

A-1937-WO-PCT_ST25
SEQUENCE LISTING

<110> AMGEN INC.
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<120> ANTI-TL1A/ANTI-TNF-ALPHA BISPECIFIC ANTIGEN BINDING PROTEINS AND
USES THEREOF

<130> A-1937-WO-PCT

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

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

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

<160> 2136

<170> PatentIn version 3.5

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A-1937-WO-PCT_ST25

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
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Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
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Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
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A-1937-WO-PCT_ST25

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Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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A-1937-WO-PCT_ST25

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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A-1937-WO-PCT_ST25

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 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
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Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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 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
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Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
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Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

A-1937-WO-PCT_ST25

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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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
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Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
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Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
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A-1937-WO-PCT_ST25

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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
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 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
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A-1937-WO-PCT_ST25

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

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

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
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Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
Page 11

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
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Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
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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
Page 12

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met
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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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 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

A-1937-WO-PCT_ST25

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A-1937-WO-PCT_ST25

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln 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
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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

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 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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 accgtctcta gt 372

A-1937-WO-PCT_ST25

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

<400> 36

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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
 115 120

<210> 37
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 <212> DNA
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<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
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A-1937-WO-PCT_ST25

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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
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Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
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<210> 39
<211> 348
<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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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
Page 17

A-1937-WO-PCT_ST25

65 70 75 80

Leu Gln Trp Ser Ser₈₅ Leu Lys Ala Ser Asp₉₀ Thr Ala Met Tyr Tyr₉₅ Cys

Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val

Thr Val Ser₁₁₅ Ser

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

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ggtaaagccc caaaagccct catctacagt gcctcttttc tctatagtgg tgtaccatac      180
aggttcagcg gatccggtag tggtactgat ttcaccctca cgatcagtag cctccagcca      240
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<210> 42
<211> 107
<212> PRT
<213> Homo sapiens

<400> 42

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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A-1937-WO-PCT_ST25

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

<400> 44
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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
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<210> 45
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 <212> DNA
 <213> Homo sapiens

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A-1937-WO-PCT_ST25

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

<400> 46

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

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1419

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 <212> PRT
 <213> Homo sapiens

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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 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

A-1937-WO-PCT_ST25

225 230 235 240

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met

Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His

Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val

His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Arg Glu Glu Gln Tyr₃₀₀ Asn Ser Thr Tyr

Arg Val Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀

Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile

Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val

Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Asp₃₆₀ Glu Leu Thr Lys Asn₃₆₅ Gln Val Ser

Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu

Trp Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀

Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val

Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met

His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser

Pro Gly₄₅₀ Lys

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<212> DNA
<213> Homo sapiens

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A-1937-WO-PCT_ST25

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

<400> 50

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Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Asp Ile Arg Asp Asp
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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

A-1937-WO-PCT_ST25

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

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1425

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 <212> PRT
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 20 25 30

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 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
 Page 26

A-1937-WO-PCT_ST25

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
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Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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Leu Ser Pro Gly Lys
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<212> DNA
<213> Homo sapiens

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Page 27

A-1937-WO-PCT_ST25

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

<400> 54

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

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

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

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Tyr Ser Thr Pro Arg
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

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

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

A-1937-WO-PCT_ST25

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
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<210> 55
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<212> DNA
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ctctccctgt ctccgggtaa a

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

<400> 56

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

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

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

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

Arg Glu Ile Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Ala
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 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
 Page 30

A-1937-WO-PCT_ST25															
225				230				235				240			
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Glu	Val	Lys 275	Phe	Asn	Trp	Tyr	Val 280	Asp	Gly	Val	Glu	Val 285	His	Asn	Ala
Lys	Thr 290	Lys	Pro	Arg	Glu	Glu 295	Gln	Tyr	Gly	Ser	Thr 300	Tyr	Arg	Val	Val
Ser 305	Val	Leu	Thr	Val	Leu 310	His	Gln	Asp	Trp	Leu 315	Asn	Gly	Lys	Glu	Tyr 320
Lys	Cys	Lys	Val	Ser 325	Asn	Lys	Ala	Leu	Pro 330	Ala	Pro	Ile	Glu	Lys 335	Thr
Ile	Ser	Lys	Ala 340	Lys	Gly	Gln	Pro	Arg 345	Glu	Pro	Gln	Val	Tyr 350	Thr	Leu
Pro	Pro	Ser 355	Arg	Glu	Glu	Met	Thr 360	Lys	Asn	Gln	Val	Ser 365	Leu	Thr	Cys
Leu	Val 370	Lys	Gly	Phe	Tyr	Pro 375	Ser	Asp	Ile	Ala	Val 380	Glu	Trp	Glu	Ser
Asn 385	Gly	Gln	Pro	Glu	Asn 390	Asn	Tyr	Lys	Thr	Thr 395	Pro	Pro	Val	Leu	Asp 400
Ser	Asp	Gly	Ser	Phe 405	Phe	Leu	Tyr	Ser	Lys 410	Leu	Thr	Val	Asp	Lys 415	Ser
Arg	Trp	Gln	Gln 420	Gly	Asn	Val	Phe	Ser 425	Cys	Ser	Val	Met	His 430	Glu	Ala
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<212> DNA
<213> Homo sapiens

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gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag      180
agaccagggg aagcccctaa gctcctgata tatgctgcat ccagtttgca aagtggggct      240
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A-1937-WO-PCT_ST25

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 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
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<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
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
 20 25 30

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

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

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

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

A-1937-WO-PCT_ST25

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
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<210> 59
 <211> 1344
 <212> DNA
 <213> Homo sapiens

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 ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300
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A-1937-WO-PCT_ST25

<212> PRT
<213> Homo sapiens

<400> 60

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

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

Lys Thr Lys Pro 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

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A-1937-WO-PCT_ST25

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

<400> 62

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

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln
 50 55 60

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

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

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

Tyr Cys Gln Gln Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr
 115 120 125

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

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

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

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 180 185 190

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 Page 36

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
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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

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<211> 455

A-1937-WO-PCT_ST25

<212> PRT
 <213> Homo sapiens

<400> 64

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 20 25 30
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 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

A-1937-WO-PCT_ST25

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

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 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

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
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A-1937-WO-PCT_ST25

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<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

A-1937-WO-PCT_ST25

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

Phe Asn Arg Gly Glu Cys
210

<210> 67
<211> 1350
<212> DNA
<213> Homo sapiens

<400> 67
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acctgcgctg tccatggtag gtccttcagt gggtactact ggaactggat ccgccagccc 120
ccagggaagg ggctggagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agatcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cactctgagg 420
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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
aaatcttctg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
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agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactgggt gaatggcaag 960
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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320
cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 68
<211> 450
<212> PRT
<213> Homo sapiens

<400> 68

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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agatgcgaca tccagatgac ccagtcctca agctccctgt ctgcgtctgt gggcgatagg 120
gtcaccatca cttgcaggtc cagccagagt gtgttatata 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 cggagggacc aagggtggaga tcaaacgaac ggtggctgca 420

A-1937-WO-PCT_ST25

ccatctgtct tcattctccc gccatctgat gaggcagttga aatctggaac tgcctctgtt 480
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
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 gagtgt 726

<210> 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

A-1937-WO-PCT_ST25

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

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

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

<400> 71
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 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120
 cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
 cagttctccc tgaagctgag ctctgtgact gccgaggaca 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 tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540
 gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagaaagtgt agcccaaatt ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
 gaactcctgg ggggaccgtc agtcttctc tccccccaa aaccaagga 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 cacaggtgta caccctgccc 1080
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 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
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<210> 72
 <211> 455
 <212> PRT
 <213> Homo sapiens

<400> 72

A-1937-WO-PCT_ST25

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

Thr Leu Ser Leu Thr Cys Thr 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

A-1937-WO-PCT_ST25

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 ccagtcctca agctccctgt ctgcgtctgt gggcgatagg 120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcceaaca taagaactac 180
ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact 300
ctcaccatca gcagcctgca gcctgaagat ttcgcaactt attactgtca gcaatattat 360
aagactcctc tcactttcgg cggagggacc aagggtggaga tcaaacgaac ggtggctgca 420

A-1937-WO-PCT_ST25

ccatctgtct tcattttccc gccatctgat gaggcagttga aatctggtac cgcctctgtt 480
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
 gcctgcgaag tcacccatca gggcctgagc tcgcccgta 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

A-1937-WO-PCT_ST25

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
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 agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc 120
 cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
 atcaggcagg ccccgaggaa 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
 accacgggtca ccgtctcctc agcctccacc aaggggccat cgggtcttccc cctggcaccc 480
 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540
 cccgaaccgg tgacgggtgc gtggaactca ggcgcctga ccagcggcgt gcacaccttc 600
 ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660
 agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720
 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcccc 780
 gcacctgaac tcctgggggg accgtcagtc ttctcttccc ccccaaaacc caaggacacc 840
 ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900
 cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 960
 ccgcgggagg agcagtacgg cagcacgtac cgtgtgggtca gcgtcctcac cgtcctgcac 1020
 caggactggc tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc 1080
 cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140
 ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa 1200
 ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260
 tacaagacca cgcctcccggt gctggactcc gacggctcct tcttctctta tagcaagctc 1320
 accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380
 gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1431

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

A-1937-WO-PCT_ST25

<400> 76

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

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

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

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

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

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

Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met
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
Page 50

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 gggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
 gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag 180
 aaaccaggga aagcccctaa ggcctgatc tatgctgcgt ccagtttgca aagtggggtc 240
 ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300
 cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360

A-1937-WO-PCT_ST25

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 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> 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

A-1937-WO-PCT_ST25

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

Phe Asn Arg Gly Glu Cys
210

<210> 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
gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420
acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600
gctgtcctac agtcctcagg actctactcc ctccagcagc tgggtgaccgt gccctccagc 660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720
gacaagaaaag ttgagccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840
atgatctccc ggaccctga ggtcacatgc gtgggtggtg acgtgagcca cgaagaccct 900
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 960
tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag 1020
gactggctga atggcaagga gtacaagtgc aaggctctcca acaaagccct cccagcccc 1080
atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140
cccccatccc gggaggagat gaccaagaac caggctagcc tgacctgcct ggtcaaaggc 1200
ttctatccca gcgacatcgc cgtggagtggt gagagcaatg ggcagccgga gaacaactac 1260
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc 1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa 1428

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

A-1937-WO-PCT_ST25

<400> 80

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc	300
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgccaaa	360
gtctcctact tgtctacagc ttcgtcgcgc gactattggg gtcaaggaac gttgggtcacc	420
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc	480
acctctgggg gcacagcggc cctgggctgc ctgggtcaagg 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 caaaaccca aggacaccct catgatctcc	840
cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tggaggtcaag	900
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa	1080
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1140
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccag	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 ggactggtga agccttcgga gaccctgtcc	1500
ctcacctgca ctgtctctgg tggtccatc agtagttact tctggagctg gatccggcag	1560
ccccaggta agggactgga gtggattggc tatactctatt acagtgggca gaccaaatac	1620
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tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt	1920
cagagcatta acaactatth aaattggtat cagcagagac cagggaagc ccctaagctc	1980
ctgatctatg ctgcatccag tttgcaaagt ggggtcccat caaggttcag tggcagtgga	2040
tctgggacag atttactct caccatcagc agtctgcaac ctgaagattt tgcaacttac	2100
tactgtcaac agagttacag taccctcgg acgttcggcc aagggaacaa gctggaaatc	2160
aaacga	2166

<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

A-1937-WO-PCT_ST25

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
Arg₃₀₅ Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Gln₄₆₀ Val Gln Leu Gln
Glu₄₆₅ Ser Gly Pro Gly Leu₄₇₀ Val Lys Pro Ser Glu₄₇₅ Thr Leu Ser Leu Thr₄₈₀
Cys Thr Val Ser Gly₄₈₅ Gly Ser Ile Ser Ser₄₉₀ Tyr Phe Trp Ser Trp₄₉₅ Ile
Arg Gln Pro Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Ile Gly Tyr Ile₅₁₀ Tyr Tyr

A-1937-WO-PCT_ST25

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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cgctgtcagt ctgtgctgac gcagccgccc tcagtgtctg gggccccagg gcagagggtc 120
accatctcct gactgggag cagttccaac atcggggcag gttatgatgt aactggtac 180
cagcagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240
ggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300
gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360
ggttcgggtgt tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420

