atcacttgta	aagccagtca	gaacgtaggt	actaacgtag	cctgggtatca	ggaaaaacca	120
ggtaaagccc	caaaagccct	catctacagt	gcctctttcc	tctatagtgg	tgtaccatcc	180
aggttcagcg	gatccggtag	tggtactgat	ttcacccctca	cgatcagtag	cctccagcca	240
gaagatttcg	ccacttatta	ctgtcaacag	tataacatct	accactcac	attcggtcag	300
ggtactaaag	tagaaatcaa	acgtacggta	gcggcccat	ctgtcttcat	cttcccgcc	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		

<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)
<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

Arg Xaa Ser Gln Ser Xaa Asn Asn Tyr Leu Asn
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<210> 643
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<400> 643

Xaa Thr Ser Ser Xaa Gln Ser
1 5

<210> 644
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<400> 644

Tyr	Xaa	Tyr	Tyr	Ser	Xaa	Ser	Thr	Asn	Tyr	Asn	Pro	Ser	Xaa	Lys	Ser
1				5				10					15		

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<400> 645

Glu Xaa Xaa Ser Tyr Tyr Xaa Phe Asp Tyr
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<210> 646

<211> 11

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<400> 646

Arg Xaa Ser Gln Ser Xaa Asn Asn Tyr Xaa Asn
1 5 10

<210> 647

<211> 7

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<400> 647

Xaa Xaa Ser Ser Xaa Gln Ser
1 5

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<400> 648

Tyr Xaa Tyr Tyr Ser Xaa Gln Thr Lys Tyr Asn Pro Ser Xaa Lys Ser
1 5 10 15

<210> 649
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1				5				10					15		

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<400> 650

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

<210> 651
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<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
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Trp	Xaa	Ser	Thr	Arg	Glu	Ser
1				5		

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<400> 653

Gln Gln Tyr Tyr Lys Thr Pro Xaa Thr
1 5

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V, W, or Y

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<400> 654

Thr Asn Xaa Xaa Xaa Trp Asn
1 5

<210> 655
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<400> 655

Thr Asn Xaa Xaa Xaa Trp Asn
1 5

<210> 656
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<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
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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
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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
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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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<400> 660

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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<400> 661

Arg	Xaa	Ser	Gln	Ser	Val	Arg	Ser	Ser	Tyr	Xaa	Xaa
1				5					10		

<210> 662

<211> 7

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<400> 662

Xaa Xaa Ser Ser Arg Xaa Thr
1 5

<210> 663
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<400> 663

Gln Gln Tyr Xaa Ser Ser Pro Thr
1 5

<210> 664
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<400> 664

Xaa Tyr Tyr Trp Asn
1 5

<210> 665

<211> 16

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<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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<400> 666

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

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

<210> 668
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<400> 668

Arg Xaa Ser Gln Ser Xaa Arg Ser Ser Tyr Xaa Xaa
1 5 10

<210> 669
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<400> 669

Xaa	Xaa	Ser	Tyr	Asp	Xaa	Asn	Asn	Lys	Xaa	Tyr	Xaa	Asp	Ser	Xaa	Lys
1				5				10						15	

Xaa

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Arg	Xaa	Ser	Gln	Xaa	Xaa	Ser	Asn	Asp	Xaa
1				5				10	

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Asp Glu Thr Glu Thr Xaa Tyr Tyr Tyr Tyr Xaa Xaa Asp Xaa
1 5 10

<210> 672
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<400> 672

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

<210> 673
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<400> 673

Gly Gly Gly Ser Gly Gly Gly Ser
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<210> 674
<211> 9
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<400> 674

Leu Gln His Asn Ser Tyr Pro Leu Thr
1 5

<210> 675
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<212> PRT
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<400> 675

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

<210> 676
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1 5 10

<210> 677
<211> 16
<212> PRT
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<400> 677

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

<210> 678

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 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

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<400> 679

Xaa Xaa Ser Tyr Glu Xaa Asn Asn Lys Leu Tyr Thr Glu Ser Xaa Lys
1 5 10 15

Xaa

<210> 680
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<220>
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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

<212> DNA

<213> Homo sapiens

<400> 682

aggtctagtc agagcctcct gtatagtaat ggatacaact atttgat 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
<211> 9
<212> PRT
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<400> 687

Met Gln Pro Leu Gln Thr Pro Leu Thr
1 5

<210> 688
<211> 51
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<400> 688
aagtccagtc agaataatattt atacagctcc aacaataaaaa actacttagc t

51

<210> 689
<211> 17
<212> PRT
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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
<212> DNA
<213> Homo sapiens

<400> 690
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21

<210> 691
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<400> 691

Val	Met	Ser	Tyr	Asp	Xaa	Asn	Asn	Lys	Leu	Tyr	Ala	Asp	Xaa	Val	Lys
1				5				10					15		

Gly

<210> 692
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<212> DNA
<213> Homo sapiens

<400> 692
caacaatatt atagtattcc gtggacg

27

<210> 693
<211> 9
<212> PRT
<213> Homo sapiens

<400> 693

Gln	Gln	Tyr	Tyr	Ser	Ile	Pro	Trp	Thr
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<210> 694
<211> 51
<212> DNA
<213> Homo sapiens

<400> 694
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<210> 695
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 696
<211> 42
<212> DNA
<213> Homo sapiens

<400> 696
actgggagca gctccaacat cggggcaggt tataatgttc ac 42

<210> 697
<211> 14
<212> PRT
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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
<211> 21
<212> DNA
<213> Homo sapiens

<400> 698
ggtaacaaca atcggccctc a 21

<210> 699
<211> 7
<212> PRT
<213> Homo sapiens

<400> 699

Gly Asn Asn Asn Arg Pro Ser
1 5

<210> 700
<211> 33
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<400> 700
cagtcctatg acagcagcct gagtggttgg gtg

33

<210> 701
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<212> PRT
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<400> 701

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val
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Gly Asn Ser His Arg Pro Ser
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Met Gln Gly Thr His Trp Pro
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Ala Ala Ser Arg Leu Gln Ser
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Ser Tyr Val Met Ser
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Gly

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Lys Ser

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Lys Ser

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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

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Glu Gly Ile Ala Val Ala Leu Thr Tyr
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30

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Asp Ser Gly Trp His Phe Ser Phe Asp Ile
1 5 10

<210> 830
<211> 15
<212> DNA
<213> Homo sapiens

<400> 830
agctatggca tgcac 15

<210> 831
<211> 51
<212> DNA
<213> Homo sapiens

<400> 831
gttatatggg ttgatggaag taatgaatac tatgcagact ccgtgaaggg c 51

<210> 832
<211> 17
<212> PRT
<213> Homo sapiens

<400> 832

Val Ile Trp Phe Asp Gly Ser Asn Glu Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 833
<211> 30
<212> DNA
<213> Homo sapiens

<400> 833
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<210> 834
<211> 10
<212> PRT

<210> 839
<211> 24
<212> DNA
<213> Homo sapiens

<400> 839
gaaatggctg gggcttttga tatc

24

<210> 840
<211> 8
<212> PRT
<213> Homo sapiens

<400> 840

Glu Met Ala Gly Ala Phe Asp Ile
1 5

<210> 841
<211> 15
<212> DNA
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<400> 841
gggtactact ggagc

15

<210> 842
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<212> DNA
<213> Homo sapiens

<400> 842
gaaatcaatc ctgttggaag aaccaactac aaaccgtccc tcaagagt

48

<210> 843
<211> 16
<212> PRT
<213> Homo sapiens

<400> 843

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

<210> 844
<211> 30
<212> DNA
<213> Homo sapiens

<400> 844
gacaatgggt ggcactatgc ttttgatatc

30

<210> 845
<211> 10
<212> PRT
<213> Homo sapiens

<400> 845

Asp Asn Gly Trp His Tyr Ala Phe Asp Ile
1 5 10

<210> 846
<211> 15
<212> DNA
<213> Homo sapiens

<400> 846
gcctactata tgcac

15

<210> 847
<211> 5
<212> PRT
<213> Homo sapiens

<400> 847

Ala Tyr Tyr Met His
1 5

<210> 848
<211> 51
<212> DNA
<213> Homo sapiens

<400> 848
tggatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcgggg c

51

<210> 849
<211> 17
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<400> 849

Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Arg
1				5				10						15	

Gly

<210> 850
<211> 27
<212> DNA
<213> Homo sapiens

<400> 850

ggcggcagct gggagggttt tgactac

27

<210> 851
<211> 9
<212> PRT
<213> Homo sapiens

<400> 851

Gly	Gly	Ser	Trp	Glu	Gly	Phe	Asp	Tyr
1				5				

<210> 852
<211> 51
<212> DNA
<213> Homo sapiens

<400> 852

ggtattagtg gtagtggtgg tagcagatac tacgcagact ccgtgaaggg c

51

<210> 853
<211> 17
<212> PRT
<213> Homo sapiens

<400> 853

Gly Ile Ser Gly Ser Gly Gly Ser Arg Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 854
<211> 24
<212> DNA
<213> Homo sapiens

<400> 854
gaagtggctg gggcttttga tatc 24

<210> 855
<211> 8
<212> PRT
<213> Homo sapiens

<400> 855

Glu Val Ala Gly Ala Phe Asp Ile
1 5

<210> 856
<211> 15
<212> DNA
<213> Homo sapiens

<400> 856
ggctactata tgcac 15

<210> 857
<211> 5
<212> PRT
<213> Homo sapiens

<400> 857

Gly Tyr Tyr Met His
1 5

<210> 858

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

<400> 858
tggatcatcc ctaacagtgg tggcacaaat tatgcccaga agtttcaggg c 51

<210> 859
<211> 17
<212> PRT
<213> Homo sapiens

<400> 859

Trp	Ile	Ile	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 860
<211> 27
<212> DNA
<213> Homo sapiens

<400> 860
ggcagcagct gggagggatt tgactac 27

<210> 861
<211> 9
<212> PRT
<213> Homo sapiens

<400> 861

Gly	Ser	Ser	Trp	Glu	Gly	Phe	Asp	Tyr
1				5				

<210> 862
<211> 15
<212> DNA
<213> Homo sapiens

<400> 862
agttatgcca tgagt 15

<210> 863
<211> 51
<212> DNA
<213> Homo sapiens

<400> 863
ggtatttagtg gtagaggtag tagcacatac tacgcagact ccgtgaaggg c 51

<210> 864
<211> 17
<212> PRT
<213> Homo sapiens

<400> 864

Gly	Ile	Ser	Gly	Arg	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1			5					10						15	

Gly

<210> 865
<211> 339
<212> DNA
<213> Homo sapiens

<400> 865
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atctcctgca ggtctagtca gagcctcctg tatagtaatg gatacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacag ctctgatct atttgggttc tagtcgggcc 180
tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgggggtt tattactgca tgcaacctct acaaactccg 300
ctcactttcg gcggagggac caaggtggag atcaaacga 339

<210> 866
<211> 112
<212> PRT
<213> Homo sapiens

<400> 866

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

<210> 867

<211> 375

<212> DNA

<213> Homo sapiens

<400> 867

gaggtgcagc tgggtggagtc tggggggaggc ctggtcaagc ctgggggggtc cctgagactc	60
tcctgtgcag cctctgaatt caccttcagt acctattaca tgagctgggt ccgccaggct	120
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 cctca	375

<210> 868
<211> 125
<212> PRT
<213> Homo sapiens

<400> 868

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

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
115 120 125

<210> 869
<211> 342
<212> DNA
<213> Homo sapiens

<400> 869

gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagtc gaatatatta tacagctcca acaataaaaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct agcctgctca tttactgggc atctacccgg	180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc	240
ctcagcagcc tgcaggctga agatgtggca gtttatttct gtcaacaata ttatagtatt	300
ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaac ga	342

<210> 870
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 870

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

<210> 871
 <211> 366

<212> DNA

<213> Homo sapiens

<400> 871

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cagggtgcagt tgggtggagtc tgggggaggc gtgggtccagc ctgggagggtc cctgagactc      60
tcctgtgcag cgtctggatt caccttcagt acttatggca tgcactgggt cccagggt      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

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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 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
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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 tgaccagtc tccagactcc ctgactgtgt ctctgggcga gggggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataaaaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct agcctgctca ttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtatt 300
ccgtggacgt tcggccaagg gaccaaggtg 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

<210> 875
<211> 366
<212> DNA
<213> Homo sapiens

<400> 875
caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt catcttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttggatat atggaagtaa taaagactat 180
gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgttgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaggaa 300
agggattcct actaccacta cggtatggac gtctggggcc aagggaccac 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

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 gcagggtata 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

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 gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cagctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgt	300
accaactatt actactacta ctccggtatg gacgtctggg gccaaaggac cacggtcacc	360
gtctcctca	369

<210> 880
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 880

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 gagtgggttat	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

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ccaggggaagg	ggctgcagtg	ggtctcagtt	attagtggta	gaggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	actccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	gaaagacggg	300
tatagcagtg	cctgggtactt	tgactactgg	ggccagggaa	ccctgggtcac	ggtctcctca	360

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

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

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

Ala Lys Asp Gly Tyr Ser Ser Ala Trp Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

<210> 885
<211> 336
<212> DNA
<213> Homo sapiens

<400> 885
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tcctgcactg ggagcggctc caacatcggg gcagggttatg atgtacactg gtaccagcag 120
cttccaggaa cagcccccaa actcctcatc tatggtaata gtcacgggcc ctcagggatc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttat 300
gtcttcggaa ctgggaccaa ggtcaccgtc ctaggt 336

<210> 886
<211> 111
<212> PRT
<213> Homo sapiens

<400> 886

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

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
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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 cctggttcctt 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

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 ttcactctca 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

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 cctcgcagac cctctcactc 60
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 cagtcccat cgagaggcct tgagtggctg ggaaggacat accagaggtc caagtggaat 180
 aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaggaac 240
 cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300
 agagaagtag tggctggccc gaggtgggtc gaccctggg gccagggaac cctgggtcacc 360
 gtctcctca 369

<210> 892
 <211> 123
 <212> PRT
 <213> Homo sapiens

<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
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 atcacttgcc gggcaagtca gagcgttacc agctatttaa attggtatca gcagaaacca 120
 gggaaaagccc ctaaactcct gatctatact gcatccagtt tgcaaagtgg gatcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 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 cctcgcagac cctctcactc	60
acctgtgccca 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 gaggtggttc 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

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	aggagtccct	180
gaccgattct	ctggctccaa	gtctggcacc	tcagcctccc	tggccatcag	tgggctccag	240
tctgaggatg	aggctgatta	ttactgtgca	acatgggatg	acaacctcaa	tggtccgcta	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

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

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<210> 899
<211> 354
<212> DNA
<213> Homo sapiens
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<400> 899
caggtgcaac tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgagggtc 60
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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

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 gatctatggt gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta atcctcagga gtgcagtttt 300
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

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
caggagcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tctatgggtgg gtccttcagt gggtactact ggagctggat ccgccagccc 120
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
<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
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattaga aatgacttag gctggtatca ggagaaacca 120
gggaaagccc ctaagcgcct gatctatgct gcatccggtt tacaagggtgg ggacccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtctacag cataatagtt accccacgtg gacgttcggc 300
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
cagggtgcagc 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
ctgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc gagagagcga 300
tggttcgggg agttattaga ctactggggc cagggaaccc tggtcaccgt ctcctca 357

<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
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
115

<210> 909
<211> 321
<212> DNA
<213> Homo sapiens

<400> 909
gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagcgtcacc 60
atcacttgcc gggcaagtca gagcattagt tactatttaa attggtatca acagaaacca 120
gggaaaagccc ctaagttcct gatctatgct gcatccagtt tacaaaagtg ggtcccatca 180
aggtttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagtt ccatcacctt cggccaaggg 300
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

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

gaggtgcacc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
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
gctggggcctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc a	351

<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

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

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagagacca 120

gggaaagccc ctaacctcct gctctttact gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcaacag tctgcaacct	240
gaggattttg caacttacta ctgtcaacag agttacagta accctcctga gagcagtttt	300
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	

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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caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc      60
acctgcgctg tctatgggtg gtccttcagt ggggtactact ggagctggat ccgccagcct      120
ccaggggaagg ggctggagtg gattgggggaa atcaatcctg ttggaagaac caactacaaa      180
ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg      240
aagctgagtt ctgtgaccgc cgcggacacg gctctgtatt actgtgcgag ggacaatggg      300
tggcactatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttca            354

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<210> 916
<211> 118
<212> PRT
<213> Homo sapiens

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<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

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<210> 917
<211> 333
<212> DNA
<213> Homo sapiens

<400> 917
gatgttgatga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60
atctcctgca ggtctagtca aagcctcgta tacagtgcg gaaacaccta cttgaattgg 120
tttcagcaga ggccaggccg atctccaagg cgcttaattt ataaggtttc taactgggac 180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgattccac actgataatc 240
agcaggggtgg aggctgagga tgttgggggtt 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
cagggacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgccagg cttctggata caccttcacc gcctactata tgcactgggt gcgacaggcc 120
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

Leu Val Thr Val Ser Ser
115

<210> 921
<211> 324
<212> DNA
<213> Homo sapiens

<400> 921
gacatccaga tgacccagtc tccatcgtcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagtag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agtgacagta ccccgatcac cttcggccaa 300
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

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
gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca acagaaacca 120
gggaaagccc ctaaattcct gatctatgct gcatccagtt tacaaagtgg ggtcccttca 180
aggtttagtg gcagtgggtc tgggacagat ttactctca 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

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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgtag cctctggatt cacctttagt agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggtag cagatactac 180
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

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
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggacagccc ctaagttcct gatctatggc gcatcccggt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagactttg caacttacta ctgtcaacag agtgacacta ccccgatcac cttcggccaa 300
gggacacgac tggagattaa acga 324

<210> 928

<211> 107
<212> PRT
<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

caggtgcagc tgggtgcaatc tggggctgag gtgaagaagc ctggggcctc agtgcaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactggat tcgacaggcc 120
cctgggcaag ggcttgagtg gctgggatgg atcatcccta acagtgggtg cacaaattat 180
gcccagaagt ttcagggcag ggtcaccatg accaggggaca cgtccatcag cacagcctac 240
atggaactga gcaggctgag atctgacgac acggccgttt attactgtgc gactggcagc 300

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

gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

60

atcacttgcc gggcaagtca gagcattagc cactatttaa attggtatca gcagaaacca	120
gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca	180
aggtttagtg 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	

<210> 933
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 933
gaggtgcacc tgttggagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60
tcttgtgcag cctctggatt cacctttagc agttatgcc a tgagttgggt ccgccagggtt 120
ccagggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatgg acagcctgag agccgaggac acggccgtat ataactgtgc gatagaagtg 300
gctggggcctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc a 351

<210> 934
<211> 117
<212> PRT
<213> Homo sapiens

<400> 934

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
115

<210> 935
<211> 7
<212> PRT
<213> Homo sapiens - Amino acids

<400> 935

Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 936
<211> 9
<212> PRT
<213> Homo sapiens - Amino acids

<400> 936

Met Gln Pro Leu Gln Thr Pro Leu Thr
1 5

<210> 937
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 937

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

Gly Gly Gly Ser
20

<210> 938
<211> 9
<212> PRT
<213> Homo sapiens - Amino acids

<400> 938

Gln Gln Tyr Tyr Ser Thr Pro Trp Thr
1 5

<210> 939
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 939

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 940
<211> 9
<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.