A-1937-WO-PCT_ST25

tcggtcactc tgttcccgcc ctcctctgag gagcttcaag ccaacaaggc cacactggtg 480
 tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540
 cccgtcaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600
 gccagcagct atctgagcct gacgcctgag cagtggaagt 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

A-1937-WO-PCT_ST25
200 205Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215<210> 85
<211> 1404
<212> DNA
<213> Homo sapiens

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<400> 85
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cgctgtgagg tgcagctggt gcagctctgga gcagaggtga aaaagcccgg ggagtctctg      120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc      180
cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc      240
agatacagcc cgtccttcca aggccaggtc accatctcag cgcacaagtc catcagtacc      300
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga      360
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc      420
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca      480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggg gtcgtggaac      540
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc      600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc      660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc      720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca      780
gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgagggtc      840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      900
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg      960
taccgtttgt tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac     1020
aagtgcaagg 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 ctttcttctt ctatagcaag ctcaccgtgg acaagagcag gtggcagcag     1320
gggaacgtct tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacgcagaag     1380
agcctctccc tgtctccggg taaa                                     1404

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

<400> 86

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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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atcacttgta aagccagtca gaacgtaggt actaacgtag cctggtatca 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 tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

<400> 89
 atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
 agatgcgagg ttacagctggt cgagtcagga ggcggctctcg tgcagcctgg cggatcactg 120
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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 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
Page 66

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
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Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
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Ser Leu Ser Leu Ser Pro Gly Lys
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33

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<400> 92

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<210> 94
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<400> 98
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<210> 101

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<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102

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<400> 102

Leu Gln His Asn Ser Tyr Pro Pro Thr
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<210> 103

<211> 33

<212> DNA

<213> Homo sapiens

<400> 103

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<400> 104

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24

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<210> 106

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1 5

<210> 107
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<400> 108

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<400> 109
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33

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<210> 112
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<400> 112

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<400> 113
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27

<210> 114
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 <223> Xaa may independently be M, G, A, V, I, or L

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 <223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

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 <213> Homo sapiens

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<210> 116
 <211> 17
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<400> 116

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 1 5 10 15

Val

<210> 117
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 <212> DNA
 <213> Homo sapiens

<400> 117
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21

<210> 118
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<400> 118

Trp Ala Ser Thr Arg Glu Ser
 1 5

<210> 119
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<210> 120
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<210> 121
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36

<210> 122
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<400> 122

Arg Ala Ser Gln Ser Val Arg Ser Ser Tyr Leu Ala
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21

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<400> 124

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<210> 126
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<400> 126

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<400> 128

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Val

<210> 129
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ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
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A-1937-WO-PCT_ST25

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

<220>
<223> Synthetic polypeptide

<400> 130

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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

Phe Ser Leu Lys₁₀₀ Leu Thr Ser Val Thr₁₀₅ Ala Ala Asp Thr Ala₁₁₀ Val Tyr
 Tyr Cys Ala₁₁₅ Arg Gly Tyr Cys Arg₁₂₀ Ser Thr Thr Cys Tyr₁₂₅ Phe Asp Tyr
 Trp Gly₁₃₀ Gln Gly Thr Leu Val₁₃₅ Thr Val Ser Ser Ala₁₄₀ Ser Thr Lys Gly
 Pro Ser Val Phe Pro Leu₁₅₀ Ala Pro Ser Ser Lys₁₅₅ Ser Thr Ser Gly Gly₁₆₀
 Thr Ala Ala Leu Gly₁₆₅ Cys Leu Val Lys Asp₁₇₀ Tyr Phe Pro Glu Pro₁₇₅ Val
 Thr Val Ser Trp₁₈₀ Asn Ser Gly Ala Leu₁₈₅ Thr Ser Gly Val His₁₉₀ Thr Phe
 Pro Ala Val₁₉₅ Leu Gln Ser Ser Gly₂₀₀ Leu Tyr Ser Leu Glu₂₀₅ Ser Val Val
 Thr Val₂₁₀ Pro Ser Ser Ser Leu₂₁₅ Gly Thr Gln Thr Tyr₂₂₀ Ile Cys Asn Val
 Asn His Lys Pro Ser Asn₂₃₀ Thr Lys Val Asp Lys₂₃₅ Lys Val Glu Pro Lys₂₄₀
 Ser Cys Asp Lys Thr₂₄₅ His Thr Cys Pro Pro₂₅₀ Cys Pro Ala Pro Glu₂₅₅ Leu
 Leu Gly Gly Pro₂₆₀ Ser Val Phe Leu Phe₂₆₅ Pro Pro Lys Pro Lys₂₇₀ Asp Thr
 Leu Met Ile₂₇₅ Ser Arg Thr Pro Glu₂₈₀ Val Thr Cys Val Val₂₈₅ Val Asp Val
 Ser His Glu Asp Pro Glu Val₂₉₅ Lys Phe Asn Trp Tyr₃₀₀ Val Asp Gly Val
 Glu Val His Asn Ala Lys₃₁₀ Thr Lys Pro Cys Glu₃₁₅ Glu Gln Tyr Gly Ser₃₂₀
 Thr Tyr Arg Cys Val₃₂₅ Ser Val Leu Thr Val₃₃₀ Leu His Gln Asp Trp₃₃₅ Leu
 Asn Gly Lys Glu₃₄₀ Tyr Lys Cys Lys Val₃₄₅ Ser Asn Lys Ala Leu₃₅₀ Pro Ala
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

355 A-1937-WO-PCT_ST25 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

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

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<223> Synthetic polynucleotide

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aggttcagcg gatccggtag tggtagtgat ttcaccctca cgatcagtag cctccagcca 240
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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt 642

<210> 132
<211> 236
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 132

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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

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
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<210> 133

<211> 642

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<400> 133

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<210> 134

<211> 234

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<223> Synthetic polypeptide

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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

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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
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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840

A-1937-WO-PCT_ST25

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140
 atgaccaaga accaggtcag cctgacctgc 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> 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

A-1937-WO-PCT_ST25

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> 137
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 137
 caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggcagccc 120
 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
 ccctccctca agagtcgagt caccatgtca atagacacgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaattggg 300
 agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc cagtgcctcc 360
 accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtctg tcctacagtc ctcaggactc 540
 tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga 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 aagccgtgag aggagcagta cggcagcacg 900
 taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga 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

<210> 138
 <211> 467
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polypeptide
 <400> 138

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<212> PRT
<213> Homo sapiens

<400> 146

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

<210> 147
<211> 21
<212> DNA
<213> Homo sapiens

<400> 147
ggtaacagca atcgccctc a

21

<210> 148
<211> 7
<212> PRT
<213> Homo sapiens

<400> 148

Gly Asn Ser Asn Arg Pro Ser
1 5

<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
 agtgcctctt 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 tgcata

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

A-1937-WO-PCT_ST25

<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 ctcttacta 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 aaccctctcc 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
gaggatgggg 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 aaccctgcc 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

A-1937-WO-PCT_ST25

<211> 54
<212> DNA
<213> Homo sapiens

<400> 195
aggacatact acaggtccaa gtggtataat gattatgcag tttctctgaa aagt 54

<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

A-1937-WO-PCT_ST25

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

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

Leu Gly Cys Leu Val 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

A-1937-WO-PCT_ST25

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

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

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

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

Gly Lys
450

<210> 199
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<400> 199
accaacagtg ttgcttgga c

21

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<400> 200

Thr Asn Ser Val Ala Trp Asn
1 5

<210> 201
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<212> DNA
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aggacatact acaggtccaa gtggtataat gattatgcag tttctgtgaa aggt

54

<210> 202
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<400> 202

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

Lys Gly

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<211> 39

<212> DNA
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gaggatgggg atagtacta ccgctacggt atggacgtc

39

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<223> Each X is independently M, G, A, V, I, or L

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (14)..(14)
<223> Xaa can be any naturally occurring amino acid

<400> 204
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Gly

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15

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Ser Tyr Asp Met His
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<212> DNA
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gttatatcat atgatggaag tattaaatac tatgcagact ccgtgaaggg c

51

<210> 208
 <211> 17
 <212> PRT
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<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
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 <212> DNA
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<400> 209
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtc

45

<210> 210
 <211> 15
 <212> PRT
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<400> 210

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

<210> 211
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 <212> DNA
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<400> 211
 agctactgga tcggc

15

<210> 212
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<400> 212

Ser Tyr Trp Ile Gly
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<210> 213
 <211> 51
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<400> 213
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51

<210> 214
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<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

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<400> 216

Ser Asn Trp Gly Leu Asp Tyr
 1 5

<210> 217

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<212> DNA

<213> Homo sapiens

<400> 217

gactatggaa tgaat

15

<210> 218

<211> 5

<212> PRT

<213> Homo sapiens

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Asp Tyr Gly Met Asn
 1 5

<210> 219

<211> 51

<212> DNA

<213> Homo sapiens

<400> 219

tggattaata cttacattgg agagcctatt tatgctgaca gcgtcaaggg c

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<211> 17

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<213> Homo sapiens

<400> 220

A-1937-WO-PCT_ST25

Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys
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Gly

<210> 221
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<213> Homo sapiens

<400> 221
ggatacagat cttatgccat ggactac

27

<210> 222
<211> 9
<212> PRT
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<400> 222

Gly Tyr Arg Ser Tyr Ala Met Asp Tyr
1 5

<210> 223
<211> 11
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<400> 223

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

<210> 224
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Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 225
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Gln Lys Tyr Asn Ser Ala Pro Trp Thr
1 5

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<400> 226

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

<210> 227
 <211> 16
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<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
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<400> 229

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

<210> 230
 <211> 15
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<220>
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<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> (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

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 1 5 10 15

<210> 231
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 <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
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<220>
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 <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
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<210> 234
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 <212> PRT
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<400> 234

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
 1 5

<210> 235
 <211> 17
 <212> PRT
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<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

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 gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
 aaaccaggga aagcccctaa gctcctgata tatgctacat ccagtttgca aagtgggggtc 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 caagagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgcccgt 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

A-1937-WO-PCT_ST25

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 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
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<400> 240

Gln Gln Tyr Gly Ser Ser Pro Ile Thr

1

5

<210> 241
 <211> 11
 <212> PRT
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<400> 241

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

<210> 242
 <211> 7
 <212> PRT
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<400> 242

Ala Ala Ser Thr Leu Gln Ser
 1 5

<210> 243
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 <212> PRT
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<400> 243

Gln Lys Tyr Asn Ser Ala Pro Leu Thr
 1 5

<210> 244
 <211> 11
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<400> 244

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

<210> 245
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<400> 245

Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 246
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 <212> PRT
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<400> 246

Leu Gln His Asn Ser Tyr Pro Leu Thr
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A-1937-WO-PCT_ST25

<210> 247
 <211> 14
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<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
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<400> 248

Gly Asn Ser Asn Arg Pro Ser
 1 5

<210> 249
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 <212> PRT
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<400> 249

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

<210> 250
 <211> 1365
 <212> DNA
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<220>
 <223> Synthetic polynucleotide

<400> 250

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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 ccagtgctc caccaagggc ccatcggctt tccccctggc accctcctcc	420
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt	540
gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagttg agcccaaatc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg	780

A-1937-WO-PCT_ST25

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atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag      840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgc      900
gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac      960
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agccccatc     1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc     1080
ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggt 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 gaggcctctcc ctgtctccgg gtaaa                     1365

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<210> 251
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<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>
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 <222> (2)..(2)
 <223> Xaa can be any naturally occurring amino acid

<400> 252

Val Xaa Gln Leu Val Tyr Phe Asp
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<210> 253
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 253

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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<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
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<400> 255

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

<210> 256
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 <212> PRT
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<400> 256

Ser Tyr Tyr Trp Ser
 1 5

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

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 gtcaccatca cttgcaggctc cagccagagt gtgttataca 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 cggagggacc aaggtggaga tcaaacgaac ggtggctgca 420
 ccatctgtct tcatcttccc gccatctgat gaggcagttga aatctggaac tgcctctggt 480
 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
 tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
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 gagtgt 726

<210> 258
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<400> 258

Tyr Ser Gly Ser Tyr Tyr Tyr Phe Asp
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<210> 259
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<400> 259

Ser Tyr Tyr Trp Ser

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5

<210> 260
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<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
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<400> 261

Leu Thr Gly Tyr Phe Asp
 1 5

<210> 262
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 <212> PRT
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<400> 262

Ser Asn Ser Ala Ala Trp Asn
 1 5

<210> 263
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 263
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33

<210> 264
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 <212> PRT
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<400> 264

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

<210> 265
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 <212> PRT
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<400> 265

Gly Tyr Tyr Trp Ser
 1 5

<210> 266
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<400> 266

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

<210> 267
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 <212> PRT
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<400> 267

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

<210> 268
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Ser Gly Ser Tyr Tyr Trp Ser
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<210> 269
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<400> 269

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

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

<210> 271
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Ser Asn Tyr Met Ser
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A-1937-WO-PCT_ST25

<210> 272
 <211> 16
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<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
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<400> 273

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

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<400> 274

Ser Tyr Ala Met His
 1 5

<210> 275
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<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
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<400> 276

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

<210> 277
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Ser Tyr Trp Ile Gly
 1 5

<210> 278
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Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
 1 5 10 15

Gly

<210> 279
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 <212> PRT
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<400> 279

Tyr Asn Trp Asn Asp Asn Trp Phe Asp
 1 5

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 <212> PRT
 <213> Homo sapiens

<400> 280

Ser Asn Tyr Met Ser
 1 5

<210> 281
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 <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
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 <212> PRT
 <213> Homo sapiens

<400> 282

Gly Tyr Ser Ser Ser Trp Tyr Tyr Phe Asp
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<210> 283
 <211> 2205
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic polynucleotide

A-1937-WO-PCT_ST25

<400> 283
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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180
caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgccaaa 360
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gtctctagtg cctccaccaa gggcccatcg gtcttcccc ttggcaccctc ctccaagagc 480
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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
ctgggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 840
cggacccttg aggtcacatg cgtgggtgtg gacgtgagcc acgaagacc ttgaggtcaag 900
ttcaactggg acgtggacgg cgtggagggtg 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
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cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga 1440
tcccaggtac agttgcagga gtcaggtcca ggactggtga agccctcgga gaccctctca 1500
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aaccagttct ccctgaagct gagctctgtg actgccgcgg acacggctgt gtattactgt 1740
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acggtcaccg tctcctcagg aggcggagga tctggtggcg gtggttctgg cggcgaggc 1860
tccgacatcc agatgacca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc 1920
accatcactt gcaggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta 1980

A-1937-WO-PCT_ST25

gtttggtacc agcagaaacc aggaaggtt cctaaactgc tcatttactg ggcattctacc 2040
 cggaatccg gggccctag tcgattcagt ggcagcgggt ctgggacaga ttctactctc 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
 Page 117

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

A-1937-WO-PCT_ST25															
465				470				475				480			
Cys	Thr	Ile	Ser	Gly 485	Asp	Ser	Val	Ser	Thr 490	Asn	Ser	Val	Ala	Trp 495	Asn
Trp	Ile	Arg	Gln 500	Pro	Pro	Gly	Lys	Gly 505	Leu	Glu	Trp	Ile	Gly 510	Arg	Thr
Tyr	Tyr	Arg 515	Ser	Lys	Trp	Tyr	Asn 520	Asp	Tyr	Ala	Val	Ser 525	Leu	Lys	Ser
Arg	Val 530	Thr	Ile	Ser	Pro	Asp 535	Thr	Ser	Lys	Asn	Gln 540	Phe	Ser	Leu	Lys
Leu 545	Ser	Ser	Val	Thr	Ala 550	Ala	Asp	Thr	Ala	Val 555	Tyr	Tyr	Cys	Ala	Arg 560
Glu	Asp	Gly	Asp	Ser 565	Tyr	Tyr	Arg	Tyr	Gly 570	Met	Asp	Val	Trp	Gly 575	Gln
Gly	Thr	Thr	Val 580	Thr	Val	Ser	Ser	Gly 585	Gly	Gly	Gly	Ser	Gly 590	Gly	Gly
Gly	Ser	Gly 595	Gly	Gly	Gly	Ser	Asp 600	Ile	Gln	Met	Thr	Gln 605	Ser	Pro	Ser
Ser	Leu 610	Ser	Ala	Ser	Val	Gly 615	Asp	Arg	Val	Thr	Ile 620	Thr	Cys	Arg	Ser
Ser 625	Gln	Ser	Val	Leu	Tyr 630	Ser	Ser	Asn	Asn	Lys 635	Asn	Tyr	Leu	Val	Trp 640
Tyr	Gln	Gln	Lys	Pro 645	Gly	Lys	Val	Pro	Lys 650	Leu	Leu	Ile	Tyr	Trp 655	Ala
Ser	Thr	Arg	Glu 660	Ser	Gly	Val	Pro	Ser 665	Arg	Phe	Ser	Gly	Ser 670	Gly	Ser
Gly	Thr	Asp 675	Phe	Thr	Leu	Thr	Ile 680	Ser	Ser	Leu	Gln	Pro 685	Glu	Asp	Val
Ala	Thr 690	Tyr	Tyr	Cys	Gln	Gln 695	Tyr	Tyr	Lys	Thr	Pro 700	Leu	Thr	Phe	Gly
Gly 705	Gly	Thr	Lys	Val	Glu 710	Ile	Lys	Arg							

Page 119

<220>

<223> Synthetic polynucleotide

<400> 285

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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 ctgcgccaaa	360
gtctcctact tgtctacagc ttcgtcgcgc gactattggg gtcaaggaac gttggtcacc	420
gtctctagt cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc	480
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acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta	600
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	660
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cggacccttg aggtcacatg cgtgggtggg gacgtgagcc acgaagacc tgaggtcaag	900
ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa	1080
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1140
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	1200
agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccag	1260
cctcccgtgc tggactccga cggctcctt ttcctctata gcaagctcac cgtggacaag	1320
agcagggtgg agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtgggt gcggatcggg aggtggcgga	1440
tcccagggtc agctgcagga gtcgggcca ggactggtga agccttcgga gaccctgtcc	1500
ctcacctgca ctgtctctgg tggctccatc agtagttact tctggagctg gatccggcag	1560
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aaccctccc tcaagagtcg agtcaccata tcaatagaca cgtccaagaa ccagttctcc	1680
ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagagaaact	1740
gggagctact acggctttga ctactggggc caggaaccc tggtcaccgt ctctcagga	1800
ggcggaggat ctggtggcgg tggttctggc ggcggaggct ccgacatcca gatgaccag	1860
tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcaagt	1920

A-1937-WO-PCT_ST25

cagagcatta acaactatTT aaattggtat cagcagagac cagggaaagc ccctaagctc 1980
 ctgatctatg ctgcatccag ttTgcaaagt ggggtcccat caaggTtcag tggcagtTga 2040
 tctgggacag atttactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 2100
 tactgtcaac agagttacag taccctcTcg acgttcggct gtgggaccaa gctggaaatc 2160
 aaacga 2166

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

<220>
 <223> Synthetic polynucleotide
 <400> 286

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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<400> 287
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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 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
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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180

A-1937-WO-PCT_ST25

ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300
agaagtacca 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

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gggaaagccc ctaagtcct 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

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ccaggaagg gactggagt gattgggtat atctattaca gtgggagcac caactacaac	180
ccctccctca agatcgagt caccatgtca atagacacgt ccaagaacca gttctccctg	240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag 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

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tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg	180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact	300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga	342

<210> 296

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 296

A-1937-WO-PCT_ST25

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

Asp Arg Val Thr Ile Thr Cys 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
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
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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
Page 128

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>
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<400> 299
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 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgg 180
 gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcagcctga agatttcgca acttattact gtcagcaata ttataagact 300
 cctctcactt tcggcggagg gaccaaggtg gagatcaaac ga 342

<210> 300
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic polypeptide

<400> 300

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
 Page 129

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
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 caggccccag ggaaaggcct tgagtgggtg agcaggacat actacaggtc caagtggat 180
 aatgattatg cagtttctgt gaaaggtcga ttcaccatca gccagacac atccaagaac 240
 acgttctacc tgcagatgaa ctctctgaga gccgaggaca cggtctgtgta 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

A-1937-WO-PCT_ST25

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	
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gggaaagccc ctaagctcct gatctatgat gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct	240
gaagattttg caacttatta ctgtctacag cataatagtt accctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acga	324

<210> 304
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 304

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

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

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

A-1937-WO-PCT_ST25

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
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ccaggcaagg ggctggagtg ggtggcagtc atatcatatg atggaaataa taaactctat 180
acagactccg tgaagggccg attcaccatc tccagagacg attccaagag cacgctgtat 240
ctgcaaataa 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
Page 132

65 70 75 80

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

Ala Arg Asp 100 Pro Thr Val Thr Leu 105 Tyr Tyr Tyr Tyr Gly Met 110 Asp Val

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

<210>	307
<211>	324
<212>	DNA
<213>	Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400>	307						
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gggaaagccc	ctaagcgcct	gatctatgat	gcatccagtt	tgcaaagtgg	gttcccatca		180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	caatcagcag	cctgcagcct		240
gaagattttg	caacttatta	ctgtctacag	cataatagtt	accctccgac	gttcggccaa		300
gggaccaagg	tggaaatcaa	acga					324

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

<220>
<223> Synthetic polypeptide

<400> 308

Asp Ile Gln Met 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

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

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

<220>
<223> Synthetic polynucleotide

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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

A-1937-WO-PCT_ST25

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
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 aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180
 caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
 gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
 ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgccaaa 360
 gtctcctact tgtctacagc ttcgtcgcgc gactattggg gtcaaggaac gttgggtcacc 420
 gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 480
 acctctgggg gcacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccggtg 540
 acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 600
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 acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 720
 gttgagccca aatcttgtga caaaactcac acatgccac cgtgcccagc acctgaactc 780
 ctgggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 840
 cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 900
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 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
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 tcccaggtac agttgcagga gtcaggtcca ggactggtga agccctcgga gaccctctca 1500
 ctcacctgta ccatctccgg ggacagtgtc tctaccaaca gtgttgcttg gaactggatt 1560
 aggcagcccc cagggaatg ccttgagtgg ataggaagga catactacag gtccaagtgg 1620

A-1937-WO-PCT_ST25

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aaccagttct ccctgaagct gagctctgtg actgccgcgg acacggctgt gtattactgt 1740
gcaagagagg atggggatag ctactaccgc tacggtatgg acgtctgggg ccaagggacc 1800
acggtcaccg tctcctcagg aggcggagga tctggtggcg gtggttctgg cggcggaggc 1860
tccgacatcc agatgaccca gtctccaagc tccctgtctg cgtctgtggg cgatagggtc 1920
accatcactt gcaggtccag ccagagtgtg ttatacagct ccaacaataa gaactactta 1980
gtttggtacc agcagaaacc aggaaagggt cctaaactgc tcatttactg ggcattctacc 2040
cgggaaatccg gggtccttag 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
Page 136

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
 Page 137

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
 Page 138

690

695

A-1937-WO-PCT_ST25
700Cys Gly Thr Lys Val Glu Ile Lys Arg
705 710<210> 313
<211> 2151
<212> DNA
<213> Artificial Sequence<220>
<223> Synthetic polynucleotide

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aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc      180
cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc      240
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accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca      480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac      540
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tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc      720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca      780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc      840
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gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg      960
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aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc     1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc     1140
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agcctctccc tgtctccggg tgggtggcgg tcgggaggtg gcggatcca ggtgcagctg     1440
caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc     1500
tctggtggct ccatcagtag ttacttctgg agctggatcc ggcagccccc aggtaagggg     1560

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A-1937-WO-PCT_ST25

ctggagtgga ttggctatat ctattacagt gggcagacca aatacaaccc ctccctcaag 1620
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 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
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 tccagtttgc aaagtggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2040
 actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2100
 tacagtaccc ctcggacgtt cggccaaggg accaagctgg aaatcaaacg a 2151