<220>
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<222> (4)..(4)
<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> 940

Xaa Gln Pro Xaa Gln Thr Pro Xaa Thr

1

5

<210> 941
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 941

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

Gly Gly Gly Ser Gly Gly Gly Ser
20

<210> 942
<211> 9
<212> PRT
<213> Homo sapiens - Amino acids

<400> 942

Gln Gln Ser Tyr Ser Thr Pro Ile Thr
1 5

<210> 943
<211> 7
<212> PRT
<213> Homo sapiens - Amino acids

<400> 943

Lys Val Ser Asn Arg Asp Ser
1 5

<210> 944
<211> 9
<212> PRT
<213> Homo sapiens - Amino acids

<400> 944

Met Gln Gly Thr His Trp Pro Leu Thr
1 5

<210> 945
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 945

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 946
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 946

Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5

<210> 947
<211> 13
<212> PRT
<213> Homo sapiens - Amino acids

<400> 947

Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val Asn
1 5 10

<210> 948
<211> 7
<212> PRT

<213> Homo sapiens - Amino acids

<400> 948

Ser Asn Asn Gln Arg Pro Ser
1 5

<210> 949

<211> 11

<212> PRT

<213> Homo sapiens

<400> 949

Ala Ala Trp Asp Asp Ser Leu Asn Gly Val Val
1 5 10

<210> 950

<211> 5

<212> PRT

<213> Homo sapiens - Amino acids

<400> 950

Ser Tyr Ser Met Asn
1 5

<210> 951

<211> 17

<212> PRT

<213> Homo sapiens

<400> 951

Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 952

<211> 15

<212> PRT

<213> Homo sapiens

<400> 952

Gly Ile Ala Ala Ala Gly Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 953

<211> 17

<212> PRT

<213> Homo sapiens - Amino acids

<400> 953

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 954

<211> 15

<212> PRT

<213> Homo sapiens - Amino acids

<400> 954

Glu Tyr Ser Ser Ser Ser Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 955

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 955

Thr Tyr Tyr Xaa Ser
1 5

<210> 956
<211> 17
<212> PRT
<213> Homo sapiens - Amino acids

<400> 956

Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 957
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 957
cgcgcggtccc aggggaatccg gaattacctc gca

33

<210> 958
<211> 10
<212> PRT
<213> Homo sapiens - Amino acids

<400> 958

Arg	Asp	Gly	Tyr	Asn	Tyr	Tyr	Phe	Asp	Tyr
1				5					10

<210> 959
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 959
gccgcctcga ctcttcagag t

21

<210> 960
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 960
cagagataca accgagcgcc ttacaca

27

<210> 961
<211> 11
<212> PRT
<213> Homo sapiens - Amino acids

<400> 961

Gly Ile Ala Val Ala Gly Asn Trp Phe Asp Pro
1 5 10

<210> 962
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 962
actgggagca gttccaacat cggggcaggt tatgatgtac ac

42

<210> 963
<211> 17
<212> PRT
<213> Homo sapiens - Amino acids

<400> 963

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 964
<211> 11
<212> PRT
<213> Homo sapiens - Amino acids

<400> 964

Ser Ile Ala Ala Arg Ala Glu Tyr Phe Gln His
1 5 10

<210> 965

<400> 965
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<210> 966
<211> 10
<212> PRT
<213> Homo sapiens - Amino acids

<400> 966

Asp Tyr Gly Asp Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 967
<211> 9
<212> PRT
<213> Homo sapiens - Amino acids

<400> 967

Arg Trp Leu Gln Leu Tyr Phe Asp Tyr
1 5

<210> 968
<211> 11
<212> PRT
<213> Homo sapiens - Amino acids

<400> 968

Val Glu Met Ala Thr Ile Asp Ala Phe Asp Ile
1 5 10

<210> 969
<211> 10
<212> PRT
<213> Homo sapiens - Amino acids

<400> 969

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

<210> 970
<211> 10
<212> PRT
<213> Homo sapiens - Amino acids

<400> 970

Ser Ile Ala Ala Arg Asp Ala Phe Asp Ile
1 5 10

<210> 971
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<220>
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<222> (14)..(14)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 971

Ser Ile Ser Ser Ser Ser Ser Phe Ile Tyr Tyr Ala Asp Xaa Val Lys
1 5 10 15

Gly

<210> 972
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 972

Ser	Ile	Ser	Ser	Ser	Ser	Ser	Phe	Ile	Tyr	Tyr	Ala	Glu	Ser	Val	Lys
1				5					10					15	

Gly

<210> 973

<211> 17

<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> (9)..(9)

<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> 973

Ser Xaa Ser Ser Ser Ser Ser Phe Xaa Tyr Tyr Xaa Asp Ser Xaa Lys
1 5 10 15

Xaa

<210> 974
<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.

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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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<222> (12)..(12)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>
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<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> 974

Ser Xaa Ser Ser Ser Ser Ser Phe Xaa Tyr Tyr Xaa Glu Ser Xaa Lys
1 5 10 15

Xaa

<210> 975
<211> 17
<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> (12)..(12)
<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>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 975

Ser Xaa Ser Ser Ser Ser Ser Phe Xaa Tyr Tyr Xaa Asp Xaa Xaa Lys
1 5 10 15

Xaa

<210> 976
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (3)..(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.

<220>

<221> MISC_FEATURE

<222> (13)..(14)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 976

Asp	Arg	Xaa	Xaa	Xaa	Pro	Xaa	Thr	Tyr	Tyr	Tyr	Tyr	Xaa	Xaa	Asp	Xaa
1				5					10					15	

<210> 977

<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.

<220>

<221> MISC_FEATURE

<222> (16)..(17)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 977

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

Xaa

<210> 978

<211> 9

<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> 978

Gln Gln Tyr Tyr Ser Xaa Pro Trp Thr
1 5

<210> 979

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 979

Thr Tyr Xaa Xaa His
1 5

<210> 980
<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.

<220>
<221> MISC_FEATURE
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 980

Val	Ile	Trp	Tyr	Asp	Xaa	Ser	Asn	Lys	Asp	Tyr	Ala	Asp	Xaa	Val	Lys
1				5				10					15		

Gly

<210> 981
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 981

Val	Ile	Trp	Tyr	Glu	Gly	Ser	Asn	Lys	Asp	Tyr	Ala	Glu	Ser	Val	Lys
1				5				10					15		

Gly

<210> 982
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(2)
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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.

<220>
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<222> (17)..(17)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 982

Xaa Xaa Trp Tyr Asp Xaa Ser Asn Lys Asp Tyr Xaa Asp Ser Xaa Lys
1 5 10 15

Xaa

<210> 983
<211> 17
<212> PRT
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<220>
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<400> 983

Xaa	Xaa	Trp	Tyr	Asp	Xaa	Ser	Asn	Lys	Asp	Tyr	Xaa	Asp	Xaa	Val	Lys
1				5				10						15	

Gly

<210> 984
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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

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Glu Glu Arg Asp Ser Tyr Tyr His Tyr Xaa Xaa Asp Xaa
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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

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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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<400> 988

Xaa Asn Asn Asn Arg Pro Ser
1 5

<210> 989
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1 5 10

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Gln Ser Tyr Glu Ser Ser Leu Ser Gly Trp Val
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Gln Ser Tyr Asp Ser Ser Xaa Ser Xaa Trp Xaa
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1 5 10

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<400> 994

Ser Tyr Xaa Xaa Ser
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<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
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<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
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<400> 997

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Xaa

<210> 998
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<400> 998

Xaa	Xaa	Ser	Xaa	Ser	Xaa	Xaa	Ser	Thr	Tyr	Tyr	Xaa	Asp	Xaa	Xaa	Lys
1				5					10					15	

Xaa

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1 5 10 15

Xaa

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<400> 1000

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1 5 10

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<400> 1001

Thr Xaa Ser Ser Ser Asn Xaa Xaa Xaa Xaa Tyr Asp Xaa His
1 5 10

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<223> Xaa may be M, G, A, V, I, or L

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<400> 1002

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1 5

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<220>
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<400> 1003

Gly Gln Ser His Arg Pro Ser
1 5

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<400> 1004

Xaa Gln Ser His Arg Pro Ser
1 5

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Gln Ser Tyr Asp Xaa Ser Leu Ser Gly Tyr Val
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<400> 1006

Ser Tyr Glu Ser Ser Leu Ser Gly Tyr Val
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Gln Ser Tyr Asp Ser Ser Xaa Ser Xaa Tyr Xaa
1 5 10

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Gln Ser Tyr Asp Xaa Ser Xaa Ser Xaa Tyr Xaa
1 5 10

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1 5 10

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1 5

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Xaa	Xaa	Ser	Xaa	Arg	Xaa	Xaa	Ser	Thr	Tyr	Tyr	Xaa	Asp	Ser	Xaa	Lys
1				5					10					15	

Xaa

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Asp	Xaa	Tyr	Ser	Ser	Ala	Trp	Tyr	Phe	Asp	Tyr
1				5					10	

<210> 1013
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<220>
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<400> 1013

Glu Gly Tyr Ser Ser Ala Trp Tyr Phe Asp Tyr

1 5 10

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<400> 1014

Asp Xaa Tyr Ser Ser Xaa Trp Tyr Phe Asp Tyr
1 5 10

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Glu Xaa Tyr Ser Ser Xaa Trp Tyr Phe Asp Tyr

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1 5 10

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Asn Tyr Xaa Xaa Asn
1 5

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<400> 1018

Asp Xaa Tyr Ser Ser Ala Trp Phe Phe Asp Tyr
1 5 10

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<211> 11

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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
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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
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<400> 1024

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1 5 10

<210> 1025
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<223> Xaa can be any naturally occurring amino acid

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<400> 1025

Arg Xaa Ser Gln Ser Xaa Thr Ser Tyr Xaa Asn
1 5 10

<210> 1026
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<400> 1026

Thr Xaa Ser Ser Xaa Gln Ser
1 5

<210> 1027
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<212> PRT
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<400> 1027

Ser Asn Ser Xaa Thr Trp Asn
1 5

<210> 1028
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<220>
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<400> 1028

Ser Gln Ser Ala Thr Trp Asn
1 5

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<400> 1030

Arg Thr Tyr Tyr Arg Ser Lys Xaa Tyr Asn Asp Tyr Xaa Xaa Ser Xaa
1 5 10 15

Lys Ser

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<400> 1031

Ser Glu Ser Asn Xaa Asp Xaa Xaa Thr Asn Xaa Xaa Asn
1 5 10

<210> 1032
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<400> 1032

Ser Glu Ser Gln Ser Asp Ile Gly Thr Asn Ala Val Asn
1 5 10

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Ser Glu Ser Gln Ser Asp Xaa Xaa Thr Asn Xaa Xaa Asn
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<210> 1034

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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

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<400> 1035

Ala	Thr	Trp	Asp	Asp	Asn	Leu	Gln	Gly	Pro	Leu
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<210> 1036

<211> 11

<212> PRT

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<400> 1036

Xaa Thr Trp Asp Asp Asn Xaa Gln Xaa Pro Xaa
1 5 10

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<400> 1037

Xaa Phe Tyr Xaa His
1 5

<210> 1038
<211> 17
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<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
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<400> 1039

Trp	Ile	Asn	Pro	Glu	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 1040
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<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
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<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

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<222> (17)..(17)

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<400> 1042

Trp	Xaa	Asn	Pro	Glu	Ser	Xaa	Xaa	Thr	Asn	Tyr	Xaa	Gln	Lys	Phe	Gln
1				5					10					15	

Xaa

<210> 1043
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<400> 1043

Glu Xaa Xaa Xaa Xaa Xaa Xaa Thr Tyr
1 5

<210> 1044
<211> 11
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<400> 1044

Arg Xaa Ser Gln Ser Xaa Ser Ser Tyr Xaa Asn
1 5 10

<210> 1045
<211> 5
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<400> 1045

Xaa Tyr Tyr Trp Ser
1 5

<210> 1046
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<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

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<220>

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<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

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<400> 1048

Glu Xaa Gln His Ser Xaa Arg Thr Asn Tyr Asn Pro Ser Xaa Lys Ser
1 5 10 15

<210> 1049
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Asp Xaa Gly Trp His Phe Ser Phe Asp Ile
1 5 10

<210> 1050
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<400> 1050

Glu Ser Gly Trp His Phe Ser Phe Asp Ile
1 5 10

<210> 1051
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<400> 1051

Asp Ser Xaa Trp His Phe Ser Phe Asp Xaa
1 5 10

<210> 1052
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<400> 1052

Glu Ser Xaa Trp His Phe Ser Phe Asp Xaa
1 5 10

<210> 1053
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<400> 1053

Arg Xaa Ser Gln Xaa Xaa Arg Asn Asp Leu Xaa
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<210> 1054
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<400> 1054

Xaa Xaa Ser Xaa Xaa Gln Xaa
1 5

<210> 1055
<211> 10
<212> PRT
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<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

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<220>

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<400> 1056

Leu	Gln	His	Gln	Ser	Tyr	Pro	Thr	Trp	Thr
1				5					10

<210> 1057

<211> 10

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<400> 1057

Xaa	Gln	His	Gln	Ser	Tyr	Pro	Thr	Trp	Thr
1				5					10

<210> 1058

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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

<210> 1059
<211> 17
<212> PRT
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<220>
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<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
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<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
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<212> PRT
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<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
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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
<211> 10
<212> PRT
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<222> (7)..(8)
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<400> 1063

Glu	Arg	Trp	Phe	Xaa	Glu	Xaa	Xaa	Asp	Tyr
1				5				10	

<210> 1064
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<400> 1064

Arg Xaa Ser Gln Ser Xaa Ser Tyr Tyr Xaa Asn
1 5 10

<210> 1065
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<400> 1065

Gln Gln Ser Tyr Ser Ser Xaa Thr
1 5

<210> 1066
<211> 17
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<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
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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> (12)..(12)

<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>

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<220>

<221> MISC_FEATURE

<222> (17)..(17)

<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

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<220>

<223> Synthetic polypeptide

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<220>

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<222> (4)..(7)

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<220>
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<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
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<400> 1070

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1 5 10 15

Xaa

<210> 1071
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<400> 1071

Glu Xaa Xaa Xaa Xaa Phe Asp Xaa
1 5

<210> 1072
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Arg Xaa Ser Gln Asn Xaa Ser Ser Tyr Xaa Asn
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<400> 1073

Thr Xaa Ser Ser Xaa Gln Ser
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<400> 1074

Glu	Xaa	Asn	Pro	Xaa	Xaa	Arg	Thr	Asn	Tyr	Lys	Pro	Ser	Xaa	Lys	Ser
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<400> 1075

Asp Asn Xaa Trp His Tyr Xaa Phe Asp Xaa
1 5 10

<210> 1076
<211> 10
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<220>
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<400> 1076

Asp Gln Gly Trp His Tyr Ala Phe Asp Ile
1 5 10

<210> 1077
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<400> 1077

Asp Gln Xaa Trp His Tyr Xaa Phe Asp Xaa
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<400> 1078

Arg Ser Ser Gln Ser Xaa Xaa Tyr Ser Asp Xaa Asn Thr Tyr Xaa Asn
1 5 10 15

<210> 1079
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<400> 1079

Arg Ser Ser Gln Ser Leu Val Tyr Ser Asp Gly Gln Thr Tyr Leu Asn
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<210> 1080
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<400> 1080

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1				5					10					15	

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<400> 1081

Lys	Val	Ser	Asn	Trp	Asp	Xaa
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<210> 1082
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<400> 1082

Lys Val Ser Asn Trp Glu Ser
1 5

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Lys Xaa Ser Asn Trp Asp Ser
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<210> 1084
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Lys Xaa Ser Asn Trp Asp Xaa
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<210> 1085

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Lys Xaa Ser Asn Trp Glu Ser
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<210> 1086

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<400> 1086

Xaa Gln Xaa Thr His Trp Pro
1 5

<210> 1087
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<400> 1087

Xaa Tyr Tyr Xaa His
1 5

<210> 1088
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<223> Xaa may independently be M, G, A, V, I, or L

<400> 1088

Trp	Xaa	Asn	Pro	Asn	Xaa	Xaa	Xaa	Thr	Asn	Tyr	Xaa	Gln	Lys	Phe	Arg
1				5					10					15	

Xaa

<210> 1089
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<212> PRT
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<220>
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<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
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<400> 1090

Trp	Xaa	Asn	Pro	Gln	Ser	Xaa	Xaa	Thr	Asn	Tyr	Xaa	Gln	Lys	Phe	Arg
1				5				10						15	

Xaa

<210> 1091
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Xaa Xaa Ser Trp Glu Xaa Phe Asp Tyr

1 5

<210> 1092
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<400> 1092

Xaa Xaa Ser Arg Xaa Gln Ser
1 5

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Gln Gln Ser Asp Ser Thr Pro Xaa Thr
1 5

<210> 1094
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<400> 1094

Gln Gln Ser Phe Ser Thr Xaa Thr
1 5

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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

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<400> 1096

Xaa Xaa Ser Xaa Ser Xaa Xaa Ser Arg Tyr Tyr Xaa Asp Ser Xaa Lys
1 5 10 15

Xaa

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<400> 1097

Xaa	Xaa	Ser	Xaa	Ser	Xaa	Xaa	Ser	Arg	Tyr	Tyr	Xaa	Asp	Xaa	Xaa	Lys
1				5					10				15		

Xaa

<210> 1098
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<400> 1098

Xaa Xaa Ser Arg Xaa Gln Ser
1 5

<210> 1099
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<400> 1099

Gln Gln Ser Asp Xaa Thr Pro Ile Thr
1 5

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<400> 1100

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1 5

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<400> 1101

Gln Gln Ser Asp Xaa Thr Pro Xaa Thr
1 5

<210> 1102
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<400> 1102

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
<212> PRT
<213> Artificial Sequence

<220>
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<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
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<400> 1104

Trp	Xaa	Xaa	Pro	Gln	Ser	Xaa	Xaa	Thr	Asn	Tyr	Xaa	Gln	Lys	Phe	Gln
1				5				10						15	

Xaa

<210> 1105
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<400> 1105

Xaa Ser Ser Trp Glu Xaa Phe Asp Tyr
1 5

<210> 1106

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<400> 1106

Arg Xaa Ser Gln Ser Xaa Ser His Tyr Xaa Asn
1 5 10

<210> 1107

<211> 8

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<400> 1107

Gln Gln Ser Phe Ser Ser Xaa Thr
1 5

<210> 1108

<211> 17

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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

<210> 1109

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<400> 1109

Gly Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Glu Ser Val Lys
1 5 10 15

Gly

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<400> 1110

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1 5 10 15

Xaa

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<400> 1111

Xaa	Xaa	Ser	Xaa	Arg	Xaa	Xaa	Ser	Thr	Tyr	Tyr	Xaa	Asp	Xaa	Val	Lys
1				5					10					15	

Xaa

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<400> 1112

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
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atcacttgcc gggcaagtca gggcattaga aatgacttag gctggatatca ggagaaacca 120
gggaaagccc ctaagcgctt gatctatgct gcatccgggt 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 ccctccaatc gggtactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag 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

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

<210> 1117

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 1117

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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 ctccctcagcc	360
tccaccaagg gcccatcgggt 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
tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttcctc	720
ttccccccaa aacccaagga caccctcatg atctcccga cccctgaggt cacgtgcgtg	780
gtgggtggacg 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 cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag	1080

gtcagcctga cctgcctggg caaaggcttc taccccagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacacctc ccatgctgga ctccgacggc	1200
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1260
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

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

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 tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagtca gaatatattta tacagctcca acaataaaaa ctacttagct 120

tggtaccagc 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

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc	480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc	540
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt 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			

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

caggtgcagt tgggtggagtc tgggggaggc gtgggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt acttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atttggatat 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 ggctgtcaca ctttcccagc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcaa cttcggcacc 600

cagacctaca catgcaacgt agatcacaag cccagcaaca ccaaggtgga caagacagtt 660

gagcgcaaat	gttgtgtcga	gtgcccaccg	tgcccagcac	cacctgtggc	aggaccgtca	720
gtcttcctct	tcccccaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acgtgcgtgg	tggtggacgt	gagccacgaa	gaccccgagg	tccagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccacggg	aggagcagtt	caacagcacg	900
ttccgtgtgg	tcagcgtcct	caccgttgtg	caccaggact	ggctgaacgg	caaggagtac	960
aagtgcaagg	tctccaacaa	aggcctccca	gccccatcg	agaaaaccat	ctccaaaacc	1020
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aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	accccagcga	catcgccgtg	1140
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tccgacggct	ccttcttcct	ctacagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	taaa				1344