<210> 314
 <211> 695
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 314

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

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

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 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

A-1937-WO-PCT_ST25

145		150		155		160									
Ala	Leu	Thr	Ser	Gly 165	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
									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

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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
 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 gacggtgtcg 540
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
 ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
 aaatcttgtg acaaaaactca cacatgccc aacgtgcccag cacctgaact cctgggggga 780
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840
 gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
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 gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140
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 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
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 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

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

A-1937-WO-PCT_ST25

<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

A-1937-WO-PCT_ST25

<400> 319
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cgctgtgagg tgcagctggg gcagctctgga gcagaggtga aaaagccccg ggagtctctg 120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgctg 180
cagatgcccc ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240
agatacagcc cgtccttcca aggccagggt accatctcag cgcacaagtc catcagtacc 300
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc 420
accaagggcc catcgggtctt ccccttgga ccctcctcca agagcacctc tgggggcaca 480
gcggccctgg gctgcctggg caaggactac ttccccgaac cgggtgacggg gtcgtggaac 540
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tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcacca gacctacatc 660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 720
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga ccctgaggtc 840
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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 ctgcctgggc aaaggcttct atcccagcga catcgccgtg 1200
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1260
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tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg 1560
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tcaggaggcg gaggatctgg tggcggtggg tctggcggcg gaggtccga catccagatg 1860
accagctctc caagctccct gtctgctgt gtgggcgata gggtcaccat cacttgacgg 1920
tccagccaga gtgtgttata cagctccaac aataagaact acttagtttg gtaccagcag 1980

A-1937-WO-PCT_ST25

aaaccaggaa aggttcctaa actgctcatt tactgggcat ctaccgggga atccggggtc 2040
 cctagtcgat tcagtggcag cgggtctggg acagatttca ctctcaccat cagcagcctg 2100
 cagcctgaag atgtggcaac ttattactgt cagcaatatt ataagactcc tctcactttc 2160
 ggcggaggga ccaaggtgga gatcaaacga 2190

<210> 320
 <211> 708
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 320

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
 Page 148

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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aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc	180
cagatgcccg 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 catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca	480
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac	540
tcaggcggcc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc	720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	900
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg	960
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1020
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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
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agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct	1680
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc	1740
tttgactact ggggccaggg aaccctggtc accgtctcct caggaggcgg aggatctggt	1800
ggcgggtggt ctggcggcgg aggtccgac atccagatga ccagtcctcc atcctccctg	1860
tctgcatctg taggagacag agtcaccatc acttgccggg caagtcagag cattaacaac	1920

A-1937-WO-PCT_ST25

tattttaaatt ggtatcagca gagaccaggg aaagccccta agctcctgat ctatgctgca 1980
tccagtttgc aaagtgggggt cccatcaagg ttcagtggca gtggatctgg gacagatttc 2040
actctcacca tcagcagtct gcaacctgaa gattttgcaa cttactactg tcaacagagt 2100
tacagtaccc ctcggacgtt cggctgtggg accaagctgg aaatcaaacg a 2151

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

<220>
<223> Synthetic polynucleotide

<400> 322

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

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

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

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

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

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

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

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
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
Page 152

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
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<210> 323
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 <400> 323

A-1937-WO-PCT_ST25

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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

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Glu Cys

<210> 324
<211> 1431
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 324

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atcaggcagg ccccagggaa aggccttgag tgggtgagca ggacatacta caggtccaag      240
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tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg      420
accacgggtca ccgtctccag tgcctccacc aaggggcccat cgggtcttccc cctggcaccc      480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc      540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc      600
ccggctgtcc tacagtcttc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc      660
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accgtggaca agagcagggt gcagcagggg aacgtcttct catgctccgt gatgcatgag     1380
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<210> 325

<211> 477

<212> PRT

<213> Artificial Sequence

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<223> Synthetic polypeptide

<400> 325

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A-1937-WO-PCT_ST25

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 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ile Ser Gly
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 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

A-1937-WO-PCT_ST25

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
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Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcacaaca taagaactac	180
ttagtttggt accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct	240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact	300

A-1937-WO-PCT_ST25

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ccatctgtct tcactttccc gccatctgat gagcagttga aatctggtac cgcctctgtt 480
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gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
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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 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

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>
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 gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc 660
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
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A-1937-WO-PCT_ST25

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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
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<210> 329
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<212> PRT
<213> Artificial Sequence
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<223> Synthetic polypeptide
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20 25 30

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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
Page 161

180

185

190

Ser Gly Val₁₉₅ His Thr Phe Pro Ala₂₀₀ Val Leu Gln Ser Ser₂₀₅ Gly Leu Tyr

Ser Leu₂₁₀ Glu Ser Val Val₂₁₅ Thr Val Pro Ser Ser₂₂₀ Leu Gly Thr Gln

Thr₂₂₅ Tyr Ile Cys Asn Val₂₃₀ Asn His Lys Pro Ser₂₃₅ Asn Thr Lys Val₂₄₀ Asp

Lys Lys Val₂₄₅ Glu Pro Lys Ser Cys Asp Lys₂₅₀ Thr His Thr Cys₂₅₅ Pro Pro

Cys Pro Ala₂₆₀ Pro Glu Leu Leu Gly₂₆₅ Pro Ser Val Phe₂₇₀ Leu Phe Pro

Pro Lys Pro₂₇₅ Lys Asp Thr Leu Met₂₈₀ Ile Ser Arg Thr₂₈₅ Pro Glu Val Thr

Cys Val₂₉₀ Val Val Asp Val₂₉₅ Ser His Glu Asp Pro Glu₃₀₀ Val Lys Phe Asn

Trp₃₀₅ Tyr Val Asp Gly₃₁₀ Val Glu Val His Asn Ala₃₁₅ Lys Thr Lys Pro Cys₃₂₀

Glu Glu Gln Tyr Gly₃₂₅ Ser Thr Tyr Arg Cys₃₃₀ Val Ser Val Leu Thr₃₃₅ Val

Leu His Gln Asp₃₄₀ Trp Leu Asn Gly₃₄₅ Lys Glu Tyr Lys Cys Lys₃₅₀ Val Ser

Asn Lys Ala₃₅₅ Leu Pro Ala Pro Ile₃₆₀ Glu Lys Thr Ile Ser₃₆₅ Lys Ala Lys

Gly Gln Pro Arg Glu Pro Gln₃₇₅ Val Tyr Thr Leu Pro₃₈₀ Pro Ser Arg Lys

Glu₃₈₅ Met Thr Lys Asn Gln₃₉₀ Val Ser Leu Thr Cys₃₉₅ Leu Val Lys Gly Phe₄₀₀

Tyr Pro Ser Asp Ile₄₀₅ Ala Val Glu Trp Glu₄₁₀ Ser Asn Gly Gln Pro₄₁₅ Glu

Asn Asn Tyr Lys₄₂₀ Thr Thr Pro Pro Val₄₂₅ Leu Lys Ser Asp Gly₄₃₀ Ser Phe

Phe Leu Tyr₄₃₅ Ser Lys Leu Thr Val₄₄₀ Asp Lys Ser Arg Trp₄₄₅ Gln Gln Gly

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

<220>
 <223> Synthetic polynucleotide

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 gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180
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 ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
 cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc 360
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 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
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<210> 331
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 331

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 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
 Page 163

A-1937-WO-PCT_ST25															
65				70				75				80			
Pro	Ser	Arg	Phe	Ser ₈₅	Gly	Ser	Gly	Ser	Gly ₉₀	Thr	Glu	Phe	Thr	Leu ₉₅	Thr
Ile	Ser	Ser	Leu ₁₀₀	Gln	Pro	Glu	Asp	Phe ₁₀₅	Ala	Thr	Tyr	Tyr	Cys ₁₁₀	Leu	Gln
His	Asn	Ser ₁₁₅	Tyr	Pro	Pro	Thr	Phe ₁₂₀	Gly	Gln	Gly	Thr	Lys ₁₂₅	Val	Glu	Ile
Lys	Arg ₁₃₀	Thr	Val	Ala	Ala	Pro ₁₃₅	Ser	Val	Phe	Ile	Phe ₁₄₀	Pro	Pro	Ser	Asp
Glu ₁₄₅	Gln	Leu	Lys	Ser	Gly ₁₅₀	Thr	Ala	Ser	Val	Val ₁₅₅	Cys	Leu	Leu	Asn	Asn ₁₆₀
Phe	Tyr	Pro	Arg	Glu ₁₆₅	Ala	Lys	Val	Gln	Trp ₁₇₀	Lys	Val	Asp	Asn	Ala ₁₇₅	Leu
Gln	Ser	Gly	Asn ₁₈₀	Ser	Gln	Glu	Ser	Val ₁₈₅	Thr	Glu	Gln	Asp	Ser ₁₉₀	Lys	Asp
Ser	Thr	Tyr ₁₉₅	Ser	Leu	Lys	Ser	Thr ₂₀₀	Leu	Thr	Leu	Ser	Lys ₂₀₅	Ala	Asp	Tyr
Glu	Lys ₂₁₀	His	Lys	Val	Tyr	Ala ₂₁₅	Cys	Glu	Val	Thr	His ₂₂₀	Gln	Gly	Leu	Ser
Ser ₂₂₅	Pro	Val	Thr	Lys	Ser ₂₃₀	Phe	Asn	Arg	Gly	Glu ₂₃₅	Cys				

<210>	332
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<220>
<223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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<210> 333
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 333

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 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

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 gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagcag 180
 aaaccaggga aagcccctaa ggcctgatc tatgatgcat ccagtttgca aagtggggctc 240
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 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
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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 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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 accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aactgggtac 180
 cagcagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240
 ggggtccctg accgattctc tggtccaag tctggcacct cagcctccct ggccatcact 300
 gggctccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360
 gggtcgggtg tcggcggagg gaccaagctg accgtcctag gtcagcccaa ggctgcccc 420
 tcggtcactc tggtcccgcc ctctctgag gagcttcaag ccaacaaggc cacactgggtg 480
 tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc agatagcagc 540
 cccgtcaagg cgggagtgga gaccaccaca ccctccaaac aaagcaacaa caagtacgcg 600
 gccgagagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660
 caggtcacgc atgaaggag caccgtggag aagacagtgg cccctacaga atgttca 717

<210> 337
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 337
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15
 Leu Arg Gly Ala Arg Cys Gln Ser Val Leu Thr Gln Pro Pro Ser Val
 20 25 30
 Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
 35 40 45
 Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Phe Pro
 50 55 60
 Gly Thr Ala Pro Lys Leu Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser
 85 90 95
 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys

100

105

110

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val Phe Gly Gly Gly Thr
 115 120 125

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

Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val
 145 150 155 160

Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys
 165 170 175

Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser
 180 185 190

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr
 195 200 205

Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His
 210 215 220

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

<210> 338
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 338
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 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240
 agatacagcc cgtccttcca aggccaggtc accatctcag cgcacaagtc catcagtacc 300
 gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga 360
 agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgccctc 420
 accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca 480
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540
 tcaggcggcc tgaccagcgg cgtgcacacc ttccggctg tcctacagtc ctcaggactc 600
 tactccctca agagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 660
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gcccaaattc 720

A-1937-WO-PCT_ST25

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acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	900
gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg	960
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1020
aagtgcgaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc	1080
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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1200
gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac	1260
tccgacggct ctttcttct ctatagcgac ctcaccgtgg acaagagcag gtggcagcag	1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1380
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<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
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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
Page 171

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 ggcgctgatc 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 cgagagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgcccg cacaagagc ttcaacaggg gagagtgt 708

<210> 341
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 341

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

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 Page 172

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

A-1937-WO-PCT_ST25

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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
acgggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc      480
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc      540
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc      600
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc      660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg      720
gacaagaaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca      780
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atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct      900
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tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag     1020
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc     1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg     1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc     1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac     1260
gacaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag cgacctcacc     1320
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct     1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa                    1428

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<210> 343
 <211> 476
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 343

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

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

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

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

50

55

60

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

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

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

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

Tyr Tyr Tyr Ser Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
130 135 140

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

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
Page 175

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

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 aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
 cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240
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 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 600

A-1937-WO-PCT_ST25

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acatgcgtgg	tgggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	900
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	960
taccgtttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	1020
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aaagggcagc	cccgagaacc	acaggtgtac	accctgcccc	catcccggga	ggagatgacc	1140
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tccgacggct	ccttcttctt	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1320
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aatgccttg	agtggatagg	aaggacatac	tacaggtcca	agtgggtataa	tgattatgca	1620
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aagctgagct	ctgtgactgc	cgcgacacg	gctgtgtatt	actgtgcaag	agaggatggg	1740
gatagctact	accgctacgg	tatggacgtc	tggggccaag	ggaccacggg	caccgtctcc	1800
tcaggaggcg	gaggatctgg	tggcggtggt	tctggcggcg	gaggctccga	catccagatg	1860
accagctctc	caagctccct	gtctgcgtct	gtgggcgata	gggtcaccat	cacttgcagg	1920
tccagccaga	gtgtgttata	cagctccaac	aataagaact	acttagtttg	gtaccagcag	1980
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cctagtcgat	tcagtggcag	cgggtctggg	acagatttca	ctctcaccat	cagcagcctg	2100
cagcctgaag	atgtggcaac	ttattactgt	cagcaatatt	ataagactcc	tctcactttc	2160
ggctgtggga	ccaaggtgga	gatcaaacga				2190

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

<220>
 <223> Synthetic polynucleotide

<400> 345

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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<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
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

A-1937-WO-PCT_ST25

gaaccggtga	cgggtgtcgtg	gaactcaggc	gccctgacca	gcggcgtgca	caccttcccc	600
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agcttgggca	cccagaccta	catctgcaac	gtgaatcaca	agcccagcaa	caccaaggtg	720
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cctgaactcc	tggtggggacc	gtcagtcttc	ctcttcccc	caaaacccaa	ggacaccctc	840
atgatctccc	ggaccctga	ggtcacatgc	gtggtggtgg	acgtgagcca	cgaagaccct	900
gaggtcaagt	tcaactggta	cgtggacggc	gtggaggtgc	ataatgcaa	gacaaagccg	960
tgtgaggagc	agtacggcag	cacgtaccgt	tgtgtcagcg	tcctcaccgt	cctgcaccag	1020
gactggctga	atggcaagga	gtacaagtgc	aaggtctcca	acaaagccct	cccagcccc	1080
atcgagaaaa	ccatctccaa	agccaaaggg	cagccccgag	aaccacaggt	gtacaccctg	1140
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ttctatccca	gcgacatcgc	cgtggagtgg	gagagcaatg	ggcagccgga	gaacaactac	1260
aagaccacgc	ctcccgtgct	ggactccgac	ggctccttct	tcctctatag	caagctcacc	1320
gtggacaaga	gcaggtggca	gcaggggaac	gtcttctcat	gctccgtgat	gcatgaggct	1380
ctgcacaacc	actacacgca	gaagagcctc	tccctgtctc	cgggtggtgg	cggatcggga	1440
ggtggcggat	cccaggtgca	gctgcaggag	tcgggcccag	gactggtgaa	gccttcggag	1500
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atccggcagc	ccccaggtaa	gggactggag	tggattggct	atatctatta	cagtgggcag	1620
accaaataca	accctccct	caagagtcga	gtcaccatat	caatagacac	gtccaagaac	1680
cagttctccc	tgaagctgag	ctctgtgacc	gctgcggaca	cggccgtgta	ttactgtgcg	1740
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tcctcaggag	gcggaggatc	tggtggcggt	ggttctggcg	gcggaggctc	cgacatccag	1860
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cgggcaagtc	agagcattaa	caactattta	aattgggtatc	agcagagacc	agggaaagcc	1980
cctaagctcc	tgatctatgc	tgcatccagt	ttgcaaagtg	gggtcccatc	aaggttcagt	2040
ggcagtggtg	ctgggacaga	tttactctc	accatcagca	gtctgcaacc	tgaagatttt	2100
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ctggaaatca	aacga					2175

<210> 347
 <211> 703
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 347

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				Ala	Ser ₂₅	Gly
				Phe	Thr	Phe
				Ser ₃₀	Ser	Tyr
Asp	Met	His ₃₅	Trp	Val	Arg	Gln
					Ala ₄₀	Pro
					Gly	Lys
					Gly	Leu
					Glu	Trp
					Val	
Ala	Val ₅₀	Ile	Ser	Tyr	Asp	Gly ₅₅
					Ser	Ile
					Lys	Tyr
					Tyr ₆₀	Ala
					Asp	Ser
					Val	
Lys	Gly	Arg	Phe	Thr	Ile ₇₀	Ser
₆₅					Arg	Asp
					Asn	Ser ₇₅
					Lys	Asn
					Thr	Leu
					Tyr ₈₀	
Leu	Gln	Val	Asn	Ser ₈₅	Leu	Arg
					Ala	Glu
					Asp ₉₀	Thr
					Ala	Val
					Tyr	Tyr
					Cys ₉₅	
Ala	Arg	Glu	Val ₁₀₀	Arg	Ser	Gly
					Ser	Tyr
					Tyr ₁₀₅	Tyr
					Tyr	Tyr
					Tyr	Tyr
					Ser ₁₁₀	Met
					Asp	
Val	Trp	Gly	Gln	Gly	Thr	Thr
		₁₁₅			Val ₁₂₀	Thr
					Val	Ser
					Ser	Ser
					Ala ₁₂₅	Ser
					Thr	Ser
					Gly	
Gly	Pro	Ser	Val	Phe	Pro	Leu
₁₃₀						Ala
					Pro	Ser
					Ser	Ser
					Lys ₁₄₀	Ser
					Thr	Ser
					Gly	
Gly	Thr	Ala	Ala	Leu	Gly ₁₅₀	Cys
₁₄₅					Leu	Val
					Lys	Asp
					Tyr ₁₅₅	Tyr
					Phe	Pro
					Glu	Pro ₁₆₀
Val	Thr	Val	Ser	Trp ₁₆₅	Asn	Ser
					Gly	Ala
					Leu ₁₇₀	Thr
					Ser	Gly
					Val ₁₇₅	His
					Thr	
Phe	Pro	Ala	Val ₁₈₀	Leu	Gln	Ser
					Ser	Ser
					Gly ₁₈₅	Leu
					Tyr	Ser
					Leu	Ser
					Ser ₁₉₀	Ser
					Val	Val
Val	Thr	Val ₁₉₅	Pro	Ser	Ser	Ser
					Ser	Ser
					Leu ₂₀₀	Gly
					Thr	Gln
					Thr	Tyr
					Tyr ₂₀₅	Ile
					Cys	Asn
Val	Asn	His	Lys	Pro	Ser	Asn
₂₁₀						Thr
					Asn ₂₁₅	Lys
					Val	Asp
					Lys ₂₂₀	Lys
					Val	Glu
					Pro	
Lys	Ser	Cys	Asp	Lys	Thr ₂₃₀	His
₂₂₅					Thr	Thr
					Cys	Pro
					Pro ₂₃₅	Cys
					Pro	Ala
					Pro	Glu
					Pro ₂₄₀	
Leu	Leu	Gly	Gly	Pro ₂₄₅	Ser	Val
					Phe	Leu
					Phe ₂₅₀	Pro
					Pro	Pro
					Lys	Pro
					Lys ₂₅₅	Asp
Thr	Leu	Met	Ile ₂₆₀	Ser	Arg	Thr
					Pro	Glu
					Val ₂₆₅	Val
					Thr	Cys
					Val ₂₇₀	Val
					Val	Val
					Asp	
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

<400> 348
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 cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120
 agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180
 caggctccag gcaaggggct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240
 tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300
 ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420
 acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540
 gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600

A-1937-WO-PCT_ST25

gctgtcctac agtcctcagg actctactcc ctcagcagcg tgggtgaccgt gccctccagc	660
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gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca	780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc	840
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct	900
gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgccaa gacaaagccg	960
tgtgaggagc agtacggcag cacgtaccgt tgtgtcagcg tcctcaccgt cctgcaccag	1020
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagccccc	1080
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg	1140
cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc	1200
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aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag caagctcacc	1320
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggtgg cggatcggga	1440
ggtggcggat cccaggtaca gttgcaggag tcagggtccag gactggtgaa gccctcggag	1500
accctctcac tcacctgtac catctccggg gacagtgtct ctaccaacag tgttgcttgg	1560
aactggatta ggcagcccc agggaaaggc cttgagtgga taggaaggac atactacagg	1620
tccaagtgggt ataagtatta tgcagtttct ctgaaaagtc gagtaaccat cagcccagac	1680
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tattactgtg caagagagga tggggatagc tactaccgct acggtatgga cgtctggggc	1800
caagggacca cggtcaccgt ctcctcagga ggcggaggat ctggtggcg tggttctggc	1860
ggcggaggct ccgacatcca gatgaccag tctccaagct ccctgtctgc gtctgtgggc	1920
gataggggtca ccatcacttg cagggtccagc cagagtgtgt tatacagctc caacaataag	1980
aactacttag tttggtacca gcagaaacca ggaaagggttc ctaaactgct catttactgg	2040
gcatctacc gggaatccgg ggtccctagt cgattcagtg gcagcgggtc tgggacagat	2100
ttcactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta ctgtcagcaa	2160
tattataaga ctctctcac tttcggcgga gggaccaagg tggagatcaa acga	2214

<210> 349
 <211> 716
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 349

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A-1937-WO-PCT_ST25

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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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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
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A-1937-WO-PCT_ST25

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agcttgggca	cccagaccta	catctgcaac	gtgaatcaca	agcccagcaa	caccaagggtg	720
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cctgaactcc	tggtggggacc	gtcagtcttc	ctcttcccc	caaaacccaa	ggacaccctc	840
atgatctccc	ggaccctga	ggtcacatgc	gtgggtggtg	acgtgagcca	cgaagaccct	900
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gactggctga	atggcaagga	gtacaagtgc	aaggtctcca	acaaagccct	cccagcccc	1080
atcgagaaaa	ccatctccaa	agccaaagg	cagccccgag	aaccacaggt	gtacaccctg	1140
cccccatccc	gggaggagat	gaccaagaac	caggtcagcc	tgacctgcct	ggtaaaggc	1200
ttctatcca	gcgacatcg	cgtggagtgg	gagagcaatg	ggcagccgga	gaacaactac	1260
aagaccacgc	ctcccgtgct	ggactccgac	ggctccttct	tcctctatag	caagctcacc	1320
gtggacaaga	gcaggtggca	gcaggggaac	gtcttctcat	gctccgtgat	gcatgaggct	1380
ctgcacaacc	actacacgca	gaagagcctc	tccctgtctc	cgggtggtgg	cggatcggga	1440
ggtggcggt	cccaggtgca	gctgcaggag	tcgggcccag	gactggtgaa	gccttcggag	1500
accctgtccc	tcacctgcac	tgtctctggt	ggctccatca	gtagttactt	ctggagctgg	1560
atccggcagc	ccccaggtaa	gtgtctggag	tggattggct	atatctatta	cagtgggcag	1620
accaaataca	accctccct	caagagtcga	gtcaccatat	caatagacac	gtccaagaac	1680
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ggcagtggt	ctgggacaga	tttactctc	accatcagca	gtctgcaacc	tgaagatttt	2100
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<220>
 <223> Synthetic polynucleotide

<400> 351

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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
 Page 190

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
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 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
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 Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 450 455 460
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
 465 470 475 480
 Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Phe Trp
 485 490 495
 Ser Trp Ile Arg Gln Pro Pro Gly Lys 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
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 Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
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 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
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 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
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 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser
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 <213> Artificial Sequence

<220>
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A-1937-WO-PCT_ST25

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 <213> Artificial Sequence

<220>
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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
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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

A-1937-WO-PCT_ST25

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 Ser 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
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 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 545 550 555 560

A-1937-WO-PCT_ST25

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
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 355

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 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
 Page 198

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

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<210>	356
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<213>	Artificial Sequence

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<223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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ggt						2163

<210> 357
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide
 <400> 357

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A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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tcctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg	180
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagaccaaa	240
tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtcaa gaaccagttc	300
tcctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa	360
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A-1937-WO-PCT_ST25