$\langle 400 \rangle$ 1122

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	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	
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

<210> 1123

<211> 651

<212> DNA

<213> Homo sapiens

```

<400> 1123
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cttccaggaa cagcccccaa actcctcatc tatggtaata gtcacccggcc ctcagggatc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat      300
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aaggcggggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccagc      540
agctatctga gcctgacgcc tgagcagtgg aagtcaccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

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<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

```

```

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

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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 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

<210> 1125

<211> 1338

<212> DNA

<213> Homo sapiens

<400> 1125

gaggtgcagc tgttgaatc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc aactatgccca 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 cctgggttctt tgactactgg ggccagggaa ccctgatcac 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 tcgagtgtccc accgtgtccc gcaccacctg tggcaggacc gtcagtcttc	720
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gtgggtgggtg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc	840
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gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc	960
aaggtctcca acaaaggcct cccagcccc atcgagaaaa ccatctcca 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 gcaggtggca gcaggggaac	1260
gtcttctcat gtcctgtgat 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

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

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 ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
 agcagagtgg aggctgagga tgttgggggt tattactgca tgcaacctct acaaactccg 300
 ctacttttcg gcggagggac caaggtggag atcaaacgaa ctgtggctgc accatctgtc 360
 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgctagcgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
 agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgcccgtc 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

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
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tcctgtgcag cctctgaatt caccttcagt acctattaca tgagctgggt ccgccaggct 120
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 ccatcggctt tccccctggc gccctgctct 420
agaagcacct ccgagagcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgct ctgaccagcg gcgtgcacac cttcccagct 540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcaac 600
ttcggcacc agacctacac atgcaacgta gatcacaagc ccagcaacac caaggtggac 660
aagacagttg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc acctgtggca 720
ggaccgtcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgaggtca cgtgcgtggg ggtggacgtg agccacgaag accccgaggt ccagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccacggga ggagcagttc 900
aacagcacgt tccgtgtggg cagcgtcctc accgttgtgc accaggactg gctgaacggc 960
aaggagtaca agtgcaaggt ctccaacaaa ggcctcccag ccccatcga gaaaaccatc 1020
tccaaaacca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag 1080
gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta cccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacacctccc 1200
atgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

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

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

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

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

gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagcgtcacc 60

atcacttgcc gggcaagtca gagcattagt tactatttaa attggtatca acagaaacca 120

gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaaagtg 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
agctcgcccg 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

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

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtgggtgggtg 780

gacgtgagcc acgaagaccc cgagggtccag ttcaactggc acgtggacgg cgtggagggtg	840
cataatgcca agacaaaagcc acgggaggag cagttcaaca gcacgttccg tgtgggtcagc	900
gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caagggtctcc	960
aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga	1020
gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccagggtcagc	1080
ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat	1140
gggcagccgg agaacaacta caagaccaca cctcccatgc tggactccga cggctccttc	1200
ttcctctaca gcaagctcac cgtggacaag agcagggtggc 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

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

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

atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagagacca 120

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gggaaagccc ctaacctcct gctctttact gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggtatc tgggacagat ttactctca ccatcaacag tctgcaacct      240
gaggattttg caacttacta ctgtcaacag agttacagta accctcctga gagcagtttt      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 gctcgcccgt cacaaagagc ttcaacaggg gagagtgt      648

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<210> 1136
<211> 216
<212> PRT
<213> Homo sapiens

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```

<400> 1136

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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 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 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> 1137

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 1137

cagggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

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 ttcagcctcc 360

accaagggcc catcggcttt ccccttggcg ccctgctcta gaagcacctc cgagagcaca	420
gcggcccttg 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 gcgcaaattgt	660
tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc	720
ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac 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
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc	1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg	1320
tctccgggta aa	1332

<210> 1138

<211> 444

<212> PRT

<213> Homo sapiens

<400> 1138

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 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	
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

<210> 1139
<211> 651
<212> DNA
<213> Homo sapiens

<400> 1139
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tcctgcactg ggagcagctc caacatcggg gcagggttata 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 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> 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

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

Lys Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 1141

<211> 1347

<212> DNA

<213> Homo sapiens

<400> 1141

gaaatacagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactt	60
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ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtgtag cacatactac	180
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
accagacct acacatgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca	660
gttgagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggaggaccg	720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccc gaccctgag	780
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acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag	960
tacaagtgca aggtctcaa caaaggcctc ccagcccca tcgagaaaac catctcaaaa	1020
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accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg	1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag cagggtggcag	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

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

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

aggtttagtg gcagtgggtc tgggacagat ttactctca 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

agctcgcccc 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

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 tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

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ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggtag cagatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc 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

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg cgtgggtggtg 780

gacgtgagcc acgaagaccc cgagggtccag ttcaactgggt acgtggacgg cgtggagggtg 840

cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg tgtgggtcagc 900

gtcttcaccg	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	agcaggtggc	agcaggggaa	cgctcttctca	1260
tgctccgtga	tgcattgaggc	tctgcacaac	cactacacgc	agaagagcct	ctccctgtct	1320
ccgggtaaa						1329

<400> 1146

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

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

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 ttactctca ccatcagcag tctgcaacct 240

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> 1149

<211> 1347

<212> DNA

<213> Homo sapiens

<400> 1149

caggtagcagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60

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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 cctgggtcacc 360

gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc 420

acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

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

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

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

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atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttactctca 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 gctcgcccgt cacaaagagc ttcaacaggg gagagtgt      648
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<210> 1152

<211> 216

<212> PRT

<213> Homo sapiens

<400> 1152

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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 Ser Ser Tyr
20           25           30
```

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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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 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 ggttactact ggagctggat ccgccagccc	120
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 ttcagcctcc	360
accaagggcc catcggctct cccctggcgc 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
tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc	720
ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac 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 ggacgcaggg gaacgtcttc	1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg	1320
tctccgggta aa	1332

<210> 1154
<211> 444
<212> PRT
<213> Homo sapiens

<400> 1154

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

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

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 gagtggttat 300
 gtcttcggaa ctgggaccaa ggtcaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
 actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc 420
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 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540
 agctatctga gcctgacgcc tgagcagtg aagtcacaca gaagctacag ctgccaggtc 600
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<210> 1156

<211> 217

<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

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 cagctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagacggg 300

tatagcagtg cctgggtactt tgactactgg ggccaggga ccttggtcac 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 cgtggtgacc gtgccctcca gcaacttcgg caccagacc 600

tacacatgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 660

aaatgttgtg tcgagtggcc accgtggcca gcaccacctg tggcaggacc gtcagtcttc 720

ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc 780

gtggtgggtg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaaagcca cgggaggagc agttcaacag cacgttccgt 900

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 960

aaggtctcca acaaaggcct cccagcccc atcgagaaaa ccatctccaa aaccaaaggg 1020

cagccccgag	aaccacaggt	gtacaccctg	cccccatccc	gggaggagat	gaccaagaac	1080
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gagagcaatg	ggcagccgga	gaacaactac	aagaccacac	ctcccatgct	ggactccgac	1200
ggctccttct	tcctctacag	caagctcacc	gtggacaaga	gcaggtggca	gcaggggaac	1260
gtctttctcat	gctccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1320
tcctgtctc	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

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

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

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 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

$\langle 210 \rangle$ 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

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 ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cagctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtggt 300

accaactatt actactacta ctccggtatg gacgtctggg gccaaaggac cacggtcacc 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	ggcaggaccg	720
tcagtcttcc	tcttcccccc	aaaacccaag	gacaccctca	tgatctcccc	gacccctgag	780
gtcacgtgcg	tggtggtgga	cgtgagccac	gaagaccccg	aggtccagtt	caactggtac	840
gtggacggcg	tggaggtgca	taatgccaa	acaaagccac	gggaggagca	gttcaacagc	900
acgttccgtg	tggtcagcgt	cctcaccgtt	gtgcaccagg	actggctgaa	cggcaaggag	960
tacaagtgca	aggtctccaa	caaaggcctc	ccagccccca	tcgagaaaac	catctccaaa	1020
accaaagggc	agccccgaga	accacaggtg	tacaccctgc	ccccatcccc	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

<400> 1162

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

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

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 attggatatca gcagaaacca 120
 gggaaagccc ctgagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caagttactt ctgtcaacag agttacagta cccctcgcag ttttggccag 300
 gggaccaagc tggagatcaa 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
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<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

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

cagggtacaac tgcagcagtc aggtccagga ctggtgaagc cctcgagac cctctcactc

60

acctgtgcc	tctccgggga	cagtgtctct	agcagcagtg	ctacttggaa	ctggatcagg	120
cagtccccat	cgagaggcct	tgagtggctg	ggaaggacat	accagaggtc	caagtggaat	180
aatgattatg	cagtatctgt	gaaaagtcga	ataaccatca	acccagacac	atccaggaac	240
cagttctccc	tgcagctgaa	ctctgtgact	cccgaggaca	cggctgtgta	ttactgtgca	300
agagaagtag	tggctggccc	gaggtggttc	gacccctggg	gccagggaac	cctggtcacc	360
gtctcctcag	cctccaccaa	gggcccacgc	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
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gttgagcgca	aatgttgtgt	cgagtgccca	ccgtgcccag	caccacctgt	ggcaggaccg	720
tcagtcttcc	tcttcccccc	aaaacccaag	gacaccctca	tgatctcccg	gacccctgag	780
gtcacgtgcg	tgggtgggga	cgtagaccac	gaagaccccg	aggtccagtt	caactgggtac	840
gtggacggcg	tggagggtgca	taatgccaag	acaaagccac	gggaggagca	gttcaacagc	900
acgttccgtg	tggtcagcgt	cctcaccgtt	gtgcaccagg	actggctgaa	cggcaaggag	960
tacaagtgca	aggtctccaa	caaaggcctc	ccagccccca	tcgagaaaac	catctccaaa	1020
accaaagggc	agccccgaga	accacagggtg	tacaccctgc	ccccatcccg	ggaggagatg	1080
accaagaacc	aggtcagcct	gacctgcctg	gtcaaaggct	tctaccccag	cgacatcgcc	1140
gtggagtggg	agagcaatgg	gcagccggag	aacaactaca	agaccacacc	tcccatgctg	1200
gactccgacg	gtccttctt	cctctacagc	aagctcaccg	tggacaagag	caggtggcag	1260
caggggaacg	tcttctcatg	ctccgtgatg	catgaggctc	tgcaacaacca	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

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

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

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

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<210> 1167
<211> 648
<212> DNA
<213> Homo sapiens
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<400>	1167					
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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	tgggtccgcta	300
ttcggcggag	ggaccaagct	gaccgtccta	ggtcagccca	aggctgcccc	ctcggtcact	360
ctgttcccg	cctctagcga	ggagcttcaa	gccacaagg	ccacactggg	gtgtctcata	420
agtgacttct	acccgggagc	cgtgacagtg	gcctggaagg	cagatagcag	ccccgtcaag	480
gcgggagtg	agaccaccac	accctccaaa	caaagcaaca	acaagtacgc	ggccagcagc	540
tatctgagcc	tgacgcctga	gcagtggaag	tcccacagaa	gctacagctg	ccaggtcacg	600
catgaaggga	gcaccgtgga	gaagacagtg	gcccctacag	aatgttca		648

$\langle 210 \rangle$	1168
$\langle 211 \rangle$	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

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

<213> Homo sapiens

<400> 1169

caggtgcaac tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgagggtc 60

tcctgcaagg cttctggata caccttcacc ggcttctata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaaccctg acagtgggtg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaaca cgtccatcag cacagcctac 240

atggagttga gtaggctgag atctgacgac acggccgtat attactgtgc gagagagggt 300

atagcagtgg ctcttaccta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggctctt cccctggcg 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 gcgcaaattgt 660

tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc 720

ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgagggtcac gtgcgtgggtg 780

gtggacgtga gccacgaaga ccccgagggtc cagttcaact ggtacgtgga cggcgtggag 840

gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtgggtc 900

agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaagggtc 960

tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc 1020

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cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc      1080
agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc      1140
aatgggcagc cggagaacaa ctacaagacc acacctccca tgctggactc cgacggctcc      1200
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc      1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg      1320
tctccgggta aa                                                                1332

```

<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

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

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 agtcagcca gagtgtttta tacagctcca acaataaaaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct agcctgctca tttactgggc atctaccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcaacaata ttatagtatt 300

ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaac gaactgtggc tgcaccatct 360

gtcttcatct	tcccgccatc	tgatgagcag	ttgaaatctg	gaactgctag	cgttggtgtgc	420
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> 1172

$\langle 211 \rangle$ 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 50 Ser Leu Leu Ile 55 Tyr Trp Ala Ser Thr Arg 60 Glu Ser Gly Val

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

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
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 ccaggcaagg ggctggagtg ggtggcagtt atttggatat 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 accgggtgacg 480
 gtgtcgtgga actcaggcgc tctgaccagc ggctgtcaca ctttcccagc tgtcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcaa cttcggcacc 600

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

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

<210> 1175

<211> 639

<212> DNA

<213> Homo sapiens

<400> 1175

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atcacttgcc gggcaagtca gagcattagc cactatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca      180
aggtttagtg 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
```

```
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
 <213> Homo sapiens

<400> 1177	
gaggtgcacc tgttggagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc	60
tcttgtgcag cctctggatt cacctttagc agttatgccca tgagttgggt cgcagggtt	120
ccagggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac	180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatgg acagcctgag agccgaggac acggccgtat ataactgtgc gatagaagtg	300
gctggggcctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc	360
aaggggcccat cgggtcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgc 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 aggacaccct catgatctcc cggacccctg aggtcacgtg cgtgggtgggtg	780
gacgtgagcc acgaagaccc cgaggtccag ttcaactgggt acgtggacgg cgtggaggtg	840
cataatgcca agacaaaagcc 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

<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
	20		
Ser	Cys	Ala	Ala
		25	
Ser	Gly	Phe	Thr
			Phe
Ser			30
Ser	Ser	Tyr	
Ala	Met	Ser	Trp
	35		
Val	Arg	Gln	Val
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Val
Ser	Gly	Ile	Ser
	50		
Gly	Arg	Gly	Gly
		55	
Ser	Thr	Tyr	Tyr
			60
Ala	Asp	Ser	Val
Lys	Gly	Arg	Phe
	65		
Thr	Ile	Ser	Arg
	70		
Asp	Asn	Ser	Lys
		75	
Asn	Thr	Leu	Tyr
			80
Leu	Gln	Met	Asp
		85	
Ser	Leu	Arg	Ala
			Glu
			90
Asp	Thr	Ala	Val
			Tyr
			95
Asn	Cys		
Ala	Ile	Glu	Val
		100	
Ala	Gly	Ala	Phe
			105
Asp	Ile	Trp	Gly
			Gln
			110
Gly	Thr	Met	
Val	Thr	Val	Ser
		115	
Ser	Ser	Ala	Ser
			120
Thr	Lys	Gly	Pro
			Ser
			125
Val	Phe	Pro	Leu
Ala	Pro	Cys	Ser
			130
Arg	Ser	Thr	Ser
			135
Glu	Ser	Thr	Ala
			140
Ala	Leu	Gly	Cys
Leu	Val	Lys	Asp
			145
Tyr	Phe	Pro	Glu
			150
Pro	Val	Thr	Val
			155
Ser	Trp	Asn	Ser
			160
Gly	Ala	Leu	Thr
			165
Ser	Gly	Val	His
			170
Thr	Phe	Pro	Ala
			Val
			175
Leu	Gln	Ser	
Ser	Gly	Leu	Tyr
			180
Ser	Leu	Ser	Ser
			185
Val	Val	Thr	Val
			190
Pro	Ser	Ser	Asn
Phe	Gly	Thr	Gln
			195
Thr	Tyr	Thr	Cys
			200
Asn	Val	Asp	His
			Lys
			205
Pro	Ser	Asn	

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

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

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 gggacagccc ctaagttcct gatctatggc gcatcccggt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca 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
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<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

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> 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 acagtgggtg cacaaattat	180
gcccagaagt ttcagggcag ggtcaccatg accaggggaca cgtccatcag cacagcctac	240
atggaaactga gcaggctgag atctgacgac acggccgttt attactgtgc gactggcagc	300
agctgggagg gatttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc	360
accaagggcc catcggctct cccctggcg ccctgctcta gaagcacctc cgagagcaca	420
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tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggg gaccgtgccc tccagcaact tcggcaccca gacctacaca	600
tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaagt	660
tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc	720
ccccaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac 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 gcctgtgcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc	1140
aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc	1200
ttcttcctct acagcaagct caccgtggac aagagcagggt 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

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		
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		
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

<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

agcagggtgg aggctgagga tgttgggggtt tattactaca tgcaaggtag acactggcct 300

ctcggcggag ggaccaaggt ggagatcaaa cgaactgtgg ctgcaccatc tgtcttcatc 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

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

<213> Homo sapiens

<400> 1185

cagggacagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgccagg cttctggata caccttcacc gcctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggttgg atcaacccta acagtgggtg cacaaactat 180

gcacagaagt ttcggggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggaaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gactggcggc 300

agctgggagg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggctct cccctggcg ccctgctcta gaagcacctc cgagagcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcaact tcggcaccca gacctacaca 600

tgcaacgtag atcacaagcc cagcaacacc aagggtggaca agacagttga gcgcaaattgt 660

tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc 720

ccccaaaaac ccaaggacac cctcatgata tcccggaccc ctgagggtcac gtgcgtgggtg 780

gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag 840

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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 acacctccca tgctggactc cgacggctcc     1200
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg 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

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<400> 1186
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Gln Gly Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5           10           15

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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

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

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

gacatccaga tgacccagtc tccatcgctc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca 180

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aggttcagtg gcagtggatc tgggacagat ttactctca 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
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
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<210> 1188

<211> 214

<212> PRT

<213> Homo sapiens

<400> 1188

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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 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

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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
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
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 1189
 cagtcctatg acagcagcct gagggttcg gtg

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
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

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

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> 1191
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1191
caccatggac tggacctgga ggatc 25

<210> 1192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1192
caccatggac tggacctgga gcatc 25

<210> 1193
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1193
caccatggac tgcacctgga ggatc 25

<210> 1194
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1194
caccatggac tggacctgga gaatc 25

<210> 1195
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1195
caccatggac tggacctgga ggg 23

<210> 1196
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1196
caccatggac tggatttgga ggatcc 26

<210> 1197
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1197
caccatggac acactttgct ccacg 25

<210> 1198
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1198
caccatggac acacttttgct acacactcc 29

<210> 1199
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1199
caccatggag tttgggctga gctg 24

<210> 1200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1200
caccatggaa ttggggctga gctg 24

<210> 1201
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1201
caccatggag ttggggctga gctg 24

<210> 1202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide
 <400> 1202
 caccatggaa ctggggctcc gc 22

<210> 1203
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
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 <400> 1203
 caccatggaa tttgggctga gctgg 25

<210> 1204
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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 <400> 1204
 caccatggag ttggggctgt gctg 24

<210> 1205
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide
 <400> 1205
 caccatggag tttgggctta gctgg 25

<210> 1206
 <211> 25
 <212> DNA
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<220>
 <223> Synthetic polynucleotide

<400> 1206
caccatggag ttttggctga gctgg 25

<210> 1207
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1207
caccatgaaa cacctgtggt tcttcctc 28

<210> 1208
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1208
caccatgaag cacctgtggt tcttcc 26

<210> 1209
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1209
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<210> 1210
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1210
caccatgggg tcaaccgcca tcc 23

<210> 1211
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1211
caccatgtct gtctccttcc tcatcttc 28

<210> 1212
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1212
gctgaggag tagagtcctg aggactgt 28

<210> 1213
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1213
caccatggac atgagggtcc ccg 23

<210> 1214
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1214
caccatggac atgagggtcc ctgc 24

<210> 1215
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1215
 caccatggac atgagggtcc tcgc 24

<210> 1216
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1216
 caccatgagg ctccctgctc agc 23

<210> 1217
 <211> 26
 <212> DNA
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 <220>
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 <400> 1217
 caccatgagg ctccttgctc agcttc 26

<210> 1218
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1218
 caccatggaa accccagcgc agc 23

<210> 1219
 <211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1219
caccatggaa gccccagcgc ag 22

<210> 1220
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1220
caccatggaa gccccagctc ag 22

<210> 1221
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1221
caccatggaa ccatggaagc cccag 25

<210> 1222
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1222
caccatggtg ttgcagaccc aggtc 25

<210> 1223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1223
caccatgggg tcccaggttc acc 23

<210> 1224
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1224
caccatgttg ccatcacaac tcattggg 28

<210> 1225
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1225
caccatgggtg tccccgttgc aattc 25

<210> 1226
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1226
acccgattgg agggcgttat ccacc 25

<210> 1227
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1227

caccatggcc tgggtcccctc tc

22

<210> 1228

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1228

caccatggcc tgggtctcctc tcc

23

<210> 1229

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1229

caccatggcc agcttccctc tcc

23

<210> 1230

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1230

caccatggcc ggcttccctc tc

22

<210> 1231

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1231
caccatgacc tgctccccctc tcc 23

<210> 1232
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1232
caccatggcc tgggctctgc tc 22

<210> 1233
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1233
caccatggcc tgggctctgc tg 22

<210> 1234
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1234
caccatggca tggatccctc tcttc 25

<210> 1235
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1235
caccatggcc tggaccgctc tc 22

<210> 1236
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1236
caccatggcc tggacccctc tc 22

<210> 1237
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1237
caccatggcc tggatccctc tcc 23

<210> 1238
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1238
caccatggcc tggaccgttc tcc 23

<210> 1239
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1239
caccatggca tgggccacac tcc 23

<210> 1240
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1240
caccatggcc tggatccctc tac 23

<210> 1241
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1241
caccatggcc tgggtctcct tctac 25

<210> 1242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1242
caccatggcc tggacccaac tcc 23

<210> 1243
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1243
caccatggct tggacccac tcc 23

<210> 1244
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1244
caccatggcc tggactcctc tcc 23

<210> 1245
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1245
caccatggcc tggactcctc ttcttc 26

<210> 1246
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1246
caccatggcc tggactcttc tccttc 26

<210> 1247
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1247
caccatggcc tgggctccac tac 23

<210> 1248
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

 <400> 1248
 caccatggcc tggactcctc tctttc 26

 <210> 1249
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1249
 caccatggcc tggatgatgc ttctcc 26

 <210> 1250
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1250
 caccatggcc tgggctcctc tg 22

 <210> 1251
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic polynucleotide

 <400> 1251
 caccatgccc tgggctctgc tc 22

 <210> 1252
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic polynucleotide

<220>

<221> misc_feature

<222> (8)..(8)

<223> K is G or T.

<400> 1252

ggagggtktg gtggtctcca ctccc

25

<210> 1253

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1253

gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaaccc 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 cttcccgcc 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaaag caccctgacg 540

ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1254

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1254

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

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

<400> 1255
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 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> 1256
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1256

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 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>
 <223> Synthetic polynucleotide

<400> 1257
 gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
 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
 agtgcctcca ccaaggggcc atcggcttcc cccctggcac cctcctccaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccag 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
 tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgtgtga ggagcagtac 900
 ggagcagcgt 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 gtcctcacc	1440
tgcgctgtcc atggtgggtc cttcagtgggt 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 ctcctcagcc	1740
tccaccaagg gcccacgggt 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> 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
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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 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

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

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

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
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaacc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaaag tcgagatcaa gcgtacggtg 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

<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

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
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 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 aggggagaggt 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

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
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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
agtcctcca ccaaggggccc 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
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
tggtagctgg 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
tgactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagccccca	1500
ggtaaggggac 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
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> 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

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

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

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

<400> 1265
gatatccaaa 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 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> 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				

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>
<223> Synthetic polynucleotide

<400> 1267
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> 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

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

<220>
<223> Synthetic polynucleotide

<400> 1269
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
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
agtcctcca ccaagggcc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcaccag 600

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
tggtagctgg 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
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 ccgctacggt 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 agcgtgggtga ccgtgccctc cagcagcttg	1980
ggcaccacga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	2040
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

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

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

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

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

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 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 cgcggccgag	540
agctatctga gcctgacgcc tgagcagtgg 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

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
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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 ttgcagtgtg 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