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gtggagatca aacgt	2175

<210> 359

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 359

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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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
 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
 Page 206

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
 Page 207

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

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 tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
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 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660
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A-1937-WO-PCT_ST25

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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1380
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ctgatctatg ccgcctcgac tcttcagagt ggtgtgccgt cgaggtttag cgggtccggg	2040
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tactgccaga gataaacg agcgccttac acattcggat gtgggacaaa agtcgagatc	2160
aagcgt	2166

<210> 361
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 361

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
			20					25					30		

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggatccgg 180
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagaccaaa 240
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A-1937-WO-PCT_ST25

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ggt						2163

<210> 363
 <211> 699
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 363

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
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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
 Page 213

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
 Page 214

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
 Page 215

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

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 cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa 240
 tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtcaa gaaccagttc 300
 tccctgaagc tgagctctgt gaccgctgcg gacacggccg tgtattactg tgcgagagaa 360
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 ggacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
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 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
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 aaatcttgtg aaaaaactca cacatgccca ccgtgccag cacctgaact cctgggggga 780
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A-1937-WO-PCT_ST25

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 agcacgtacc gttgtgtcag 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 acaagaccac gcctcccgtg 1260
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 gtggagatca aacgt 2175

<210> 365
 <211> 703
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polynucleotide
 <400> 365

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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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys
 Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser
 Asn₃₈₅ Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀
 Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp₄₁₅ Lys Ser
 Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala
 Leu His Asn₄₃₅ His Tyr Thr Gln Lys₄₄₀ Ser Leu Ser Leu Ser₄₄₅ Pro Gly Gly
 Gly Gly₄₅₀ Ser Gly Gly Gly Gly₄₅₅ Ser Gln Val Gln Leu₄₆₀ Val Glu Ser Gly
 Gly₄₆₅ Gly Val Val Gln Pro₄₇₀ Gly Arg Ser Leu Arg₄₇₅ Leu Ser Cys Ala Ala₄₈₀
 Ser Gly Phe Thr Phe₄₈₅ Ser Ser Tyr Asp Met₄₉₀ His Trp Val Arg₄₉₅ Gln Ala
 Pro Gly Lys Cys₅₀₀ Leu Glu Trp Val Ala₅₀₅ Val Ile Ser Tyr Asp₅₁₀ Gly Ser
 Ile Lys Tyr₅₁₅ Tyr Ala Asp Ser Val₅₂₀ Lys Gly Arg Phe Thr₅₂₅ Ile Ser Arg
 Asp Asn₅₃₀ Ser Lys Asn Thr Leu₅₃₅ Tyr Leu Gln Val Asn₅₄₀ Ser Leu Arg Ala
 Glu₅₄₅ Asp Thr Ala Val Tyr₅₅₀ Tyr Cys Ala Arg Glu₅₅₅ Val Arg Ser Gly Ser₅₆₀
 Tyr Tyr Tyr Tyr Tyr₅₆₅ Ser Met Asp Val Trp₅₇₀ Gly Gln Gly Thr Thr₅₇₅ Val
 Thr Val Ser Ser₅₈₀ Gly Gly Gly Gly Ser₅₈₅ Gly Gly Gly Gly Ser₅₉₀ Gly Gly

A-1937-WO-PCT_ST25

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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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
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cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600
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gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 780
gcacctgaac tcctgggggg accgtcagtc ttctcttccc ccccaaaacc caaggacacc 840
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A-1937-WO-PCT_ST25

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aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac 1740
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ttggtcaccg tctctagtgg aggcggagga tctggtggcg gtggttcttg cggcggaggc 1860
tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttg cgaccgtgtg 1920
acgattacct gtcgcgcgtc ccaggaatc cggaattacc tcgcatggta tcagcaaaaa 1980
cccggaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg 2040
tcgaggttta gcgggtccgg gtcaggtacg gactttactc tcacaatttc cagcctgcag 2100
cccgaagatg tagctaccta ttactgccag agatacaacc gagcgcctta cacattcgga 2160
caagggacaa aagtcgagat caagcgt 2187

<210> 367
<211> 707
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 367

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

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

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

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
Page 221

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
Page 222

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
 Page 223

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

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tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
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A-1937-WO-PCT_ST25

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gggaccaagc tgaccgtcct aggt 2184

<210> 369
<211> 706
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic polynucleotide
<400> 369

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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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 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

A-1937-WO-PCT_ST25

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

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tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
attaggcagc cccagggaa 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
accacgggtca 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 accgtgccca 780

A-1937-WO-PCT_ST25

gcacctgaac	tcctgggggg	accgtcagtc	ttcctcttcc	ccccaaaacc	caaggacacc	840
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cctgaggtca	agttcaactg	gtacgtggac	ggcgtggagg	tgcataatgc	caagacaaag	960
ccgtgtgagg	agcagtacgg	cagcacgtac	cgttgtgtca	gcgtcctcac	cgtcctgcac	1020
caggactggc	tgaatggcaa	ggagtacaag	tgcaaggctt	ccaacaaagc	cctcccagcc	1080
cccacgcaga	aaaccatctc	caaagccaaa	gggcagcccc	gagaaccaca	ggtgtacacc	1140
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tacaagacca	cgcctcccgt	gctggactcc	gacggctcct	tcttcctcta	tagcaagctc	1320
accgtggaca	agagcagggt	gcagcagggg	aacgtcttct	catgctccgt	gatgcatgag	1380
gctctgcaca	accactacac	gcagaagagc	ctctccctgt	ctccgggtgg	tggcggatcg	1440
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tgggtccgcc	aggctccagg	caaggggctg	gagtgggtgg	cagttatatc	atatgatgga	1620
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aagaacacgc	tgtatctgca	agtgaacagc	ctgagagctg	aggacacggc	tgtgtattac	1740
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caagggacca	cggtcaccgt	ctctagtgga	ggcggaggat	ctggtggcgg	tggttctggc	1860
ggcggaggct	ccgacatcca	gatgaccag	tctccatcct	ccctgtctgc	atctgtagga	1920
gacagagtca	ccatcacttg	ccgggcaagt	caggacatca	gaaatgattt	aggctggtat	1980
cagcagaaac	cagggaaagc	ccctaagcgc	ctgatctatg	ctgcgtccag	tttgcaaagt	2040
ggggtcccat	caaggttcag	cggcagtgga	tctgggccag	aattcactct	cacaatcagc	2100
agcctgcagc	ctgaagattt	tgcaacttat	tactgtctac	aacataatag	ttatccgctc	2160
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<210> 371
 <211> 710
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 371

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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
 Page 230

305 310 315 320
 Trp Leu Asn Gly Lys₃₂₅ Glu Tyr Lys Cys Lys₃₃₀ Val Ser Asn Lys Ala₃₃₅ Leu
 Pro Ala Pro Ile₃₄₀ Glu Lys Thr Ile Ser₃₄₅ Lys Ala Lys Gly Gln₃₅₀ Pro Arg
 Glu Pro Gln₃₅₅ Val Tyr Thr Leu Pro₃₆₀ Pro Ser Arg Glu Glu₃₆₅ Met Thr Lys
 Asn Gln₃₇₀ Val Ser Leu Thr Cys₃₇₅ Leu Val Lys Gly Phe₃₈₀ Tyr Pro Ser Asp
 Ile₃₈₅ Ala Val Glu Trp Glu₃₉₀ Ser Asn Gly Gln₃₉₅ Pro Glu Asn Asn Tyr Lys₄₀₀
 Thr Thr Pro Pro Val₄₀₅ Leu Asp Ser Asp Gly₄₁₀ Ser Phe Phe Leu Tyr₄₁₅ Ser
 Lys Leu Thr Val₄₂₀ Asp Lys Ser Arg Trp₄₂₅ Gln Gln Gly Asn Val₄₃₀ Phe Ser
 Cys Ser Val₄₃₅ Met His Glu Ala Leu₄₄₀ His Asn His Tyr Thr₄₄₅ Gln Lys Ser
 Leu Ser₄₅₀ Leu Ser Pro Gly Glu₄₅₅ Gly Gly Ser Gly Glu₄₆₀ Gly Gly Ser Gln
 Val₄₆₅ Gln Leu Val Glu Ser₄₇₀ Gly Gly Gly Val Val₄₇₅ Gln Pro Gly Arg Ser₄₈₀
 Leu Arg Leu Ser Cys₄₈₅ Ala Ala Ser Gly Phe₄₉₀ Thr Phe Ser Ser Tyr₄₉₅ Asp
 Met His Trp Val₅₀₀ Arg Gln Ala Pro Gly₅₀₅ Lys Gly Leu Glu Trp₅₁₀ Val Ala
 Val Ile Ser₅₁₅ Tyr Asp Gly Ser Ile₅₂₀ Lys Tyr Tyr Ala Asp₅₂₅ Ser Val Lys
 Gly Arg₅₃₀ Phe Thr Ile Ser Arg₅₃₅ Asp Asn Ser Lys Asn₅₄₀ Thr Leu Tyr Leu
 Gln₅₄₅ Val Asn Ser Leu Arg₅₅₀ Ala Glu Asp Thr Ala₅₅₅ Val Tyr Tyr Cys Ala₅₆₀
 Arg Glu Val Arg Ser₅₆₅ Gly Ser Tyr Tyr Tyr₅₇₀ Tyr Tyr Ser Met Asp₅₇₅ Val
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 Page 231

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

<210> 372
 <211> 2187
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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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 ccgtctcctc agcctccacc aagggcccat cggctcttccc cctggcaccc 480
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 cccgaaccgg tgacgggtgtc gtggaactca ggcgcctga ccagcggcgt gcacaccttc 600
 ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 660
 agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720

A-1937-WO-PCT_ST25

gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgcccc	780
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ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac	900
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	960
ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac	1020
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc	1080
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc	1140
ctgcccccat cccgggagga gatgaccaag aaccagggtca gcctgacctg cctggtcaaa	1200
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accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtgg tggcggatcg	1440
ggagggtggcg gatccgaggt acaactggtg gaatcagggtg gaggtttggt gcagccgggg	1500
agatcgctca ggcttagctg tgcggcatcg gggtttactt tcgatgatta tgcgatgcat	1560
tgggtccggc aagcgcctgg aaaatgtctc gagtgggttt cgcgcattac gtggaatagc	1620
ggacacatcg attatgcaga cagtgtggag ggcagattca caatctcacg agacaatgct	1680
aagaacagcc tgtaccttca gatgaactca cttcgcgcgg aagataccgc cgtatactac	1740
tgcgccaaag tctcctactt gtctacagct tcgtcgtcgc actattgggg tcaaggaacg	1800
ttggtcaccg tctctagtgg aggcggagga tctggtggcg gtggttcttg cggcggaggc	1860
tccgatatcc aaatgacaca atcaccatcg tcgctttcag cgtctgttg cgcacctgtg	1920
acgattacct gtcgcgcgtc ccagggaatc cggaattacc tcgcatggta tcagcaaaaa	1980
cccggaaaag caccgaagct cctgatctat gccgcctcga ctcttcagag tgggtgtgccg	2040
tcgaggttta gcgggtccgg gtcaggtacg gactttactc tcacaatttc cagcctgcag	2100
cccgaagatg tagctaccta ttactgccag agatacaacc gagcgcctta cacattcgga	2160
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<210> 373
 <211> 707
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 373

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1				5					10					15	

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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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
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cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600
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A-1937-WO-PCT_ST25

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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	960
ccgtgtgagg agcagtacgg cagcacgtac cgttgtgtca gcgtcctcac cgtcctgcac	1020
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc	1080
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accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
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gaggctgatt attactgcca gtcctatgac agcagcctga gtggttcggt 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
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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn

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
 Page 239

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 cccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240
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 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
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A-1937-WO-PCT_ST25