```

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<210> 1274
<211> 214
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic polypeptide

```

```

<400> 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

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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cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tgggggtcttg 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 gacaagaaaag 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
aaggctctca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg	1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1140
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gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtgca gttacagcag	1380
tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt	1440
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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 cagcctccac caagggccca	1740
tcggctcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	1800
tgcttggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg	1860

accagcggcg tgcacacctt cccggctgtc ctacagtctt caggactcta ctccctcgag	1920
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat	1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaatcttg 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

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

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

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>

<223> Synthetic polynucleotide

<400> 1277

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc

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 tctaccggg 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> 1278

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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			

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

<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 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

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```

<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

```

```

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1281
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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180

agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tggggctcttg actactgggg ccaggggaacc ctggtcaccg tctctagtgct ctccaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag 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 ccatctccaa agccaaaggg	1020
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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tggattggct atatctatta cagtgggcag accaaaataca acccctccct caagagtcga	1560
gtcaccatat caatagacac gtccaagaac cagtttctccc tgaagctgag ctctgtgacc	1620
gctgcggaca cggccgtgta ttactgtgct agagaaactg ggagctacta cggctttgac	1680

tactgggggcc	agggaaccct	ggtcaccgtc	tcctcagcct	ccaccaaggg	cccatcggtc	1740
ttccccctgg	caccctcctc	caagagcacc	tctggggggca	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	ccaaggtgga	caagaaagtt	gagcccaaat	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

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

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

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

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

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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 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> 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

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

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
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tggtaccagc agaaaccagg aaaggttcct 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
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<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

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 ccggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg	120
cccgaggaaag 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 cgggtgcgtg 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 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 ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtaca gttgcaggag	1380
tcaggccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg	1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc	1500

cttgagtgga	taggaaggac	atactacagg	tccaagtgg	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	gcccacggt	cttccccctg	gcacctcct	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>	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

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

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

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

<220>
<223> Synthetic polynucleotide

<400> 1289
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 cttcccgcc 360
tctgatgagc agttgaaatc tggtagcgcc 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 aggggagaggt 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

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
<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 ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 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 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

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> 1293
<211> 2046
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1293
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 cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca 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 caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg 840
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc 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 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 tccgggtggt ggcggatcgg gaggtggcgg atccgaggta	1380
caactggtgg aatcagggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga	1500
aaagggtcgc agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctctacttg	1680
tctacagctt cgtcgtcga ctattggggt caaggaacgt 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 gcttgggcac ccagacctac	1980
atctgcaacg tgaatcacaa gcccagcaac accaagggtgg 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

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

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

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

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 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> 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

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
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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 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> 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

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
 cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 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
 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 aagacaaaagc 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 accagggtcag cctgacctgc ctggtcaaag 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 gggtgcgcca gatgcccggg	1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg	1560
tccttccaag gccagggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag	1620
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt	1680
cttgactact ggggccaggg aaccctgggt accgtctcta gtgcctccac 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> 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

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

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

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
<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 ttactctca 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 gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt 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

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

<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
aggtttagcg ggtccgggtc aggtacggac ttactctca 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> 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

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
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
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaatct 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 aagccgtgtg aggagcagta cggcagcacg	900
taccgttgtg 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 ggtacaactg	1380
gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca	1440
tcggggttta 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 gggtaagga acgttgggtc ccgtctctag tgcctccacc	1740
aagggcccat cggctctccc 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> 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

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

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

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

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 ttcacttca 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 gcctcgagag caccctgacg 540

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

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 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 tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag 540
agctatctga gcctgacgcc tgagcagtg 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

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 agaaaactggg 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

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
taccgttggtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg 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 ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggagggtg 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 gggctcttgac	1680
tactggggcc agggaaacct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc	1740
ttccccctgg caccctctc 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 ccaagggtga caagaaagt 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

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

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

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1313
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttcct aaactgctca tttactgggc atctacccgg 180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc 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 aacacaaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaaga gcttcaacag gggagagtgt	660

<210> 1314
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <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		

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

<210> 1315
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1315
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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 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> 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		

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> 1317
<211> 2061
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1317
caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 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 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
aagaaagtgt agcccaaata 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
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtgta 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 ggtggagggt tggtgcagcc 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 ggggtcaagg aacgttggtc	1740
accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag	1800
agcacctctg ggggcacagc ggccctgggc tgcttggtca aggactactt ccccgaaccg	1860
gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	1920
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg	1980

ggcaccacaga 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

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

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

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

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 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
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc	480
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

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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 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> 1321
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1321
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tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 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 tctaccggg 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
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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

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

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cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggct caagtgggtat 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
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 cacagggtgta caccctgccc	1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	1140
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accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg	1260
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cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat	1560
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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	gcttggggcac	ccagacctac	1980
atctgcaacg	tgaatcacia	gccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

<210>	1324
<211>	682
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

$\langle 400 \rangle$ 1324

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

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

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

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

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

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> 1325

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1325

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gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgccaa      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
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<210> 1326

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1326

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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 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

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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
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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 cctcatgac	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 tccaacaaag ccctcccagc ccccatcgag	1020
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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc	1500
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tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	1620
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga	1680
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaacct agtcaccgtc	1740
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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
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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

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

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

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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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 gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttccccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tggggcaccca 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

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 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 aggggagaggt 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

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 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
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
tcccggaccc 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
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 tggtaggctcc 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 ggccagggaa ccctgggtcac cgtctcctca	1740
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	1800
ggcacagcgg ccctgggctg cctgggtcaag 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

<210> 1334
 <211> 683
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1334

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

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

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

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> 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 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 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 gcccaaattct 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

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 ctgtctgctg ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttacttgggc atctaccggg 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 aacacaaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1338
<211> 220
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1338

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

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 catcgggggt 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
agtacggtgg ctgcaccatc tgtcttcac ttcccggcat 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
tcccggaccc 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
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 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
accacgggtca cagtctctc agcctccacc aaggggcccat cggctcttccc cctggcaccc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtctc 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

<400> 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

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

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

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 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
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg 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 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	

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
 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 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> 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

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
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 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 gcccaaggcc 360
 aacccactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
 ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
 ggagccccg 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 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 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 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 ccagggaacc ctagtcaccg tctcctcagc ctccaccaag	1740
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	1800
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg gaactcaggc	1860
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc	1920
ctcgagagcg tggtgaccgt gccctccagc agcttgggca ccagaccta 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

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

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

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

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 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 tgcctacag tcctcaggac tctactccct cgaaagcgtg	540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag	600
cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt	645

<210> 1348
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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 ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg 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> 1350
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<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

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
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360
aaccctactg 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 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 tcgggagggtg gcggatccca ggtgcagctg	1380
caggagtccg 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 cagcctccac caagggccca	1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	1800
tgcctggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccctg	1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag	1920

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1980

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 2031

<210> 1352

<211> 677

<212> PRT

<213> Artificial Sequence

<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

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

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

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
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> 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	

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
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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> 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	

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
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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 ggccctcggac accgccatgt attactgtgc gagaagtaac	300
tgggggtcttg 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 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 tgggtggcga tcgggagggtg gcggatccca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg	1500
aaaggccttg agtggatagg aaggacatac tacagggtcca 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	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggtg	1860
tcgtggaact	caggcgcctt	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	1920
tcaggactct	actccctcga	gagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	1980
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	2040
cccaaattctt	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

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

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

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

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

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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 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 ccaagggtgga caagaaagtt gagcccaaat cttgt                      645
```

<210> 1360

<211> 215

<212> PRT

<213> Artificial Sequence

<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

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

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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 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

<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

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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ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt	300
agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca	360
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga	420
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg	480
aaggtggata acgcccctca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc	540
aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa	600
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccggt cacaaagagc	660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc	720
ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	780
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aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa	1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtaaaagg cttctatccc	1140
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gcgcctggaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat 1560
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 taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc 1680
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 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 1920
 tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980
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 gagcccaa at cttgt 2055

<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

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

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

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
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 cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tggggcaccca 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

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

<400> 1367
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggaaca 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> 1368
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1368

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

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>
<223> Synthetic polynucleotide

<400> 1369
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 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 caaaaaccca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagtg caaggctctc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
cctcccgctg tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260

agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1320
 cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga 1380
 tccgagggtgc 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 gggccaggga accctgggtca ccgtctctag tgcctccacc 1740
 aaggggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
 tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac 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

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

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

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

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 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 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 tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaaagttga gcccaaatct tgt 633

<210> 1372
<211> 211
<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

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 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 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> 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

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
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 actgtgcgag 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
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt ccccccaaaa 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
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 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> 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

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

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

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

<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 ttactctca 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
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gccc aaatct 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

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>
<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 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 aagtcacaca 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

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

<220>
<223> Synthetic polynucleotide

<400> 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
gctgcacat 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

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 cggatccgag	1380
gtgcagctgg tgcagtctgg agcagagggtg 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 actgtgagag aagtaactgg	1680
ggtcttgact actggggcca gggaaccctg gtcaccgtct ctagtgctc caccaagggc	1740
ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac 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 agcccaaatac ttgt	2034

<210> 1382
 <211> 678
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

<400> 1382

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

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

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

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

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 gcagtggatc tgggacagat ttcacttca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggctctt 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 agaaaagttga gccc aaatct tgt 633

<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

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
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> 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

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
caggtagcgt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaaccagtg ttgcttgga cttgattagg 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 tgctgtgta ataacttcta tcccagagag 480
gccaaagtac agtggaagggt ggataacgcc ctccaatcgg gtaactccca ggagagtgtc 540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660

cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac	780
accctcatga tctcccgac 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
gccccatcg agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acagggtgtac	1080
accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gaggggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga	1380
tcgggagggtg gcggatccga ggtacaactg gtggaatcag gtggagggtt ggtgcagccg	1440
gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg	1500
cattgggtcc ggcaagcgcc tggaaaagg ctcgagtggtg 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 aaggggccat cggctctccc cctggcaccc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc	1980
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	2040
gtggacaaga aagttgagcc caaatcttgt	2070

<210> 1388
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1389
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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 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> 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
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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

Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215

<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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

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
caggtacagt 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 ctctgtttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtgggaagg 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 tggaggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgtttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca	1020
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	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 ggtgcagctg gtgcagtctg gagcagagg gaaaaagccc	1440
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc	1500
ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggg	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctttgac tactggggcc agggAACcct ggtcaccgtc	1740
tctagtgcct ccaccaaggg cccatcgggtc 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	ccaaggtgga	caagaaagtt	2040
gagcccaa	attgt					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
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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

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

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

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

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

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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
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc      420
tgcctggtca aggactactt ccccgaaacc gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t              651
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<210> 1396

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1396

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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 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> 1397

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1397
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaaccc 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 cttcccgcca 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

<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

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
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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
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
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca 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 cagggtgtaca 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
tgcgctgtcc atggtgggtc cttcagtgggt tactactgga actggattcg ccagccacca	1500
gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaacccg	1560

tcctctaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg	1620
ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgcgagagg atattgtaga	1680
agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctcctcaact	1740
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact	1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag	1860
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag	1920
gacagcacct acagcctcga aagcacctg acgctgagca aagcagacta cgagaaacac	1980
aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc	2040
aacaggggag agtgt	2055

$\langle 210 \rangle$	1400
$\langle 211 \rangle$	685
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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

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

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

<210> 1401
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1401
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgtaga 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 acgagcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttccccgctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaaagttga gcccaaattct 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

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
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 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

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

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
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc	300
tacttgtcta cagcttcgtc gctcgactat tggggctcaag gaacgttgggt caccgtctct	360
agtgccctcca ccaagggccc atcggctctt cccctggcac cctcctcaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccagg	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtgggt 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
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 cggatcccag	1380
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc	1440
tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagccccca	1500
ggtaagggac tggagtggat tggctatatc tattacagtg ggagaccaa 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> 1406
 <211> 683
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1406

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

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

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

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
gggaaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggctctt ccccctggca 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 agaaaagttga 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

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 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 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> 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

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggt 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 gaacgttggt caccgtctct 360
agtgccctcca ccaaggggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
ggggggcacag 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
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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
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 gtgtataat	1560
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag	1620
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga	1680
gaggatgggg atagctacta ccgctacgg atggacgtct ggggccaagg gaccacggtc	1740
accgtctcct caactgtggc 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> 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

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

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

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

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 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
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctggtca aggactactt ccccgaaaccg gtgacgggtgt cgtggaactc aggcgccctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

651

<210> 1414

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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 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 tctaccggg agccgtgaca gtggcctgga aggagatag cagccccgtc 480
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgcccgag 540
 agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1416
<211> 217
<212> PRT
<213> Artificial Sequence

<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

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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaaag 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 gaaccggtga cggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagacctt catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggacccctga	ggtcacatgc	780
gtgggtgg	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
tccctgtctc	cgggtgggtg	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	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

<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

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

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

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

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 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 tggggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gccc aaatct 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

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
 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 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
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

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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

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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 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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaaag 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
ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540

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 ataatagcaa 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 ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcagggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tcctgtctc 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
tactggggcc agggaaaccct ggtcaccgtc tcctcaactg tggctgcacc atctgtcttc	1740
atcttcccg ccatctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	1800
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg	1860
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcgaa	1920
agcacctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	1980
acccatcagg gcctgagctc gccggtcaca 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
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

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

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

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

<210> 1425
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1425
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 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 agaaagttga gcccaaattct tgt	633

<210> 1426
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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> 1427
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1427
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
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
 agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1428
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1428

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

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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tgggggtcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360

ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag 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
aaggctctca 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 gcagggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag	1380
tcaggccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg	1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc	1500
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ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg	1620
agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc	1680
tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcaact	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> 1430
 <211> 685
 <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

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

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

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
tgggtaccagc agaaaccagg aaaggttcct 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
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> 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

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

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

<400> 1435
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tccatggtgg gtccttcagt gggttactact ggaactggat ccgccagcca 120

ccaggggaagg ggctagagtg gattgggggaa atcaatcatg ctggaaacac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgctgacct ctgtgaccgc cgcggaacacg gctgtgtatt actgtgagag aggatattgt	300
agaagtacca 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 cgtggtgacc 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 ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc	900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc 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 tccgggtggt ggcggatcgg gaggtggcgg atccgaggta	1380
caactgggtg aatcagggtg aggtttggtg cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgccctgga	1500
aaagggtctg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1620

atgaactcac	ttcgcgcgga	agataccgcc	gtatactact	gcgccaaagt	ctcctacttg	1680
tctacagctt	cgtcgctcga	ctattgggggt	caaggaacgt	tggtcaccgt	ctctagtact	1740
gtggctgcac	catctgtctt	catctttccc	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
aacagggggag	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

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

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

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

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 accatcgtcg 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 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> 1438
<211> 211
<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

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 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 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> 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

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 tccatggtgg gtccttcagt ggttactact 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 ggccaggga ccttagtcac cgtctcctca	360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcaaaaag cgtggtgacc 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 gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggcagccccg 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 ggcggatcgg gaggtggcgg atccgaggtg	1380

cagctggtgc agtctggagc agaggtgaaa aagccccgggg agtctctgaa gatctcctgt	1440
aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgccccggg	1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagccccg	1560
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag	1620
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt	1680
cttgactact ggggccaggg aaccctgggtc accgtctcta gtcagcccaa ggccaacccc	1740
actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagtg	1800
tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc	1860
cccgtaagg cgggagtgga gaccacaaaa ccctccaaac agagcaacaa caagtacgcg	1920
gccgagagct acctgagcct gacgcccag cagtgggaagt cccacagaag ctacagctgc	1980
caggtcacgc atgaaggggag caccgtggag aagacagtgg cccctacaga atgttca	2037

<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

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

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

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
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 ccaaggtgga 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

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

<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 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> 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

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>
<223> Synthetic polynucleotide

<400> 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 actgtgcgag agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggcccttg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagtga 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
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 ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccga ggtacaactg	1380
gtggaatcag gtggagggtt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca	1440
tcggggttta 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 gggtaagga acgttgggtca ccgtctctag tactgtggct	1740
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca agtacagtg gaagggtgat	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

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

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

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

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 cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg 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 tcaggcggcc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct tgt 633

<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

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 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 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

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
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 catcggctct 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 aagggtggaca agaaagtga gccc aaatct 660
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttctctt tcccccaaa acccaaggac accctcatga tctccggac 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 gcccccatcg agaaaacccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctgggtc 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 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 gggctcttgac	1680
tactggggcc agggaaaccct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc	1740
actctgttcc cgccctcctc tgaggagctc caagccaaca aggccacact agtgtgtctg	1800
atcagtgact tctacccggg agctgtgaca gtggcctgga aggagatgg cagccccgtc	1860
aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcgcccgag	1920
agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccaggtc	1980
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a	2031

<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

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

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

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

<400> 1455
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 ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaagggtga 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

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>
<223> Synthetic polynucleotide

<400> 1457
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 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> 1458
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

<220>
<223> Synthetic polynucleotide

<400> 1459
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
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 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 aggtacaact ggtggaatca ggtggagggt tggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcggggttt actttcgatg attatgcgat gcattgggtc	1500
cggcaagcgc ctggaaaagg gtcgagtggt gtttccgcca ttacgtggaa tagcggacac	1560
atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac	1620
agcctgtacc ttcagatgaa ctcacttcgc 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 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> 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

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

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

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

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
gatatccaaa tgacacaatc accatcgctcg 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 attcggacaa 300

```

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggctctt ccccttgga      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 gccc aaatct 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
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

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
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc 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 aacacaaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaaga 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

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
caggtagagt 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
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420

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
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
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
accagatata gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680
agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtcag	1740
cccaaggcca accccactgt cactctgttc ccgcccctct ctgaggagct ccaagccaac	1800
aaggccacac tagtgtgtct gatcagtgac ttctaccggg gagctgtgac agtggcctgg	1860
aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc	1920

aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtccac 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

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

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

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

<210> 1467

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1467

cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc

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 caaaagcgtg	540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag	600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat 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		

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

gagggtacaac tgggtggaatc aggtgggaggt ttgggtgcagc cgggggagatc 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 gaacgttggc caccgtctct	360
agtacggtag ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	420
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	480
tggaaggtag 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 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
tcccgaggag agatgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat	1140
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1200
acgcctcccc tgctggactc cgacggctcc ttcttcctct atagcaagct caccgtggac	1260
aagagcaggc ggcagcaggc gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggagggtggc	1380
ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg	1440
tccctcacct gcgctgtcca tgggtgggtcc ttcagtggtt actactggaa ctggattcgc	1500
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac	1560
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	1620

tccttgacgc	tgacctctgt	gaccgccgcg	gacacggctg	tgtattactg	tgcgagagga	1680
tattgtagaa	gtaccacctg	ctactttgac	tactggggcc	agggaaccct	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	agcaccctga	cgctgagcaa	agcagactac	1980
gagaaacaca	aagtctacgc	ctgcgaagtc	acccatcagg	gcctgagctc	gcccgtcaca	2040
aagagcttca	acaggggaga	gtgt				2064

<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

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

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

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

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
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 gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tggggggcaca 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> 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

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 catggatatca 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 catcgggtctt ccccctggca 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> 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

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

gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt	60
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 gaacgttggt 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 cctcatgac	780
tccccggacc 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
tccccggagg 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 tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg      1440
tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg      1500
cagccccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagaccaaa      1560
tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc      1620
tccctgaagc tgagctctgt gaccgctgcg 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
aaggtggata acgcccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc      1920
aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa      1980
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc      2040
ttcaacaggg gagagtgt                                                    2058

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<210> 1476
<211> 686
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic polypeptide

```

```

<400> 1476

```

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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

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

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

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> 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
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 cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

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 gcaaaaaaccc 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 ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

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
gagggtacaac tgggtggaatc aggtggagggt ttgggtgcagc cgggggagatc gctcaggctt 60
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
agtacgggtg ctgcaccatc tgtcttcac tccccgccat 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 gtgcaaggct tccaacaaag ccctcccagc ccccatcgag 1020
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080
tcccgggagg agatgacca gaaccaggct agcctgacct gcctgggtcaa aggccttctat 1140

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

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

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

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 tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tgggtaccagc agaaaccagg aaaggttcct 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
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 ccaaattctg 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

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 accatcgctc 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 attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca 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

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
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggccctcgac accgccatgt attactgtgc gagaagtaac 300
tgggggtcttg 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
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 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 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 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 ctgcgctgtc	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 ccagggaacc ctagtcaccg tctcctcaac tgtggctgca	1740
ccatctgtct tcactttccc gccatctgat gagcagttga aatctggaac tgcctctgtt	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> 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

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

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

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

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 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 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 tggggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gccc aaatct tgt	633

<210> 1490
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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 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

$\langle 210 \rangle$	1492
$\langle 211 \rangle$	215
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<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

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 ccgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaaag 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
aaccctactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540

tacgcgcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac	600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt	660
tcagacaaaa ctcacacatg 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 ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggagggtg gcggatccca ggtgcagctg	1380
caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc	1440
tctggtggct ccatcagtag ttacttctgg agctggattc ggagcccc aggttaaggga	1500
ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag	1560
agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct	1620
gtgaccgtg 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

<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

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

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

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

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> 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	

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
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
 ggctgtcaca ctttcccggc tgcctacag tcctcaggac tctactccct cgaaagcgtg 540
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
 cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt cttgt 645

<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

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 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
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 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 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 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 tgggtggcggg tcgggaggtg 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 cgcggacacg gctgtgtatt actgtgcaag agaggatggg	1680
gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggt caccgtctcc	1740
tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	1800
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	1860

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

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

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

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
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tgggtaccagc agaaaccagg aaaggttcct 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
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> 1502
<211> 217
<212> PRT
<213> Artificial Sequence

<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

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

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> 1504
 <211> 215
 <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

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
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tccatggtgg gtccttcagt gggttactact ggaactggat tcgccagcca 120

ccaggggaagg ggctagagtg gattgggggaa atcaatcatg ctggaaacac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgctgacct ctgtgaccgc cgcggaacacg 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 cgtggagggtg cataatgcca agacaaagcc gtgtgaggag	900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	960
aatggcaagg agtacaagtg caaggctctc aacaaagccc tcccagcccc catcgagaaa	1020
accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc	1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccagc	1200
cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag	1260
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc 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	gtcgtctgac	tattggggtc	aaggaacgtt	ggtcaccgtc	1740
tctagtactg	tggctgcacc	atctgtcttc	atcttcccg	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>	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

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

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

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 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 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> 1508
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1508

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

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

<400> 1509
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 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 tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

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>

<223> Synthetic polynucleotide

<400> 1511

cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatgggtg gtccttcagt ggttactact ggaactggat tcgccagcca	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 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 gctcgcccgt cacaaagagc	660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc	720
ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	780
cggacccctg aggtcacatg cgtggtggtg 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
cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag	1260
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga	1380

tccgaggtgc	agctggtgca	gtctggagca	gaggtgaaaa	agccccgggga	gtctctgaag	1440
atctcctgta	agacttctga	atacagcttt	accagctact	ggatcggctg	ggtgcgccag	1500
atgccccggga	aaggcctgga	gtggatgggg	atcatctatc	ttggtgactc	agataaccaga	1560
tacagcccgt	ccttccaagg	ccaggtcacc	atctcagccg	acaagtccat	cagtaccgcc	1620
tacctgcagt	ggagcagcct	gaaggcctcg	gacaccgcca	tgtattactg	tgcgagaagt	1680
aactgggggtc	ttgactactg	gggccaggga	accctgggtca	ccgtctctag	tcagcccaag	1740
gccaaaccca	ctgtcactct	gttcccgccc	tcctctgagg	agctccaagc	caacaaggcc	1800
acactagtgt	gtctgatcag	tgacttctac	ccgggagctg	tgacagtggc	ctggaaggca	1860
gatggcagcc	ccgtcaaggc	gggagtggag	accaccaaac	cctccaaaca	gagcaacaac	1920
aagtacgcgg	ccgagagcta	cctgagcctg	acgcccgagc	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

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

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

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

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 ctcaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaaa 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 ccaagggtgga caagaaaagt gagcccaa at cttgt 645

<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

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 tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagttga 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

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
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 actgtgcgag agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 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 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
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 tgcctggtca aaggcttcta tcccagcgac 1140

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

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

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

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>
<223> Synthetic polynucleotide

<400> 1519
gatatccaaa tgacacaatc accatcgtcg 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 catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagttga gcccaaattct tgt 633

<210> 1520
<211> 211

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1520

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

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

<220>
<223> Synthetic polynucleotide

<400> 1521
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 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 gcccaaattct 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

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1523
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 agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420
tctgttgtgt gcctgctgaa taacttctat ccagagagg 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 tcttctcttt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc 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 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 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 aaacctcca aacagagcaa caacaagtac	1920
gcggccgaga gctacctgag cctgacgccc gagcagtgga agtcccacag aagctacagc	1980
tgccagggtca cgcataagg gagcaccgtg gagaagacag tggcccctac agaattgtca	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

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

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

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

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 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 ccttcccggc 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

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 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 tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1528
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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
caggtagcagt 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 cctcaacggt 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 tctcccggac ccctgaggtc 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
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acagggtgtac	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 gggaaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga	1380
tcgggagggtg 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
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 cctgacgtg	1980
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg	2040
agctcgcccc 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

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

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

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

<210> 1531
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1531
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc ggcgcgtccca 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 ccccctggca	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 agaaagttga 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			

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

<210> 1533
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1533
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttcct aaactgctca ttactgggc 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 gtgacgggtg 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> 1534
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1534

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

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> 1535
<211> 2061
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1535
caggtacagt 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 cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgtttgtg 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
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 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 ctttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga	1380
tcgggagggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc	1440
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc	1500
ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggg	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctttgac tactggggcc agggAACcct 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 cgcgcccgag agctacctga gcctgacgcc cgagcagtgg 1980
aagtcaccaca gaagctacag ctgccagggtc acgcatgaag ggagcaccgt ggagaagaca 2040
gtggccccta cagaatgttc a 2061

<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

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

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

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

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
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 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 ccaagggtga caagaaagtt gagcccaaat 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

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

gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

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 gagcctccac caagggccca	360
tcggtcttcc 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

<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

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

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 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> 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

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
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaaa 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 cttcccgcca	360
tctgatgagc agttgaaatc tggtagccgc 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> 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	

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
gagggtacaac tgggtggaatc aggtggagggt 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 tgggggtcaag gaacgttggt caccgtctct	360
agtgccctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggacacag cggccctggg ctgcctggtc 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
cccaaactctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca 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
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 cggatcccag	1380
gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc	1440
tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggattcg caagccacca	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	gcccacggt	cttccccctg	gcacctcct	ccaagagcac	ctctgggggc	1800
acagcggccc	tgggctgcct	ggtcaaggac	tacttccccg	aaccggtgac	ggtgtcgtgg	1860
aactcaggcg	ccctgaccag	cggcgtgcac	accttcccgg	ctgtcctaca	gtcctcagga	1920
ctctactccc	tcgagagcgt	ggtgaccgtg	ccctccagca	gcttggggcac	ccagacctac	1980
atctgcaacg	tgaatcacia	gccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

$\langle 210 \rangle$	1546
$\langle 211 \rangle$	682
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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

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

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

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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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 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

<400> 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

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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcc      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> 1550

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt	60
agctgtgcgg catcgggggtt tacttttcgat 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 tgggggtcaag gaacgttggt caccgtctct	360
agtgctcca ccaaggggccc 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
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat 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
tcaaagcca aagggcagcc ccgagaacca cagggtgtaca 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 ggacagaccaa atacaacccc 1560
 tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620
 ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680
 tactacggct ttgactactg gggccaggga 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> 1552
 <211> 680
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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

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

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
gatatccaaa 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
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1554
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1554

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

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 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> 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

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 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
agtgccctcca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccagg 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgaggtca 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
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 gattaggaag 1500
 cccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat 1560
 gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 1620
 ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 1680
 gaggatgggg atagctacta ccgctacggt atggacgtct ggggccaagg gaccacggtc 1740
 accgtctcct cagcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 1800
 agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg 1860
 gtgacgggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920
 ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980
 ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040
 aaagttgagc ccaaattctt 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

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

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

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

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 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 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>
<223> Synthetic polypeptide

<400> 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

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
gaaatttgtg 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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtaaccgc 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> 1562
<211> 214
<212> PRT
<213> Artificial Sequence

<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

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
gagggtgcagc 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
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg 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 tggggggacc gtcagtcttc 720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
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tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggctctcca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020
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 cgggtgggtg cggatcggga ggtggcggat cccaggtgca gttacagcag	1380
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tggattgggg aaatcaatca tgctggaaac accaactaca acccgccct caagagtcga	1560
gtcaccatat cattagacac gtccaagaac cagtttctcc tgacgctgac ctctgtgacc	1620
gccgcggaca cggctgtgta ttactgtgcg agaggatatt gtagaagtac cacctgctac	1680
tttgactact ggggccaggg aaccctagtc accgtctcct cagcctccac caagggccca	1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	1800
tgcctggtca aggactactt ccccgaaacc gtgacgggtg cgtggaactc aggcgccctg	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

<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

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

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

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
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 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

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
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 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> 1568
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1568

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

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
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccggaag 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 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 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 cccagccccc atcgagaaaa ccatctccaa agccaaaggg	1020
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 gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtgca gctgcaggag	1380
tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt	1440
ggctccatca gtagttactt ctggagctgg attcgggaagc ccccaggtaa gggactggag	1500
tggattggct atatctatta cagtgggcag accaaataca acccctccct caagagtcga	1560
gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc	1620
gctgcggaca cggccgtgta ttactgtgcg agagaaactg ggagctacta cggctttgac	1680
tactggggcc agggaaaccct ggtcaccgtc tcctcagcct ccaccaaggg cccatcggtc	1740
ttccccctgg caccctctc 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 gagcccaaatt cttgt	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

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

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

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

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
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 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 tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a

651

<210> 1572

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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
 gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagg agaaaccagg aaaggttcct 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 aacacaaaagt ctacgcctgc 600
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1574
<211> 220
<212> PRT
<213> Artificial Sequence

<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

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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc 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
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
ctcaaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc	780
gtgggtgggtg 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 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 gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtaca gttgcaggag	1380
tcaggtcag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg	1440
gacagtgtct ctaccaacag tggtgcttgg aactggatta ggaagcccc 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 ctctcagcc	1740
tccaccaagg gcccatcgggt 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 gccagcaac accaagggtg acaagaaagt tgagcccaaa	2040
tcttgt	2046

<210> 1576

<211> 682

<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

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

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

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 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

tctgatgagc	agttgaaatc	tggtaccgcc	tctgttgtgt	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>	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

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
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 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 gcctcaagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                          642

```

```

<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

```

```

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

<400> 1581
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 actgtgcgag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 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 ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc	900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc 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 tccgggtggg ggcggtcgg gaggtggcgg atccgaggta	1380
caactggtgg aatcagggtg aggtttgggt cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt gggtcggaa agcgcttga	1500
aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgcaaaagt ctctacttg	1680
tctacagctt cgtcgctcga ctattggggg caaggaacgt tggtcaccgt ctctagtgcc	1740
tccaccaagg gcccatcggg cttccccctg gcacctcct 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 tgaatcacaa gcccagcaac accaaggtgg 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

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

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

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

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

ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccaggagaaa 120

cctggccagg	ctcccaggct	cctcatctat	ggtgcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtctggggaca	gacttcactc	tcaccatcag	cagactggag	240
cctgaagatt	ttgcagtgtg	ttactgtcag	cagtatggta	gctcacctac	cttcggccaa	300
gggacacgac	tggagattaa	acgaacggtg	gctgcaccat	ctgtcttcat	cttcccgcca	360
tctgatgagc	agttgaaatc	tggtaccgcc	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>	1584
<211>	214
<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

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 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
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> 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

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

caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tccatgggtgg gtccttcagt gggtactact 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 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 ccctcaaaaag 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 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 accaggctcag 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 ggcggatcgg gaggtggcgg atccgaggtg	1380
cagctgggtg agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatctcctgt	1440
aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcaa gatgcccggg	1500
aaaggcctgg agtggatggg gatcatctat cttgggtgact cagataccag atacagcccg	1560
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag	1620
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactgggggt	1680
cttgactact ggggccaggg aaccctgggt accgtctcta gtgcctccac caagggccca	1740

tcggtctttcc	ccctggcacc	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcctgggtca	aggactactt	ccccgaaccg	gtgacggtgt	cgtggaactc	aggcgccctg	1860
accagcggcg	tgcacacctt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtgggtga	ccgtgccctc	cagcagcttg	ggcacccaga	cctacatctg	caacgtgaat	1980
cacaagccca	gcaacaccaa	ggtggacaag	aaagttgagc	ccaaatcttg	t	2031

$\langle 210 \rangle$	1588
$\langle 211 \rangle$	677
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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

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

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

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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 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
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt                        642
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<210> 1590

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1590

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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
```

```
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

<210> 1591

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1591
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca 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> 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

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>
<223> Synthetic polynucleotide

<400> 1593
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc

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 ccccttgga cccctctcca 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 aagggtggaca agaaagtga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttcctct tcccccaaaa 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
aagtgc aagg 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 tcgggagggtg gcggatccga ggtacaactg	1380
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
 gcttcgctgc tcgactattg gggtaagga acgttggtca ccgtctctag tgcctccacc 1740
 aaggggcccat 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> 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

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

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

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

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 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 gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1596
<211> 214
<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

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 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> 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

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

cagggtgcagc 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 catcggctct 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 aagggtggaca agaaagtga gcccaaattct	660
tgtgacaaaa ctcacacatg 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
aagtgcaagg tctccaacaa agccctccca 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 ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtgcagctg	1380

gtgcagtcctg	gagcagaggt	gaaaaagccc	ggggagtcctc	tgaagatctc	ctgtaagact	1440
tctgaataca	gctttaccag	ctactggatc	ggctgggtgc	gcaagatgcc	cgggaaaggc	1500
ctggagtgga	tggggatcat	ctatcttgg	gactcagata	ccagatacag	cccgtccttc	1560
caaggccagg	tcaccatctc	agccgacaag	tccatcagta	ccgcctacct	gcagtggagc	1620
agcctgaagg	cctcggacac	cgccatgtat	tactgtgcga	gaagtaactg	gggtcttgac	1680
tactggggcc	agggaaccct	ggtcaccgtc	tctagtcct	ccaccaagg	cccacggtc	1740
ttccccctgg	caccctctc	caagagcacc	tctgggggca	cagcggccct	gggctgcctg	1800
gtcaaggact	acttccccga	accggtgacg	gtgtcgtgga	actcaggcgc	cctgaccagc	1860
ggcgtgcaca	ccttcccg	tgctctacag	tcctcaggac	tctactccct	cgagagcgtg	1920
gtgaccgtgc	cctccagcag	cttgggcacc	cagacctaca	tctgcaacgt	gaatcacaag	1980
cccagcaaca	ccaagggtgga	caagaaagtt	gagcccaa	cttgt		2025

$\langle 210 \rangle$	1600
$\langle 211 \rangle$	675
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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

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

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
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tgggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccggg 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

<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

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

<400> 1603
 gatatccaaa tgacacaatc accatcgctc 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> 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

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>
<223> Synthetic polynucleotide

<400> 1605
cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga 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 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 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
tggtgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc 1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacagggtga caccctgccc 1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc 1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200

accacgcctc ccggtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg	1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtgggtggcgg atcgggaggt	1380
ggcggatccg aggtacaact ggtggaatca ggtggagggt tggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcggggttt actttcgatg attatgcgat gcattgggtc	1500
cggaaagcgc ctggaaaagg gctcgagtgg gtttccgcc ttacgtggaa tagcggacac	1560
atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac	1620
agcctgtacc ttcagatgaa ctcacttcgc gcggaagata ccgccgtata ctactgcgcc	1680
aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtcaagg aacgttggtc	1740
accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag	1800
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt cccgaaccg	1860
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	1920
ctacagtcct caggactcta ctccctcgag agcgtgggtga ccgtgccctc cagcagcttg	1980
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	2040
aaagttgagc ccaaattctg t	2061

<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

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

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

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

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 ctgtctgctg ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaagggttcct aaactgctca ttacttgggc 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
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<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

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

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
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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

tggtgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaaacca 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 ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat	1560
accagatata gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680
agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtgcc	1740
tccaccaagg gcccacgggt 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 accaagggtg acaagaaagt tgagcccaaa	2040
tcttgt	2046

<210> 1612
 <211> 682
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 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

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

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

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>
<223> Synthetic polynucleotide

<400> 1613
gaaatttgtt 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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 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> 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

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

<220>
<223> Synthetic polynucleotide

<400> 1615
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 gtcgactat 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
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660

agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa	720
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc	780
tcccggaccc ctgaggtcac atgcgtggtg 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
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac	1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc	1380
ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg	1440
tccttcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc	1500
aagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac	1560
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	1620
tccttgacgc 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
gagcccaaat 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

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

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

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

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 accatcgctcg 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

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gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggctctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccgctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gccc aaatct tgt                                  633

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```

<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

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 ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg 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> 1620
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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 catcgggggtt tactttcgat 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 gaacgttgggt caccgtctct 360
agtacggtgg ctgcaccatc tgtcttcac tccccgcat ctgatgagca gttgaaatct 420

ggaactgcct ctgttggtg 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
tcccggaacc ctgagggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc	840
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag	900
gagcagtacg gcagcacgta ccgttggtgc agcgtcctca ccgtcctgca ccaggactgg	960
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaaag 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 ttcttctct 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
tacaacccct ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc	1620
tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa	1680
actgggagct actacggctt tgactactgg ggccaggga cctgggtcac cgtctcctca	1740
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> 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

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

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

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

<220>

<223> Synthetic polynucleotide

<400> 1623

gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg

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
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> 1624
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <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			

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

<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

tggtaccagg 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
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		

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

<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 ccggaagcgc 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 ctgttggtg 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 cctcatgac	780
ttccggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc	840
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag	900
gagcagtacg gcagcacgta ccgttggtg agcgtcctca ccgtcctgca ccaggactgg	960
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaaag ccctcccagc ccccatcgag	1020
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca	1080
tcccgaggagg 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 tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc	1440
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttg ttggaactgg	1500
attaggaagc ccccagggaaggaggccttgag tggataggaa ggacatacta caggccaag	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	aagggcccat	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	gcaccagac	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

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

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

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

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 accatcgctc gtttcagcgt 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
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtagcggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtcg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagtga gccc aaatct 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

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 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 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> 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

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 ccgggggagtc 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 ggccctcgac 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 accaaaacct 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 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	tggtggcgga	tcgggaggtg	gcggatccca	ggtgcagtta	1380
cagcagtcgg	gcgcaggact	gttgaagcct	tcggagaccc	tgtccctcac	ctgcgctgtc	1440
catggtgggt	ccttcagtgg	ttactactgg	aactggattc	gcaagccacc	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	ccagggaacc	ctagtcaccg	tctcctcagc	ctccaccaag	1740
ggcccatcgg	tcttccccct	ggcacccctc	tccaagagca	cctctggggg	cacagcggcc	1800
ctgggctgcc	tggtcaagga	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

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

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

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

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

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

<210> 1635
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1635
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggaaca 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 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 ccaagggtgga caagaaaagt gagcccaa at 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

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> 1637
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1637
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> 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

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

<210> 1639
<211> 2031
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1639
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc 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
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc 360
aaccacctg 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 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 ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggaggtg gcggatccca ggtgcagctg	1380
caggagtcgg gcccaggact 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
tttgactact ggggccaggg aaccctggtc accgtctcct cagcctccac caagggccca	1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	1800
tgcctggtca aggactactt cccggaaccg gtgacggtgt cgtggaactc aggcgccctg	1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag	1920
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat	1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t	2031

<210> 1640
 <211> 677
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1640

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 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

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 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

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> 1641
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1641
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 gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctctc 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 ccaaggtgga caagaaagt gagcccaaat cttgt 645

<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

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
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaagggttcct aaactgctca ttacttgggc atctaccggg 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> 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

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
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccggaagag 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
aaccctactg 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 ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctccggac ccctgaggtc 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 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 gagggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggaggtg gcggatccca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggaa gccccaggg	1500
aaaggccttg agtggatagg aaggacatac tacaggtcca agtgggataa tgattatgca	1560
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg	1620
aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg	1680
gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggg caccgtctcc	1740
tcagcctcca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct	1800
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	1860
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	1920
tcaggactct actccctcga gagcgtgggtg accgtgccct ccagcagctt gggcacccag	1980
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	2040
cccaaattctt 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

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

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

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

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 gagcccaaatt 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

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
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> 1650
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1650

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

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 tccatgggtg gtccttcagt gggtactact ggaactggat tcgcaagcca 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 gctcgcccgt cacaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720

ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	780
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag	840
ttcaactggt 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 tggtaaagg cttctatccc	1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1200
cctcccgtgc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag	1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga	1380
tccgaggtag aactggtgga atcaggtgga ggtttggtgc agccggggag atcgctcagg	1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggaaa	1500
gcgcttgaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat	1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg	1620
taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc	1680
tcctacttgt ctacagcttc gtcgctcgac tattggggtc aaggaaacgtt ggtcaccgtc	1740
tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	1800
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1860
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag	1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc	1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	2040
gagcccaaata cttgt	2055

<210> 1652

<211> 685

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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 gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca 360

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ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtagcggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtaggaca agaaagtga gcccaaattct tgt                                633

```

```

<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

```

```

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
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 tgagcagtgg aagtcccaca gaagctacag ctgccaggtc	600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a	651

$\langle 210 \rangle$	1656
$\langle 211 \rangle$	217
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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 tccatgggtg gtccttcagt ggttactact ggaactggat tcgcaagcca 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 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 cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	780
cggacccctg aggtcacatg cgtgggtgggtg gacgtgagcc acgaagaccc tgagggtcaag	840
ttcaactgggt acgtggacgg cgtgggaggtg 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 tgcatgaggc tctgcacaac	1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga	1380
tccgaggtgc agctggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag	1440
atctcctgta agacttctga atacagcttt accagctact ggatcggctg ggtgcgcaag	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 accctgggtc ccgtctctag tgcctccacc	1740
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	1800
gccctgggct gcctggtcaa 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> 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

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

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

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 gtcacacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggg 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> 1660
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1660

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

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 ggcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccggggtc aggtacggac ttactctca 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

<400> 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

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
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 actgtgagag agaaactggg 300

agctactacg gcttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg	360
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc	420
tctgtttgtgt gcctgctgaa taactttctat cccagagagg ccaaagtaca gtggaaggtg	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 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 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 tatgcatgc 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 cgttgggtcac cgtctctagt	1740
gcctccacca agggcccatc ggtcttcccc ctggcacct cctccaagag cacctctggg	1800

ggcacagcgg	ccctgggctg	cctgggtcaag	gactacttcc	ccgaaccggt	gacggtgtcg	1860
tggaactcag	gcgccctgac	cagcggcggtg	cacaccttcc	cggctgtcct	acagtcctca	1920
ggactctact	ccctcgagag	cgtgggtgacc	gtgccctcca	gcagcttggg	cacccagacc	1980
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	2040
aaatcttgt						2049

<210>	1664
<211>	683
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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 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 catcggtctt cccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtaggaca agaaagttga gcccaaattct 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

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 ctcagggggtc      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 aggagatag cagccccgtc      480
aaggcggggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag      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

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

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc

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 ctgagcaaaag 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 agtgcaagggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccagggt cagcctgacc tgcctggtca 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 aaaaagcccc gggagtctct gaagatctcc	1440
tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg caagatgccc	1500
gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc	1560


```

ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg      1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgcgag aagtaactgg      1680
ggctcttgact actggggcca gggaaccctg gtcaccgtct ctagtgcctc caccaagggc      1740
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg      1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc      1860
ctgaccagcg gcgtgcacac cttcccggt gtcctacagt cctcaggact ctactccctc      1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg      1980
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaadc ttgt          2034

```

<210> 1670
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1670

```

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

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

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

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

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 ttactctca 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> 1672
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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 catggatatca 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 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>
<223> Synthetic polypeptide

<400> 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

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

caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc	60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa 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 tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtgggaagg 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

tcgggaggtg	gcggatccga	ggtacaactg	gtggaatcag	gtggaggttt	ggtgcagccg	1440
gggagatcgc	tcaggcttag	ctgtgcggca	tcggggttta	ctttcgatga	ttatgcatg	1500
cattgggtcc	ggaaagcgcc	tggaaaaggg	ctcgagtggg	tttccgcat	tacgtggaat	1560
agcggacaca	tcgattatgc	agacagtgtg	gagggcagat	tcacaatctc	acgagacaat	1620
gctaagaaca	gcctgtacct	tcagatgaac	tcacttcgcg	cggaagatac	cgccgtatac	1680
tactgcgcc	aagtctccta	cttgtctaca	gcttcgtcgc	tcgactattg	gggtcaagga	1740
acgttggtca	ccgtctctag	tgcctccacc	aagggcccat	cggctctccc	cctggcaccc	1800
tcctccaaga	gcacctctgg	gggcacagcg	gccctgggct	gcctgggtcaa	ggactacttc	1860
cccgaaccgg	tgacggtgtc	gtggaactca	ggcgccctga	ccagcggcgt	gcacaccttc	1920
ccggctgtcc	tacagtcttc	aggactctac	tcctcgaga	gcgtgggtgac	cgtgccctcc	1980
agcagcttgg	gcaccagac	ctacatctgc	aacgtgaatc	acaagcccag	caacaccaag	2040
gtggacaaga	aagttgagcc	caaatcttgt				2070

$\langle 210 \rangle$	1676
$\langle 211 \rangle$	690
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<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

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

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

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

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
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaagggttcct aaactgctca ttactgggc atctaccgg 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
tgcttggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

<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

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

<400> 1679
 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 ctaggtcagc ccaaggctgc cccctcggtc 360
 actctgttcc cgccctctc 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> 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

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>
<223> Synthetic polynucleotide

<400> 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 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
cccgtcacaa 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

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccgggagaac	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 gcaagatgcc cgggaaaaggc 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
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> 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
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

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

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 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

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 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
tgcttggtca aggactactt cccgaaccg 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

<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

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
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120
ggaaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccggggtc aggtacggac ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaaatc 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> 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

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
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tactttcgat 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
agtcctcca ccaaggggccc atcgggtcttc 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
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780

cctgagggtca catgcgtggt 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 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 atgggtgggtc cttcagtggt 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 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 ggcctgagct cgcccgtcac aaagagcttc	2040
aacaggggag agtgt	2055

<210> 1688
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

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

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>
<223> Synthetic polynucleotide

<400> 1689
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 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 tggggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gccc aaatct tgt	633

<210> 1690
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1690

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 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

<220>
<223> Synthetic polynucleotide

<400> 1691
gatatccaaa 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
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
ctgagcaaaag cagactacga gaaacacaaaa gtctacgcct gcgaagtcac ccatcagggc	600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt	642

<210> 1692
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <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			

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1693
gagggtacaac 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
agtgccctcca ccaagggtccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540

tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc	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 atcccgaggag	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 gaagcccca	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 aactgtggct	1740
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaagggtgat	1860
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc	1920
acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc	1980
tacgcctgcg aagtcacca 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

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

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

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

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 ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtcctt 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> 1696
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc ggcgcgtccca 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
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> 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

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
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 ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
ggggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt 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 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 cagggtgtaca 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 cggatcccag	1380
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc	1440
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggaag	1500
ccccaggga aaggccttga gtggatagga aggacatact acagggtcaa 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 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	aacacaaagt	ctacgcctgc	gaagtcaccc	atcagggcct	gagctcgccc	2040
gtcacaaaga	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
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

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

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

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

<210> 1701

<211> 651

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1701
gacatccaga tgacccagtc tccaagctcc ctgtctgctg ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaagggttcct aaactgctca ttacttgggc atctacccgg 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
tgcctggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg 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

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> 1703

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1703

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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 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 tgagcagtg aagtcccaca gaagctacag ctgccaggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651
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<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
```

```
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

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg	120
cccgggaaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggccctcggac 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 gacaagaaaag 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
aaggctctca acaaagccct ccagcccc 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 gcaggaggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtgg cggatcggga ggtggcggat ccaggtgca gttacagcag	1380
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
 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
 ctcgaaaagca ccctgacgct gagcaaaagca gactacgaga aacacaaaagt 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

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

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

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

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
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
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tggggaccca 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

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 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
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggaaca 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> 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

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
cccggaag 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 cgggtgctgt 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 caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
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tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggctctca acaaagccct ccagcccc 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 gcagggtggca gcagggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtgca gctgcaggag	1380
tcgggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt	1440
ggctccatca gtagttactt ctggagctgg attcgggaagc ccccaggtaa 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 tcctcaactg tggctgcacc atctgtcttc	1740
atcttcccg c 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
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

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

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

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

<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
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 catcggctctt ccccctggca 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 agaaaagttga gcccaaactct 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

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
 cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120
 tttccaggaa cagcccccaa actcctcatc caaggaaca gcaatcggcc ctcaggggctc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
 gtgttcggcg gagggaccaaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
 actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
 ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
 aaggcggggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
 agctatctga gcctgacgcc tgagcagtgg 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

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
gagggtgcagc 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
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg 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 tggggggacc gtcagtcttc 720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt 900
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aagggtctcca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020
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 gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtaca gttgcaggag	1380
tcagggtccag gactgggtgaa 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 ctctcaact	1740
gtggctgcac catctgtctt catcttccc ccatctgatg agcagttgaa atctggaact	1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag	1860
gtggataacg cctccaatc gggtaactcc caggagagtgc 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

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

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

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

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 ttactgggc atctaccg 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
tgcctgggtca aggactactt ccccgaccg 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> 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

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 gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 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> 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

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 tccatggtgg 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 ggccagggaa ccctagtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct 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 acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcggtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc	900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag 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 tccgggtggt ggcggtcgg gaggtggcgg atccgaggta	1380
caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggaa agcgcctgga	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 caaggaacgt tggtcaccgt ctctagtact	1740
gtggctgcac catctgtctt catcttcccc ccactctgatg 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

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

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

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

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
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 cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

ttcccggtg 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

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

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 ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacgggtg 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

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

<400> 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

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 tccatgggtgg gtccttcagt gggtactact 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 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 cacatgcccc cctgtgcccag 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 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 gcctcccgtg	1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggtg	1380
cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt	1440
aagacttctg aatacagctt taccagctac tggatcggct gggtgcgcaa gatgcccggg	1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccc	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 cacactagtg	1800
tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc	1860
cccgtaagg cgggagtgga gaccacaaa ccctccaaac agagcaacaa caagtacgcg	1920
gccgagagct acctgagcct gacgcccag cagtggaaagt cccacagaag ctacagctgc	1980
caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca	2037

<210> 1730
<211> 679
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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 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
 ggctgtcaca ctttcccggc tgcctacag tcctcaggac tctactccct caaaagcgtg 540
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
 cccagcaaca ccaagggtgga caagaaagtt gagcccaaatt 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

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 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 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> 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	

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
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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 ctcagcctcc 360
accaagggcc catcggctctt cccctgggca 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 gcccaaatct	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
aagtgcagg 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 tcgggagggt gcggatccga ggtacaactg	1380
gtggaatcag gtggagggtt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca	1440
tcggggttta 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
gcttcgtcgc tcgactattg gggtaagga acgttgggtc ccgtctctag tactgtggct	1740
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaagggtgat	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> 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

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

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

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

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

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
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga	360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac	420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc	540
tccagcagct tggggaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gccc aaatct tgt	633

<210> 1738
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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 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> 1740
<211> 214
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Synthetic polypeptide

```

```

<400> 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

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
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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 gctgcctggg 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
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 agaaaacat ctccaaagcc	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 tcgggagggtg gcggatccga ggtgcagctg	1380
gtgcagtctg gagcagaggt gaaaaagccc ggggagtctc tgaagatctc ctgtaagact	1440
tctgaataca gctttaccag ctactggatc ggctgggtgc gcaagatgcc cgggaaaggc	1500
ctggagtggg tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc	1560
caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc	1620
agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac	1680

tactgggggcc	agggaaccct	ggtcaccgtc	tctagtcagc	ccaaggccaa	ccccactgtc	1740
actctgtttcc	cgccctcctc	tgaggagctc	caagccaaca	aggccacact	agtgtgtctg	1800
atcagtgact	tctacccggg	agctgtgaca	gtggcctgga	aggcagatgg	cagccccgtc	1860
aaggcggggag	tggagaccac	caaaccctcc	aaacagagca	acaacaagta	cgcgggccgag	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>
<223> Synthetic polypeptide

<400> 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

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

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

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

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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 ctttccggc tgcctacag tcctcaggac tctactccct caaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaagggtgga caagaaagtt gagcccaaat cttgt                      645
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<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

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

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagg agaaaccagg aaaggttcct 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
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

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 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 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
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg 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 tctcaaagc 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
ggcggatccg aggtacaact ggtggaatca ggtggagggt ttggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcgggggtt actttcgatg attatgcgat gcattgggtc	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 gtactgtggc 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 aacacaaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040
 gtcacaaaga 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

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

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

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

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 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 cgggtgacggt 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> 1750
<211> 211
<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

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
tgggtaccagg agaaaccagg aaagggttcct aaactgctca tttactgggc atctaccg 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

<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

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
 caggtagagt 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
 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 agcccccatc 1020
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080
 ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc 1140

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

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

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

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

<400> 1755
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 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 ccaagggtga caagaaaagt gagcccaaatt 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

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>
<223> Synthetic polynucleotide

<400> 1757
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tactttcgat 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 gaacgttgggt 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 ccccaaaaac ccaaggacac cctcatgatc 780
tcccggaacc ctgaggtcac atgcgtggtg 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 gggagggtggc	1380
ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg	1440
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt 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

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

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

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

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
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 cgggtgacggt 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> 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

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 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 catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtcg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aagggtggaca agaaaagttga gccc aaatct 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

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 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
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
tacaaccctt 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
aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc	1920
aaggacagca cctacagcct cgaaaagcacc ctgacgctga gcaaagcaga ctacgagaaa	1980
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc	2040
ttcaacaggg gagagtgt	2058

<210> 1764
<211> 686
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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>
<223> Synthetic polynucleotide

<400> 1765
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 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 agaaagttga gcccaaattct tgt	633

<210> 1766
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1766

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 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

<220>
<223> Synthetic polynucleotide

<400> 1767
gatatccaaa tgacacaatc accatcgctc 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

```

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggctctt ccccttgga      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

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<210> 1768
<211> 211
<212> PRT
<213> Artificial Sequence

```

```

<220>
<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

```

```

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1769
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

agtacggtgg ctgcaccatc tgtcttcac	ttccccccat ctgatgagca gttgaaatct	420
ggaactgcct ctgttggtg 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 cctcatgatc	780
tcccggaccc ctgaggtcac atgcgtggtg	gtggacgtga gccacgaaga ccctgaggtc	840
aagttcaact ggtacgtgga cggcgtggag	gtgcataatg ccaagacaaa gccgtgtgag	900
gagcagtacg gcagcacgta ccgttggtg	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
acgcctcccc tgctggactc cgacggctcc	ttcttcctct atagcaagct caccgtggac	1260
aagagcagggt ggcagcaggg gaacgtcttc	tcatgctccg tgatgcatga ggctctgcac	1320
aaccactaca cgcagaagag cctctccctg	tctccgggtg gtggcggatc gggagggtggc	1380
ggatcccagg tacagttgca ggagtcagg	ccaggactgg tgaagccctc ggagaccctc	1440
tcactcacct gtaccatctc cggggacagt	gtctctacca acagtgttgc ttggaactgg	1500
attaggaagc ccccagggaaggccttgag	tggataggaa ggacatacta cagggtccaag	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
 agctcgcccg 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

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

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

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

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

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagg agaaaccagg aaagggtcct 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 ccccgaaaccg 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> 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

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

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gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga cctgtgtgacg      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
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aagggtggaca 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

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
cccgaggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac 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 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 tcgggaggtg gcggatccca ggtgcagtta	1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc	1440
catggtgggt ctttcagtgg ttactactgg aactggattc gcaagccacc aggggaagggg	1500

ctagagtgga	ttggggaaat	caatcatgct	ggaaacacca	actacaacc	gtccctcaag	1560
agtcgagtca	ccatatcatt	agacacgtcc	aagaaccagt	tctccctgac	gctgacctct	1620
gtgaccgccg	cggacacggc	tgtgtattac	tgtgcgagag	gatattgtag	aagtaccacc	1680
tgctactttg	actactgggg	ccagggaacc	ctagtcaccg	tctcctcaac	tgtggctgca	1740
ccatctgtct	tcatctttcc	gccatctgat	gagcagttga	aatctggaac	tgctctgttt	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>	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

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

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

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

<210> 1777
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1777
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 acgagcctcc 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 tggggaccca 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

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 caaggaaca 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 cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaagggtga caagaaaagt 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

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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
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
aaccctactg tctctgtgtt 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 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 agaaaacat ctccaagcc 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 tggtaggcga tcgggaggtg gcggatccca ggtgcagctg 1380
 caggagtcgg gcccgaggact 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
 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 aacacaaaagt 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

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

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

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

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 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 catcggctctt ccccctggca 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 agaaaagttga 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

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 caaggaaca gcaatcggcc ctcaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaaa 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 caagaaaagt 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

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
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 tctctagtca gccaaggcc 360
aaccctactg 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 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 agccctccca gccccatcg agaaaaccat ctccaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 1080

aagaaccagg tcagcctgac ctgcctgggc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tggcggcgga tcgggaggtg gcggatccca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggaa gccccaggg	1500
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
tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	1800
ggaactgcct ctgttgtgtg 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

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

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

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

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 tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct 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
tgcctgggtca aggactactt ccccgaaccg 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> 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

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 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 caagaaaagt gagcccaaatt cttgt 645

<210> 1792
<211> 215

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1792

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

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
caggtgcagt 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 cgcggacacg gctgtgtatt actgtgagag 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
caciaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt caciaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtcctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgagggtcaag 840

ttcaactggg 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 ccaggtcagc ctgacctgcc tggtaaagg cttctatccc	1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1200
cctcccgtagc tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag	1260
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac	1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga	1380
tccgaggtagc aactgggtga atcagggtga ggtttggtgc agccggggag atcgctcagg	1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccgga	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 tattggggtc aaggaaagtt 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

<400> 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

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

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

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
 aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctgggt caaggactac 420
 ttccccgaac cgggtgacggt gtcgtggaac tcaggcgcgc tgaccagcgg cgtgcacacc 480

ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct 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	

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
 cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300
 gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt cccctggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
 ttccccgaac cgggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaaagttga gccc aaatct 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

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
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatgggtgg gtccttcagt gggttactact 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 ggccaggga ccttagtcac cgtctcctca 360
acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480
aagggtggata 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
cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgaggtcaag	840
ttcaactggt 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 tggtaaaagg 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 ccgggtggtg gcggatcggg aggtggcgga	1380
tccgaggtgc agctggtgca gtctggagca gaggtgaaaa agcccgggga gtctctgaag	1440
atctcctgta agacttctga atacagcttt accagctact ggatcggctg ggtgcgcaag	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 accctggtca ccgtctctag tcagcccaag	1740
gccaacccca ctgtcactct gttcccgccc tcctctgagg agctccaagc caacaaggcc	1800
acactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca	1860
gatggcagcc ccgtcaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac	1920
aagtacgcgg ccgagagcta cctgagcctg acgcccagc agtggaagtc ccacagaagc	1980
tacagctgcc aggtcacgca tgaaggagc 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

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

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

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

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 gcagggttatg 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
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> 1802
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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 catcggctctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttccccgctg 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>
<223> Synthetic polypeptide

```

```

<400> 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

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
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 actgtgagag agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360

gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc	420
tctgtttgtgt gcctgctgaa taactttctat cccagagagg ccaaagtaca gtggaaggtg	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
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 tgcctggtca 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 cggggtttac 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 ttctatcca 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

<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

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

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

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 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 catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tggggaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga 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

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

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 cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc	540
tccagcagct tggggaccca 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	

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
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 actgtgagag 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 ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgagggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaca 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 tgccctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcattgctc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggagggtg cggtatccgag	1380
gtgcagctgg tgcagtctgg agcagagggtg aaaaagcccg gggagtctct gaagatctcc	1440
tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg caagatgccc	1500
gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc	1560
ccgtccttcc aaggccagggt caccatctca gccgacaagt ccatcagtac cgcctacctg	1620

cagtggagca	gcctgaaggc	ctcggacacc	gccatgtatt	actgtgcgag	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	gagcagtggg	agtcccacag	aagctacagc	1980
tgccagggtca	cgcataaagg	gagcaccgtg	gagaagacag	tggcccctac	agaatgttca	2040

$\langle 210 \rangle$	1812
$\langle 211 \rangle$	680
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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

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

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

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 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 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>
<223> Synthetic polypeptide

<400> 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

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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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca      120
gggaaaagccc 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 cgggtgacggg 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
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<210> 1816

<211> 211

<212> PRT

<213> Artificial Sequence

<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

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

caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc	60
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 cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtgggaagg ggataacgcc ctccaatcgg gtaactcca ggagagtgtc	540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa	600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	660
cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttctct 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 agccctcca	1020
gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080
accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gaggggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcgga	1380
tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg	1440

```

gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg      1500
cattgggtcc ggaaagcgcc 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 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
agctcgcccg tcacaaagag cttcaacagg ggagagtgt                                2079

```

<210> 1818
 <211> 693
 <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

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

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

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

<400> 1819
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggctctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagtga gcccaaattct 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

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>
<223> Synthetic polynucleotide

<400> 1821
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 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
tgcctggtca aggactactt ccccgaaaccg gtgacgggtgt 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> 1822
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1822

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

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

<220>
<223> Synthetic polynucleotide

<400> 1823
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggattagg 120
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggatat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
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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 ctcacacatg cccaccgtgc 720
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 780
accctcatga tctcccgga cctgaggtc acatgcgtgg tggaggacgt gagccacgaa 840
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aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1020
gccccatcg agaaaacat ctcaaagcc aaagggcagc cccgagaacc acaggtgtac 1080

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct 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 gcaagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggt	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctctgac tactggggcc agggaaccct ggtcaccgtc	1740
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc	1800
caagccaaca aggccacact agtgtgtctg atcagtgact tctaccgagg 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

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

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

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

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 caaggaaca 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 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

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 aaaggttcct aaactgctca ttactgggc atctaccgg 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
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 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

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 gcaaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcgagaaa 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

<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

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
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

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 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
 agtgcctcca ccaagggtccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
 gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt 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 ctccggacc 780
 cctgaggtca catgcgtggt 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 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 ctccctagcc	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 tgaatcaciaa gccagcaac 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

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

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

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

<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
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
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

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

<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 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 aggggagaggt 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

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
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 gaacgttgggt caccgtctct 360
agtcctcca 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 gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca 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 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
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag	1380
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc	1440
tgcactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagccccca	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
aagggcccat cggctctccc cctggcacc tcctccaaga gcacctctgg gggcacagcg	1800
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	1860
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1920
tccctcgaga gcgtggtgac 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

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

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

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

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 ggtccgggtc aggtacggac ttactctca 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
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaaag 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			

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 ctgtctgctg ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggagcct aaactgctca ttactgggc 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

$\langle 210 \rangle$	1844
$\langle 211 \rangle$	220
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	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

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggt 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
agtgccctcca ccaagggtccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540

tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc	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 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
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc	1440
tgtaccatct ccggggacag tgtctctacc aacagtgtt 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 cagcctccac 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 cacaagcca gcaacaccaa ggtggacaag	2040

aaagttgagc ccaaatcttg 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

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

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

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

<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 ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 300
gtgttcggcg aagggaccaa 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

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

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 gagggttaga agcagttact tagcctggta ccagcagaaa 120

cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtggt gtctggggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagtattggtg 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

<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	

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
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgcatgt attactgtgc gagaagtaac 300

tggggtcttg actactgggg ccaggggaacc ctggtcaccg tctctagtgc ctccaccaag	360
ggccccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg 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
ctcttcccccc 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
aaggctctcca 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 gcagggtggca gcaggggaac	1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tcctgtctc cgggtgggtg cggatcggga ggtggcggat cccaggtgca gttacagcag	1380
tcgggcgcag gactgttgaa gccttcggag accctgtccc tcacctgcg tgtccatggt	1440
gggtccttca gtggttacta ctggaactgg attcgccagc caccagggaa ggggctagag	1500
tggattgggg aaatcaatca tgctggaaac accaactaca acccgctcct 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 ccccgaaaccg gtgacgggtgt cgtggaactc aggcgccctg	1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag	1920
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat	1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg 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	

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

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

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

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 ctcagggggtc 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 aggagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540
agctatctga gcctgacgcc tgagcagtg 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

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

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 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

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 ccgggggagtc tctgaagatc 60

tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccggaaaaa aactggagtg 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 cgggtgctgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcaaaaagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag 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 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 cgggtgggtg 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
tactgggggca agggaaacct ggtcaccgtc tcctcagcct ccaccaaggg cccatcggtc	1740
ttccccctgg caccctcctc caagagcacc tctggggggca 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 ccaagggtgga caagaaagtt gagcccaaat 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

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

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

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

<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 ctcaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg aagggacca gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc 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> 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

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

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

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt 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 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 aacacaaaagt ctacgcctgc      600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660
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<210> 1862

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1862

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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
```

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

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 ccgggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg	120
cccggaaaaa aactggagtg 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
ctcaaaagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag ttgagcccaa atcttgtgac	660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	840
gtggaggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt	900
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aaggctctca acaaagccct ccagcccc 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
tccctgtctc cgggtggtgg cggatcggga ggtggcggat ccaggtaca gttgcaggag	1380
tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg	1440

gacagtgtct ctaccaacag tgttgcttgg aactggatta ggagagcccc 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 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
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tgagcccaaa 2040
tcttgt 2046

<210> 1864
<211> 682
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1864

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

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

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

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 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 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> 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

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 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> 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

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
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatgggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120
ccagggaaga agctagagtg 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 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 ctgagggtcaa gttcaactgg 840
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgtgtgagga gcagtacggc 900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
aaagccaaaag ggagcccccg agaaccacag gtgtacaccc tgcccccac cggggaggag 1080
atgaccaaga accagggtcag 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 gccggatcgg gaggtggcgg atccgaggta	1380
caactgggtg aatcaggtgg aggtttgggt cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga	1500
aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg	1680
tctacagctt cgtcgtcga ctattggggg aaaggaacgt tggtcaccgt ctctagtgcc	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 gcttggggcac ccagacctac	1980
atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa	2040
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

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

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

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 gagtgtaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgag 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 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

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

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 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> 1874
<211> 217
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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 tccatgggtgg 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
 ggacacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcaaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggg 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 gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggcagccccc 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 tccgggtggt ggcggatcgg gaggtggcgg atccgaggtg	1380
cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt	1440
aagacttctg aatacagctt taccagctac tggatcggct gggcgcgcca gatgcccggg	1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg	1560
tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag	1620
tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggt	1680
cttgactact ggggcaaggg aaccctggtc accgtctcta gtgcctccac caagggccca	1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	1800
tgcttggtca 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> 1876
 <211> 677
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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

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

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
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 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> 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

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
gatatccaaa 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
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaaatc 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

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
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 ctcagcctcc 360
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggcccttg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagtga gcccaaactc 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac 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	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	ccttcttcct	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	tggtggcgga	tcgggaggtg	gcggatccga	ggtacaactg	1380
gtggaatcag	gtggaggttt	ggtgcagccg	gggagatcgc	tcaggcttag	ctgtgcggca	1440
tcggggttta	ctttcgatga	ttatgcatg	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	gggtaaagga	acgttgggtc	ccgtctctag	tgccctccacc	1740
aagggcccat	cggctcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	1800
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgc	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

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

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

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

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 tgaccagtc 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 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> 1884
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1884

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

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 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> 1886

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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 agaaaactggg 300
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360
 accaagggcc catcggctct cccctggca 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 gccc aaatct	660
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
aagtgc aagg 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
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggagggtg 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 gggctctgac	1680
tactggggca agggaaacct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc	1740
ttccccctgg caccctctc caagagcacc tctgggggca cagcgccctt 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 gagcccaa at cttgt	2025

<210> 1888
<211> 675
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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

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

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 ttactgggc atctaccgg 180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcgaggg gaccaaggtg gagatcaaac gaacggtggc 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 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	

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
gatatccaaa tgacacaatc accatcgtcg 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
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> 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	

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
caggtagagt 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 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 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 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 ggtggagggt tggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcggggttt 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 gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag	1800
agcacctctg ggggcacagc ggccctgggc tgccctgggtca aggactactt ccccgaaccg	1860
gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	1920

ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040
aaagttgagc ccaaattcttg 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

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

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

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

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

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 tcggcgaggg 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
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	660

<210> 1896
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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	ctcagggggtc	180
cctgaccgat	tctctggctc	caagtctggc	acctcagcct	ccctggccat	cactggggtc	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	tgagcagtgg	aagtcccaca	gaagctacag	ctgccaggtc	600
acgcatgaag	ggagcacctg	ggagaagaca	gtggccccta	cagaatgttc	a	651

<210>	1898
<211>	217
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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
cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggatat 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 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 agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtgggtggacg 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 ccgggaaaagg cctggagtgg atggggatca tctatcttgg tgactcagat	1560
accagatata gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680

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agaagtaact ggggtcttga ctactggggc aagggaaccc 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
atctgcaacg tgaatcaca gcccagcaac accaagggtgg acaagaaagt tgagcccaaa      2040
tcttgt                                           2046

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<210> 1900
 <211> 682
 <212> PRT
 <213> Artificial Sequence

<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

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

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

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
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagggttaga 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 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

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 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
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 cctcatgac	780
tccccggacc 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
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
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
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc	1620
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga	1680
tattgtagaa gtaccacctg ctactttgac tactggggca agggaaccct 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> 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

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

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

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

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 ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca 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 agaaaagttga gcccaaattct tgt 633

<210> 1906
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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 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> 1908
<211> 214
<212> PRT
<213> Artificial Sequence

<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

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
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 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
tcccgggagg agatgacca gaaccaggtc agcctgacct gcctgggtcaa aggtttctat 1140

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

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

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

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 accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg 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 tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagtga 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

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 ctgtctgctg ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggagcct aaactgctca ttacttgggc 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> 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

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

<400> 1915
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggt 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
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
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac 780
tcccggaacc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc 840
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900

gagcagtagc gcagcacgta ccgttggtgc agcgtcctca ccgtcctgca ccaggactgg	960
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag	1020
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca	1080
tcccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggccttctat	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 caggtccaag	1560
tggataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc	1620
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac	1680
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggcaaaggg	1740
accacggtca ccgtctctc agcctccacc aagggcccat cggctcttccc cctggcaccc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtcctc aggactctac tcctcgaga 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

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

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

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

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 ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 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 tggggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gccc aaatct 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

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 gagtgtaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta 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
ctgagcaaa	cagactacga	gaaacacaaa	gtctacgcct	gcgaagtcac	ccatcagggc	600
ctgagctcgc	ccgtcacaaa	gagcttcaac	aggggagagt	gt		642

<210>	1920
<211>	214
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc 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 gccaaggcc 360
aaccctactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540

tacgcgcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac	600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt	660
tcagacaaaa ctcacacatg 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
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 tcgggagggtg gcggatccca ggtgcagtta	1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgtgtc	1440
catggtgggt ctttcagtgg ttactactgg aactggattc gccagccacc agggaaagggg	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 cgggtgctgtg gaactcaggc	1860
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	1920
ctcgagagcg tgggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac	1980
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag 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

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

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

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>
<223> Synthetic polynucleotide

<400> 1923
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

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

<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 ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300

gggaccaagc tggaaatcaa acgaacgggtg gctgcacccat 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

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1927
gagggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccggaaaaa aactggagtg 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

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	tctcccgga	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	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	ccttcttctt	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	tggtggcgga	tcgggaggtg	gcggatccca	ggtgcagctg	1380
caggagtcgg	gcccaggact	ggtgaagcct	tcggagaccc	tgtccctcac	ctgcactgtc	1440
tctggtggct	ccatcagtag	ttacttctgg	agctggattc	ggcagcccc	aggtaaggga	1500
ctggagtgga	ttggctatat	ctattacagt	gggcagacca	aataacaacc	ctccctcaag	1560
agtcgagtca	ccatatcaat	agacacgtcc	aagaaccagt	tctccctgaa	gctgagctct	1620
gtgaccgctg	cggacacggc	cgtgtattac	tgtgcgagag	aaactgggag	ctactacggc	1680
tttgactact	ggggcaaggg	aaccctggtc	accgtctcct	cagcctccac	caagggccca	1740
tcggctcttc	ccctggcacc	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcttggtca	aggactactt	ccccgaaccg	gtgacggtgt	cgtggaactc	aggcgccctg	1860

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag 1920
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg 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

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

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

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

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

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 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> 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

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 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> 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

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

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc	360
aaccccactg tcaactctgtt 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 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 agccctcca gccccatcg agaaaacat ctccaagcc	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 tcgggagggtg gcggatccca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaaact ggattaggca gccccaggg	1500
aaaggccttg agtggatagg aaggacatac tacaggcca agtggataa tgattatgca	1560
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg	1620
aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg	1680

gatagctact accgctacgg tatggacgtc tggggcaaag ggaccacggt caccgtctcc	1740
tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	1800
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	1860
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	1920
tcaggactct actccctcga gagcgtgggtg accgtgccct ccagcagctt gggcacccag	1980
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

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

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

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

<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 aagggaccaa 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> 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

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

<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			
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> 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
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt	300
agaagtacca cctgctactt tgactactgg ggccaggga ccttagtcac cgtctcctca	360
acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga	420
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg	480
aagggtggata 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
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag	840
ttcaactggg acgtggacgg cgtggagggtg cataatgcc aagacaaagcc 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 tggctaaagg 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 aactggtgga atcagggtgga ggtttggtgc 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 ggcgtgcaca cttcccggc tgtcctacag	1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc	1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	2040
gagcccaaat 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

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

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

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

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 gagggttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 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> 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

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 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 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> 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

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
cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 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
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
cacaaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtcctt cctcttcccc ccaaaacca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagaccc tgagggtcaag 840
ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagtg caaggctctc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccagc 1200

cctcccgtgc tggactccga cggctccttc ttcctctata 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
aactgggggtc ttgactactg gggcaaggga accctgggtca ccgtctctag tgcctccacc 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 gcaccagac 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

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

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

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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1947
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 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 agaaagtga gcccaaattct tgt 633

<210> 1948
<211> 211
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1948

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

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> 1949
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1949
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
 attacctgtc gcgcggtcca 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> 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

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
 ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaaactggg 300
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360
 gctgcaccat ctgtcttcat cttcccgcc 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
 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac 900
 ggtagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaagggt 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 tatgcatgc 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 ggtaaaggaa 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

<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	

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

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

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

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 ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

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 caaggaaca 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 tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540
agctatctga gcctgacgcc tgagcagtggt 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

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
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
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360
gctgcaccat ctgtcttcat cttcccgcga 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 tcttctcttt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780

cctgagggtca catgcgtggt 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
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
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 actggggcaa gggaaccctg gtcaccgtct ctagtgcctc caccaagggc	1740
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	1860
ctgaccagcg gcgtgcacac cttcccggt gtcctacagt cctcaggact ctactccctc	1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	1980
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatac 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

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

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

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

<210> 1959
 <211> 633
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1959
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
 gggaaaagccc 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
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
 ttccccgaac cgggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca 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		

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> 1961
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1961
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> 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

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
 cagggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
 cagccccag ggaaaaaact 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 cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
 cagttgaaat ctggaactgc ctctgttgtg 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 ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac	780
accctcatga tctcccgac ccctgaggtc 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 ctccaaagcc aaagggcagc cccgagaacc acagggtgac	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 gggtaaagga	1740
acgttgggtca ccgtctctag tgcctccacc aaggggccat cggtcttccc cctggcaccc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtctc aggactctac tccctcgaga gcgtggtgac 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

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

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

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

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 aaaggttcct aaactgctca tttactgggc atctacccgg	180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact	300
cctctcactt tcggcgaagg gaccaaggtg gagatcaaac gagcctccac caagggccca	360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc	420
tgcttggtca aggactactt ccccgaaccg 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

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 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
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> 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

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
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
cagccccag ggaaaaaact 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 cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtggaaagg ggataacgcc ctccaatcgg gtaactccca 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 tctcccgac ccctgaggtc acatgcgtgg tggtaggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca	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 ctttcttcct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggtagcgga	1380
tcgggagggtg gcggatccga ggtgcagctg gtgcagtctg gagcagagg gaaaaagccc	1440
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc	1500
ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttgg	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctcttgac tactggggca agggaaccct ggtcaccgtc	1740

tctagtcgct	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	ccaagggtgga	caagaaagtt	2040
gagcccaa	attgt					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

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

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

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

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

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gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaagggtcct aaactgctca tttactgggc atctaccgg      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 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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<210> 1972

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

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gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga cctgtgtgacg      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 cgcccttacac attcggagaa      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
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<210> 1974

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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

gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt	60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg	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
agtgctcca ccaaggggccc 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
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat 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
tcaaagcca aagggcagcc ccgagaacca cagggtgtaca 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 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 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

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<210> 1976
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1976

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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

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

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 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
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 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
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tggggaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gccc aaatct 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

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 accatcgctc 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 taactccag 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

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
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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 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
cccaaacttt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
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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	cggatcccag	1380
gtgcagctgc	aggagtcggg	cccaggactg	gtgaagcctt	cggagaccct	gtccctcacc	1440
tgcactgtct	ctggtggctc	catcagtagt	tacttctgga	gctggattcg	gcagccccc	1500
ggtaaggga	tggagtggat	tggctatata	tattacagt	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	aagtacagt	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

<220>
<223> Synthetic polypeptide

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

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

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

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 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> 1983
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1983
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 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

<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

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
 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 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> 1986
 <211> 214
 <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

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
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg 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
agtcctcca ccaagggcc atcggcttcc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
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cctgaggtca 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 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
gaggatgggg atagctacta ccgctacggg atggacgtct ggggcaaagg 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> 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

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

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

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>
<223> Synthetic polynucleotide

<400> 1989
gacatccaga tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggaacct aaactgctca ttactgggc atctaccgg 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
tgcctgggtca aggactactt ccccgaaaccg gtgacgggtgt cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540

agcgtggtga 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

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

<220>
 <223> Synthetic polynucleotide

<400> 1991
 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 cgccctctc 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> 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

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
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1993
 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
 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 ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	720
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc	780
gtgggtgggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	840
gtggaggtgc ataatgccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt	900
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aaggtctcca acaaagccct cccagccccc 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 gcaggtggca gcaggggaac	1260
gtcttctcat 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 acccgccct 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 aacacaaagt 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

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

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

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

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 gagtgtaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg aaccaggct 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	gctgcctggt	caaggactac	420
ttccccgaac	cggtgacggt	gtcgtggaac	tcaggcgccc	tgaccagcgg	cgtgcacacc	480
ttcccggtg	tcctacagtc	ctcaggactc	tactccctca	aaagcgtggt	gaccgtgccc	540
tccagcagct	tgggcaccca	gacctacatc	tgcaacgtga	atcacaagcc	cagcaacacc	600
aaggtggaca	agaaaagttga	gccccaaatct	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

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 gagtggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420

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> 1999
 <211> 2034
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1999
 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
 tggggctcttg actactgggg ccagggaacc 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 tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaaggtg 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
aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa 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 gcaggaggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtgggtg 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 cgcccggtgta ttactgtgcg agagaaactg ggagctacta cggctttgac	1680
tactggggca agggaaaccct ggtcaccgtc tcctcaactg tggctgcacc atctgtcttc	1740
atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgtg	1800
aataacttct atcccagaga ggccaaagta cagtggaaagg tggataacgc cctccaatcg	1860
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcgaa	1920
agcacctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	1980

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

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

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

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>
 <223> Synthetic polynucleotide

<400> 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
 gaagatTTTtg caacttacta ctgtcaacag agttacagta CCCctcggac gttcggccaa 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 tactccctca aaagcgtggg gaccgtgccc 540
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gccc aaatct tgt 633

<210> 2002
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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

<220>
<223> Synthetic polynucleotide

<400> 2003
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	gagtgggttcg	300
gtgttcggcg	aagggaccaa	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	gtggcccccta	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

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
<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
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgcatgt attactgtgc gagaagtaac 300

tggggtcttg actactgggg ccaggggaacc ctggtcaccg tctctagtgc ctccaccaag	360
ggcccatcgg tcttccccct ggcacccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgtg 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
ctcttcccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc	780
gtgggtgggtg 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
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 cgggtgggtg cggatcggga ggtggcggat cccaggtaca gttgcaggag	1380
tcaggccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg	1440
gacagtgtct ctaccaacag tggtgcttgg aactggatta ggcagcccc 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 aaagggacca 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 cacccatcag 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

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

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

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

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

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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggaacct aaactgctca tttactgggc atctacccgg      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
tgcctggtca aggactactt ccccgaaaccg gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651
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<210> 2008

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2008

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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
```

```
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 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> 2009

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2009
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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgag 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> 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

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
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc

acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca	120
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgtgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt	300
agaagtacca 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 cgtggtgacc 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 ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc	900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc 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 gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggta	1380
caactggtgg aatcagggtg aggtttgggt cagccgggga gatcgctcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgccctgga	1500
aaagggtcgc agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560

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agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag      1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaaagt ctcctacttg      1680
tctacagctt cgtcgtcga ctattgggggt aaaggaacgt tggtcaccgt ctctagtact      1740
gtggctgcac catctgtctt catcttccccg ccatctgatg agcagttgaa atctggaact      1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaaagt acagtggaag      1860
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag      1920
gacagcacct acagcctcga aagcaccttg acgctgagca aagcagacta cgagaaacac      1980
aaagtctacg cctgcgaagt caccatcag ggctgagct cgcccgtcac aaagagcttc      2040
aacaggggag agtgt                                         2055

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<210> 2012
<211> 685
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic polypeptide

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```

<400> 2012

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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 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

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

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 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
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2013
gatatccaaa tgacacaatc accatcgctg 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
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 tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagttga gccc aaatct 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

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

<210> 2015
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2015
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 acgaacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggtagccgc 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

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

caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc	60
acctgcgctg tccatgggtg 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 ccgaaccggt gacggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttggtg 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
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aacctctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag	1080
atgaccaaga accaggctcag 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 tccgggtggt ggcggatcgg 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
cccgtcaagg cgggagtgga gaccaccaa ccctccaaac agagcaacaa caagtacgcg	1920
gccgagagct acctgagcct gacgcccag cagtggaagt cccacagaag ctacagctgc	1980
caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca	2037

<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

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

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

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

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
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 gagtgggttcg 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 ccaagggtgga caagaaaagt gagcccaa at 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

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 attggatatca 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 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> 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

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
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 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 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 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 ctgcctgggc aaaggcttct atcccagcga catcgccgtg 1140

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

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

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 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

<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 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 cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagtga 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

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

<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 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> 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

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
caggtgcagc 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 ctcagcctcc 360
accaagggcc catcggctctt ccccttgga cccctctcca 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 agaaagtga gccc aaatct 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttctctt 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 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 ctttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tggTggcgga tcgggaggtg gcggatccga ggtgcagctg	1380
gtgcagtctg gagcagaggt gaaaaagccc ggggagTctc tgaagatctc ctgtaagact	1440
tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc	1500
ctggagtgga tggggatcat ctatcttggT gactcagata ccagatacag cccgtccttc	1560
caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc	1620
agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggTcttgac	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 cgcgcccgag	1920
agctacctga gcctgacgcc cgagcagtgg 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

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

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

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

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 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> 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

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 tgacccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
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 tcggcgaggg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360
gtctttcatct 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> 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

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
caggtagcagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120
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 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 gccaccgtg cccagcacct 720

gaactcctgg ggggaccgtc agtcttcctc ttccccccaa 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 cacagggtgta 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 aggtacaact ggtggaatca ggtggagggt ttggtgcagcc 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
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
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

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

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

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 ggtccggggtc aggtacggac ttactctca 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 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> 2038
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 2038

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

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 aaagggttcct aaactgctca ttactgggc atctaccgg 180
gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcgaggg 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
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	660

<210> 2040
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120
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 cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc	420
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggct	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
atctccccga 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
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 aagggaaccc tggtcaccgt ctctagtcag	1740
cccaaggcca accccactgt cactctgttc ccgcccctct 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 agtggcccct	2040
acagaatgtt ca	2052

<210> 2042
 <211> 684
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 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

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

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

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
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 ccaaggtgga 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

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
gagggtacaac tgggtggaatc aggtggaggt ttgggtgcagc cggggagatc gctcaggctt

agctgtgcgg catcgggggtt tacttttcgat 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 gaacgttggg 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
ttccggaccc 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
ttccgggagg 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 tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg	1440
tcctcacct gcgctgtcca tgggtgggtcc ttcagtgggt 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	tactggggca	agggaaccct	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	agcacccctga	cgctgagcaa	agcagactac	1980
gagaaacaca	aagtctacgc	ctgcgaagtc	acccatcagg	gcctgagctc	gcccgtcaca	2040
aagagcttca	acagggggaga	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

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

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

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

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 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 catcgggtctt ccccttgga 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
aagggtggaca agaaagtga gccc aaatct tgt 633

<210> 2048
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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 ggtccgggtc aggtacggac ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 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 tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2050
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 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

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 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
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
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320

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

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

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

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
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 cgggtgacggg 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> 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

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 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 gcgtgcctcc accaagggcc catcgggtcctt ccccctggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtagcggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtcg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaaagttga gcccaaattct 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

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggt tacttttcgat 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 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 ccccaaaaac ccaaggacac cctcatgac 780
ttccggaccc ctgagggtcac 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 gaaccagggtc agcctgacct gcctgggtcaa aggcttctat	1140
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1200
acgcctccccg tgctggactc cgacggctcc ttcttcctct 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 ccccagggaaggaggccttgag tggataggaa ggacatacta caggtccaag	1560
tggtataatg 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 cctgacgtg	1980
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg	2040
agctcgccccg 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

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

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

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

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 ttactgggc atctaccgg 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
tgcctggtca aggactactt cccgaaccg gtgacgggtg cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

651

<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

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
 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 gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gcccaaattct 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

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
gagggtgcagc 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
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gccaaggcc 360
aaccacctg 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 gcccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctgggtc 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 ctgcgctgtc	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 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 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

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

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

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>
<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
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt ccccttgga 360

ccctcctcca	agagcacctc	tgggggcaca	gcggccctgg	gctgcctggt	caaggactac	420
ttccccgaac	cggtgacggt	gtcgtggaac	tcaggcgccc	tgaccagcgg	cgtgcacacc	480
ttcccggtg	tcctacagtc	ctcaggactc	tactccctca	aaagcgtggt	gaccgtgccc	540
tccagcagct	tgggcaccca	gacctacatc	tgcaacgtga	atcacaagcc	cagcaacacc	600
aaggtggaca	agaaagtga	gccccaatct	tgt			633

<210>	2066
<211>	211
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 2066

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

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

<220>
<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 aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc	480
ggcgtgcaca ccttccccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg	540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag	600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt	645

<210> 2068
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <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	

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
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 2069
 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
 tggggctctg 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 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
aagtgcgaagg 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 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 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

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

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

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

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 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 catcggtctt ccccctggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
 ttccccgaac cggtgacggg 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> 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

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 gcagggttatg 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 aagggaccaaa 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 ccaagggtgga caagaaagtt gagcccaaat 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

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 ggtcaccatc tcagccgaca agtccatcag taccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgcatgt attactgtgc gagaagtaac 300

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 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 tcgggagggtg gcggatccca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg	1500
aaaggccttg agtggatagg aaggacatac tacagggtcca agtggataa tgattatgca	1560
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg	1620
aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg	1680
gatagctact accgctacgg tatggacgtc tggggcaaag ggaccacggt caccgtctcc	1740
tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	1800

ggaactgcct ctgttggtg cctgctgaat aacttctatc ccagagaggc caaagtacag 1860
 tggaagggtgg 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> 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

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

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

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

<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 atctacccgg      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
tgcctggtca aggactactt ccccgaaaccg gtgacgggtg cgtggaactc aggcgccctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651
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<210> 2078

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2078

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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
```

```
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

<212> DNA

<213> Artificial Sequence

<220>

<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 gagtgggttcg 300
gtgttcggcg aagggaacaa 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 ccaagggtga caagaaagtt gagcccaaat cttgt 645

<210> 2080
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<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

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

<210> 2081

<211> 2064

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2081

cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc

acctgcgctg tccatggtgg gtccttcagt ggttactact 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 ggccaggga cctagtcac cgtctcctca	360
acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga	420
actgcctctg ttgtgtgcct gctgaataac ttctatcca 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
ctggggggac cgtcagtctt cctcttcccc ccaaaacca aggacaccct catgatctcc	780
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc 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 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 ccgggtgggt gcggatcggg aggtggcgga	1380
tccgaggtag aactggtgga atcagggtgga ggtttggtgc 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	gtcgtctgac	tattggggta	aaggaacgtt	ggtcaccgtc	1740
tctagtactg	tggctgcacc	atctgtcttc	atcttcccgc	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	acagggggaga	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

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

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

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

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 accatcgctc gtttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccggggtc 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 cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagttga gccc aaatct 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

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 gagtgtaga 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 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> 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

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 tccatgggtg gtccttcagt ggttactact 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
acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420
actgcctctg ttgtgtgcct gctgaataac ttctatcca 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 acatgccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc 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 caagaccag 1200
cctcccgctg tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320

cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga	1380
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
aactgggggtc ttgactactg gggcaaggga accctggtca ccgtctctag tcagcccaag	1740
gccaacccca ctgtcactct gttcccgccc tcctctgagg agctccaagc caacaaggcc	1800
acactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca	1860
gatggcagcc ccgtcaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac	1920
aagtacgcgg ccgagagcta cctgagcctg acgcccgagc agtggaagtc ccacagaagc	1980
tacagctgcc aggtcacgca tgaagggagc 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

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

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

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

<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 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 caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt 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

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

<210> 2091
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2091
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 cttcggcgaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaaagttga gcccaaattct 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

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 tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120
ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgcgag 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
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt ccccccaaaa 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
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
aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc	1920
aaggacagca cctacagcct cgaaagcacc 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		

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

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

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

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 accatcgctc gtttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagaac cgaagctcct 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 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 gccc aaatct 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

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 tggaatatcaa 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 agaaagtga gcccaaatct 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

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
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 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 ccctcatgat ctcccgacc 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 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 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 actgtgagag aagtaactgg	1680
ggtcttgact actggggcaa 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 cgcatgaagg 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

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

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

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

<210> 2101
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2101
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
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcctt caaaagcgtg 540

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaatt 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

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

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 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 ccccttgga 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

aagggtggaca agaaaagttga gcccaaatct 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

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
caggtagcgt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggattagg 120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtgggtat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
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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 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 aagtgaagg tctccaacaa agccctccca	1020
gccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acagggtgtac	1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagggggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag	1260
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gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggaggcgga	1380
tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggagggtt ggtgcagccg	1440
gggagatcgc tcaggcttag ctgtgcggca tcgggggtta 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 tactgtggct gcaccatctg tcttcatctt cccgccatct	1800
gatgagcagt tgaatatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc	1860
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag	1920
agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgtg	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

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

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

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

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

gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc ggcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

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 gctgcctggg caaggactac 420
 ttccccgaac cggtgacggg 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> 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

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
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttcct 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 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	

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
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
cagccccccag ggaaaaaact 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 cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgtttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtgggaagg 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 tggaggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgtttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca	1020
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acagggtgtac	1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagggggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcgga	1380
tcgggagggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc	1440
ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc	1500
ggctgggtgc gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggg	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctttgac tactggggca agggaaacct ggtcaccgtc	1740
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc	1800

caagccaaca	aggccacact	agtgtgtctg	atcagtgact	tctaccgagg	agctgtgaca	1860
gtggcctgga	aggcagatgg	cagccccgtc	aaggcggggag	tggagaccac	caaaccctcc	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
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<220>
<223> Synthetic polypeptide

$\langle 400 \rangle$ 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

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

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

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 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

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

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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 gagggaccaaa 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 caagaaaagt gagcccaaat cttgt                      645
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<210> 2114

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 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

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
tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctacccgg 180
gaatccggggg 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 aggcgccctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t 651

<210> 2116
<211> 217
<212> PRT
<213> Artificial Sequence

<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

Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
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Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
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Asp Lys Lys Val Glu Pro Lys Ser Cys
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