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gtggacaaga	aagttgagcc	caaatcttgt	gacaaaactc	acacatgccc	accgtgcccc	780
gcacctgaac	tcctgggggg	accgtcagtc	ttcctcttcc	ccccaaaacc	caaggacacc	840
ctcatgatct	cccggacccc	tgaggtcaca	tgctggtggg	tggacgtgag	ccacgaagac	900
cctgaggtca	agttcaactg	gtacgtggac	ggcgtggagg	tgcataatgc	caagacaaag	960
ccgtgtgagg	agcagtacgg	cagcacgtac	cgttgtgtca	gcgtcctcac	cgtcctgcac	1020
caggactggc	tgaatggcaa	ggagtacaag	tgcaaggtct	ccaacaaagc	cctcccagcc	1080
cccacgaga	aaaccatctc	caaagccaaa	gggcagcccc	gagaaccaca	ggtgtacacc	1140
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tacaagacca	cgctctccgt	gctggactcc	gacggctcct	tcttctctta	tagcaagctc	1320
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caagggacca	cggtcaccgt	ctctagtgga	ggcggaggat	ctggtggcgg	tggttctggc	1860
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gacagagtca	ccatcacttg	ccgggcaagt	caggacatca	gaaatgattt	aggctggtat	1980
cagcagaaac	cagggaaagc	ccctaagcgc	ctgatctatg	ctgcgtccag	tttgcaaagt	2040
ggggtcccat	caaggttcag	cggcagtgga	tctgggccag	aattcactct	cacaatcagc	2100
agcctgcagc	ctgaagattt	tgcaacttat	tactgtctac	aacataatag	ttatccgctc	2160
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<210> 377
 <211> 710
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 377

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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

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aggcttagct gtgcggcatc ggggtttact ttcgatgatt atgcgatgca ttgggtccgg 180
caagcgctg gaaaagggt cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
gattatgcag acagtgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
ctgtaccttc agatgaactc acttcgcgcg gaagataccg ccgtatacta ctgcgccaaa 360
gtctcctact tgtctacagc ttcgtcgtc gactattggg gtcaaggaac gttggtcacc 420
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcacccctc ctccaagagc 480
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccgggtg 540

A-1937-WO-PCT_ST25

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accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa	720
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc	780
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cggacccttg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag	900
ttcaactggg acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag	960
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg	1020
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accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1140
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	1200
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ctcacctgcg ctgtccatgg tgggtccttc agtgggttact actggaactg gattcgccag	1560
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cccaggctcc tcatctatgg tgcattcagc agggccactg gcatcccaga caggttcagt	2040
ggcagtggtt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt	2100
gcagtgtatt actgtcagca gtatggtagc tcacctacct tcggccaagg gacacgactg	2160
gagattaaac ga	2172

<210> 379
 <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
 Page 246

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
 Page 247

[illegible]

A-1937-WO-PCT_ST25

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acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctctgcagg	1920
gccagtcaga gtgttagaag cagttactta gcctggtacc agcagaaacc tggccaggct	1980
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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	

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
 290 295 300
 Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 450 455 460
 Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
 465 470 475 480
 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
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A-1937-WO-PCT_ST25

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

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A-1937-WO-PCT_ST25

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<210> 383
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 <213> Artificial Sequence

<220>
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<400> 383

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

A-1937-WO-PCT_ST25

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
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Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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

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

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

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

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

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

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

Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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
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 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

A-1937-WO-PCT_ST25

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
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aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgctg 180
cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc 240
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A-1937-WO-PCT_ST25

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gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg      960
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<210> 385

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 385

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

A-1937-WO-PCT_ST25

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
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Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
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 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
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 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
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 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
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 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Leu Asp Thr Ser
 515 520 525
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 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

A-1937-WO-PCT_ST25

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

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Cys Gly Thr Arg Leu Glu Ile Lys Arg
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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<210> 387
 <211> 705
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 387

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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
 Page 262

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
 Page 263

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

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tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600
gctgtcctac agtcctcagg actctactcc ctacgcagcg tggtgaccgt gccctccagc 660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840

A-1937-WO-PCT_ST25

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<212> PRT
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<223> Synthetic polynucleotide
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Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

A-1937-WO-PCT_ST25

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

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

Val Trp Gly Gln Gly Thr 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

A-1937-WO-PCT_ST25

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 325 330 335
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 340 345 350
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 355 360 365
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 405 410 415
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445
 Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 450 455 460
 Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu
 465 470 475 480
 Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr Tyr Trp
 485 490 495
 Asn Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Glu
 500 505 510
 Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 515 520 525
 Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu
 530 535 540
 Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
 545 550 555 560
 Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 565 570 575
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 580 585 590

A-1937-WO-PCT_ST25

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

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

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

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

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

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

Tyr Gly Ser Ser Pro Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys
690 695 700

Arg
705

<210> 390
<211> 2172
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc 180
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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tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
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A-1937-WO-PCT_ST25

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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag      960
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aagctcctga tctatgccgc ctcgactctt cagagtgggt tgccgtcgag gtttagcggg     2040
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<210> 391
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 391

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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
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 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
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 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
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 Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile
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 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
 Page 271

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

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A-1937-WO-PCT_ST25

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 <212> PRT
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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			

A-1937-WO-PCT_ST25

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 Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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

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<211> 2181
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<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggtt actactggaa ctggattcgc 180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360
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gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 840
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A-1937-WO-PCT_ST25

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 accaaggtgg agatcaaacg t 2181

<210> 395
 <211> 705
 <212> PRT
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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
 Page 277

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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
Page 278

325

330

335

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr

Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu

Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀

Leu Asp Ser Asp Gly₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp

Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His

Glu Ala Leu₄₃₅ His Asn His Tyr Thr Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro

Gly Gly₄₅₀ Gly Gly Ser Gly Gly₄₅₅ Gly Gly Ser Gln Val₄₆₀ Gln Leu Val Glu

Ser Gly Gly Gly Val Val₄₇₀ Gln Pro Gly Arg Ser₄₇₅ Leu Arg Leu Ser Cys₄₈₀

Ala Ala Ser Gly Phe₄₈₅ Thr Phe Ser Ser Tyr₄₉₀ Asp Met His Trp Val₄₉₅ Arg

Gln Ala Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Val Ala Val Ile Ser₅₁₀ Tyr Asp

Gly Ser Ile₅₁₅ Lys Tyr Tyr Ala Asp₅₂₀ Ser Val Lys Gly Arg₅₂₅ Phe Thr Ile

Ser Arg₅₃₀ Asp Asn Ser Lys Asn₅₃₅ Thr Leu Tyr Leu Gln₅₄₀ Val Asn Ser Leu

Arg Ala Glu Asp Thr Ala₅₅₀ Val Tyr Tyr Cys Ala₅₅₅ Arg Glu Val Arg Ser₅₆₀

Gly Ser Tyr Tyr Tyr₅₆₅ Tyr Tyr Ser Met Asp₅₇₀ Val Trp Gly Gln Gly₅₇₅ Thr

Thr Val Thr Val₅₈₀ Ser Ser Gly Gly Gly₅₈₅ Gly Ser Gly Gly Gly₅₉₀ Gly Ser

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu

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

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

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

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

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

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

Arg
705

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

<220>
<223> Synthetic polynucleotide

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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc 180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtcaa gaaccagttc 300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360
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A-1937-WO-PCT_ST25

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 aagctcctga tctatgccg ctcgactctt cagagtgggt tgccgtcgag gtttagcggg 2040
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 gagatcaagc gt 2172

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 <212> PRT
 <213> Artificial Sequence
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 <223> Synthetic polynucleotide
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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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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<223> Synthetic polynucleotide

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 gtcctaggt 2169

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

<220>
 <223> Synthetic polynucleotide
 <400> 399

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
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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
 Page 285

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

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

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

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

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

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

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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
Page 286

325

330

335

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr

Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu

Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀

Leu Asp Ser Asp Gly₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp

Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His

Glu Ala Leu₄₃₅ His Asn His Tyr Thr Glu Lys Ser Leu Ser₄₄₅ Leu Ser Pro

Gly Gly₄₅₀ Gly Gly Ser Gly Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln

Ser Gly Ala Glu Val Lys₄₇₀ Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀

Lys Thr Ser Glu Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg

Gln Met Pro Gly₅₀₀ Lys Cys Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly

Asp Ser Asp₅₁₅ Thr Arg Tyr Ser Pro₅₂₀ Ser Phe Gln Gly Gln₅₂₅ Val Thr Ile

Ser Ala Asp Lys Ser Ile Ser₅₃₅ Thr Ala Tyr Leu Gln₅₄₀ Trp Ser Ser Leu

Lys Ala Ser Asp Thr Ala₅₅₀ Met Tyr Tyr Cys Ala₅₅₅ Arg Ser Asn Trp Gly₅₆₀

Leu Asp Tyr Trp Gly₅₆₅ Gln Gly Thr Leu Val₅₇₀ Thr Val Ser Ser Gly₅₇₅ Gly

Gly Gly Ser Gly₅₈₀ Gly Gly Gly Ser Gly₅₈₅ Gly Gly Gly Ser Gln₅₉₀ Ser Val

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

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

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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 agggaaccct agtcaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780
gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccg 840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgtg tgaggagcag 960

A-1937-WO-PCT_ST25

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 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
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 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
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 accaagggtg agatcaaacg t 2181

<210> 401
 <211> 705
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 401

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr
 Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu
 Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp
 Glu₃₈₅ Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀
 Leu Asp Ser Asp₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp
 Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His
 Glu Ala Leu₄₃₅ His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro
 Gly Gly₄₅₀ Gly Gly Ser Gly₄₅₅ Gly Gly Ser Gln Val₄₆₀ Gln Leu Val Glu
 Ser₄₆₅ Gly Gly Gly Val₄₇₀ Val Gln Pro Gly Arg Ser₄₇₅ Leu Arg Leu Ser Cys₄₈₀
 Ala Ala Ser Gly Phe₄₈₅ Thr Phe Ser Ser Tyr₄₉₀ Asp Met His Trp Val₄₉₅ Arg
 Gln Ala Pro Gly₅₀₀ Lys Cys Leu Glu Trp₅₀₅ Val Ala Val Ile Ser₅₁₀ Tyr Asp
 Gly Ser Ile₅₁₅ Lys Tyr Tyr Ala Asp₅₂₀ Ser Val Lys Gly Arg₅₂₅ Phe Thr Ile
 Ser Arg₅₃₀ Asp Asn Ser Lys Asn₅₃₅ Thr Leu Tyr Leu Gln Val₅₄₀ Asn Ser Leu
 Arg₅₄₅ Ala Glu Asp Thr Ala₅₅₀ Val Tyr Tyr Cys Ala₅₅₅ Arg Glu Val Arg Ser₅₆₀
 Gly Ser Tyr Tyr Tyr₅₆₅ Tyr Tyr Ser Met Asp₅₇₀ Val Trp Gly Gln Gly₅₇₅ Thr
 Thr Val Thr Val₅₈₀ Ser Ser Gly Gly₅₈₅ Gly Gly Ser Gly Gly₅₉₀ Gly Gly Ser
 Gly Gly₅₉₅ Gly Ser Asp Ile Gln₆₀₀ Met Thr Gln Ser Pro Ser Ser Leu

A-1937-WO-PCT_ST25

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

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cgctgtcagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 120
tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc 180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
tacaaccctg ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaccct agtcaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtga caagaaagtt 720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 780
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg 840
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900

A-1937-WO-PCT_ST25

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 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1080
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
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 ggggcagggt atgatgtaca ctggtaccag cagcttcag gaacagcccc caaactcctc 1980
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 ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac 2100
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 gtcctaggt 2169

<210> 403
 <211> 701
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide
 <400> 403

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

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

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

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 Page 293

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
Page 294

325

330

335

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr

Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu

Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀

Leu Asp Ser Asp Gln₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp

Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His

Glu Ala Leu₄₃₅ His Asn His Tyr Thr Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro

Gly Gly₄₅₀ Gly Gly Ser Gly Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln

Ser Gly Ala Glu Val Lys₄₇₀ Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀

Lys Ala Ser Gly Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg

Gln Met Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly

Glu Ser Glu₅₁₅ Thr Arg Tyr Ser Pro₅₂₀ Ser Phe Gln Gly Gln₅₂₅ Val Thr Ile

Ser Ala Asp Lys Ser Ile Ser₅₃₅ Thr Ala Tyr Leu Gln₅₄₀ Trp Ser Ser Leu

Lys Ala Ser Asp Thr Ala₅₅₀ Met Tyr Tyr Cys Ala₅₅₅ Arg Ser Asn Trp Gly₅₆₀

Leu Asp Tyr Trp Gly₅₆₅ Gln Gly Thr Leu Val₅₇₀ Thr Val Ser Ser Gly₅₇₅ Gly

Gly Gly Ser Gly₅₈₀ Gly Gly Gly Ser Gly₅₈₅ Gly Gly Gly Ser Gln₅₉₀ Ser Val

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

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

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

<220>
<223> Synthetic polynucleotide

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tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt actactggaa ctggattcgc 180
cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
tacaacccgt ccctcaagag tcgagtcacc atatcattag acacgtccaa gaaccagttc 300
tccctgacgc tgacctctgt gaccgccgcg gacacggctg tgtattactg tgcgagagga 360
tattgtagaa gtaccacctg ctactttgac tactggggcc agggaaccct agtcaccgtc 420
tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 480
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gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgccttacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
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gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccg 840
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
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A-1937-WO-PCT_ST25

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 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
 gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
 cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1320
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 tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc 1440
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 ggcacctcag cctccctggc catcactggg ctccaggctg aggatgaggc tgattattac 2100
 tgccagtcct atgaaagcag cctgagtggg tcggtgttcg gcggagggac caagctgacc 2160
 gtcctaggt 2169

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

<220>
 <223> Synthetic polynucleotide

<400> 405

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr
 Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu
 Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp
 Glu₃₈₅ Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀
 Leu Asp Ser Asp₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp
 Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His
 Glu Ala Leu₄₃₅ His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro
 Gly Gly₄₅₀ Gly Gly Ser Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln
 Ser Gly Ala Glu Val₄₇₀ Lys Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀
 Lys Ala Ser Glu Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg
 Gln Met Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly
 Glu Ser Glu₅₁₅ Thr Arg Tyr Ser Pro₅₂₀ Ser Phe Gln Gly Gln₅₂₅ Val Thr Ile
 Ser Ala Asp Lys Ser Ile Ser₅₃₅ Thr Ala Tyr Leu Gln₅₄₀ Trp Ser Ser Leu
 Lys Ala Ser Asp Thr Ala₅₅₀ Met Tyr Tyr Cys Ala₅₅₅ Arg Ser Asn Trp Gly₅₆₀
 Leu Asp Tyr Trp Gly₅₆₅ Gln Gly Thr Leu Val₅₇₀ Thr Val Ser Ser Gly₅₇₅ Gly
 Gly Gly Ser Gly₅₈₀ Gly Gly Gly Ser Gly₅₈₅ Gly Gly Gly Ser Gln₅₉₀ Ser Val
 Leu Thr Gln₅₉₅ Pro Pro Ser Val Ser₆₀₀ Gly Ala Pro Gly Gln₆₀₅ Arg Val Thr

A-1937-WO-PCT_ST25

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
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tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 960
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ggt 2163

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<211> 699
<212> PRT
<213> Artificial Sequence
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<223> Synthetic polynucleotide
<400> 407

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20 25 30

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

Gly Tyr Ile Tyr Tyr Ser Gly 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

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Lys	Leu	Ser	Ser	Val ₈₅	Thr	Ala	Ala	Asp	Thr ₉₀	Ala	Val	Tyr	Tyr	Cys ₉₅	Ala
Arg	Glu	Thr	Gly ₁₀₀	Ser	Tyr	Tyr	Gly	Phe ₁₀₅	Asp	Tyr	Trp	Gly	Gln ₁₁₀	Gly	Thr
Leu	Val	Thr ₁₁₅	Val	Ser	Ser	Ala	Ser ₁₂₀	Thr	Lys	Gly	Pro	Ser ₁₂₅	Val	Phe	Pro
Leu	Ala ₁₃₀	Pro	Ser	Ser	Lys	Ser ₁₃₅	Thr	Ser	Gly	Gly	Thr ₁₄₀	Ala	Ala	Leu	Gly
Cys ₁₄₅	Leu	Val	Lys	Asp	Tyr ₁₅₀	Phe	Pro	Glu	Pro	Val ₁₅₅	Thr	Val	Ser	Trp	Asn ₁₆₀
Ser	Gly	Ala	Leu	Thr ₁₆₅	Ser	Gly	Val	His	Thr ₁₇₀	Phe	Pro	Ala	Val	Leu ₁₇₅	Gln
Ser	Ser	Gly	Leu ₁₈₀	Tyr	Ser	Leu	Ser	Ser ₁₈₅	Val	Val	Thr	Val	Pro ₁₉₀	Ser	Ser
Ser	Leu	Gly ₁₉₅	Thr	Gln	Thr	Tyr	Ile ₂₀₀	Cys	Asn	Val	Asn	His ₂₀₅	Lys	Pro	Ser
Asn	Thr ₂₁₀	Lys	Val	Asp	Lys	Lys ₂₁₅	Val	Glu	Pro	Lys	Ser ₂₂₀	Cys	Asp	Lys	Thr
His ₂₂₅	Thr	Cys	Pro	Pro	Cys ₂₃₀	Pro	Ala	Pro	Glu	Leu ₂₃₅	Leu	Gly	Gly	Pro	Ser ₂₄₀
Val	Phe	Leu	Phe	Pro ₂₄₅	Pro	Lys	Pro	Lys	Asp ₂₅₀	Thr	Leu	Met	Ile	Ser ₂₅₅	Arg
Thr	Pro	Glu	Val ₂₆₀	Thr	Cys	Val	Val	Val ₂₆₅	Asp	Val	Ser	His	Glu ₂₇₀	Asp	Pro
Glu	Val	Lys ₂₇₅	Phe	Asn	Trp	Tyr	Val ₂₈₀	Asp	Gly	Val	Glu	Val ₂₈₅	His	Asn	Ala
Lys	Thr ₂₉₀	Lys	Pro	Cys	Glu	Glu ₂₉₅	Gln	Tyr	Gly	Ser	Thr ₃₀₀	Tyr	Arg	Cys	Val
Ser ₃₀₅	Val	Leu	Thr	Val	Leu ₃₁₀	His	Gln	Asp	Trp	Leu ₃₁₅	Asn	Gly	Lys	Glu	Tyr ₃₂₀
Lys	Cys	Lys	Val	Ser ₃₂₅	Asn	Lys	Ala	Leu	Pro ₃₃₀	Ala	Pro	Ile	Glu	Lys ₃₃₅	Thr
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
 Page 303

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
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Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
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 <211> 2163
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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ggt 2163

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<400> 409

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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

A-1937-WO-PCT_ST25

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
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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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A-1937-WO-PCT_ST25

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

<220>
<223> Synthetic polynucleotide

<400> 411

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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

Arg Gly Tyr Cys₁₀₀ Arg Ser Thr Thr Cys₁₀₅ Tyr Phe Asp Tyr Trp₁₁₀ Gly Gln
 Gly Thr Leu₁₁₅ Val Thr Val Ser Ser₁₂₀ Ala Ser Thr Lys Gly₁₂₅ Pro Ser Val
 Phe Pro₁₃₀ Leu Ala Pro Ser Ser₁₃₅ Lys Ser Thr Ser Gly₁₄₀ Gly Thr Ala Ala
 Leu Gly Cys Leu Val Lys₁₅₀ Asp Tyr Phe Pro Glu₁₅₅ Pro Val Thr Val Ser₁₆₀
 Trp Asn Ser Gly Ala₁₆₅ Leu Thr Ser Gly Val₁₇₀ His Thr Phe Pro Ala₁₇₅ Val
 Leu Gln Ser Ser₁₈₀ Gly Leu Tyr Ser Leu₁₈₅ Ser Ser Val Val Thr₁₉₀ Val Pro
 Ser Ser Ser₁₉₅ Leu Gly Thr Gln Thr₂₀₀ Tyr Ile Cys Asn Val₂₀₅ Asn His Lys
 Pro Ser₂₁₀ Asn Thr Lys Val Asp₂₁₅ Lys Lys Val Glu Pro₂₂₀ Lys Ser Cys Asp
 Lys Thr His Thr Cys Pro₂₃₀ Pro Cys Pro Ala Pro₂₃₅ Glu Leu Leu Gly Gly₂₄₀
 Pro Ser Val Phe Leu₂₄₅ Phe Pro Pro Lys Pro₂₅₀ Lys Asp Thr Leu Met₂₅₅ Ile
 Ser Arg Thr Pro₂₆₀ Glu Val Thr Cys Val₂₆₅ Val Val Asp Val Ser₂₇₀ His Glu
 Asp Pro Glu₂₇₅ Val Lys Phe Asn Trp₂₈₀ Tyr Val Asp Gly Val₂₈₅ Glu Val His
 Asn Ala₂₉₀ Lys Thr Lys Pro Cys₂₉₅ Glu Glu Gln Tyr Gly₃₀₀ Ser Thr Tyr Arg
 Cys Val Ser Val Leu Thr₃₁₀ Val Leu His Gln Asp₃₁₅ Trp Leu Asn Gly Lys₃₂₀
 Glu Tyr Lys Cys Lys₃₂₅ Val Ser Asn Lys Ala₃₃₀ Leu Pro Ala Pro Ile₃₃₅ Glu
 Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu

355

360

365

Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp
 Glu₃₈₅ Ser Asn Gly Gln Pro₃₉₀ Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀
 Leu Asp Ser Asp Gly₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp
 Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His
 Glu Ala Leu₄₃₅ His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro
 Gly Gly₄₅₀ Gly Gly Ser Gly Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln
 Ser Gly₄₆₅ Ala Glu Val Lys₄₇₀ Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀
 Lys Ala Ser Gly Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg
 Gln Met Pro Gly₅₀₀ Lys Cys Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly
 Glu Ser Glu₅₁₅ Thr Arg Tyr Ser Pro₅₂₀ Ser Phe Gln Gly Gln₅₂₅ Val Thr Ile
 Ser Ala₅₃₀ Asp Lys Ser Ile Ser₅₃₅ Thr Ala Tyr Leu Gln₅₄₀ Trp Ser Ser Leu
 Lys₅₄₅ Ala Ser Asp Thr Ala₅₅₀ Met Tyr Tyr Cys Ala₅₅₅ Arg Ser Asn Trp Gly₅₆₀
 Leu Asp Tyr Trp Gly₅₆₅ Gln Gly Thr Leu Val₅₇₀ Thr Val Ser Ser Gly₅₇₅ Gly
 Gly Gly Ser Gly₅₈₀ Gly Gly Gly Ser Gly₅₈₅ Gly Gly Gly Ser Gln₅₉₀ Ser Val
 Leu Thr Gln₅₉₅ Pro Pro Ser Val Ser₆₀₀ Gly Ala Pro Gly Gln₆₀₅ Arg Val Thr
 Ile Ser₆₁₀ Cys Thr Gly Ser Ser₆₁₅ Ser Asn Ile Gly Ala₆₂₀ Gly Tyr Asp Val
 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

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

<220>
 <223> Synthetic polynucleotide

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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
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttccccggc tgtcctacag 600
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 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
 gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200

A-1937-WO-PCT_ST25

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
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 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
 tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc 1440
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 tcctgtaagg cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 1560
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 gtcctaggt 2169

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 <213> Artificial Sequence
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 <223> Synthetic polynucleotide
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 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

<220>
<223> Synthetic polynucleotide

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cagccaccag ggaaggggct agagtggatt ggggaaatca atcatgctgg aaacaccaac 240
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atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260

A-1937-WO-PCT_ST25

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 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
 tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc 1440
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 accgtctcta gtggaggcgg aggatctggt ggcggtggtt ctggcggcgg aggctccgac 1860
 atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1920
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 aaagccccta agctcctgat ctatgctgcg tccagtttgc aaagtggggt cccatcaagg 2040
 ttcagcggca gtggatctgg gccagaattc actctcaca tcagcagcct gcagcctgaa 2100
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 accaaggtgg agatcaaacg t 2181

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 <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
 Page 318

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 Ser Gly Gly Gly Ser
 580 585 590

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

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

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

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
 Page 319

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

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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 tacacgcaga agagcctctc cctgtctccg ggtggtggcg gatcgggagg tggcggatcc 1440
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 gcagaatccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 1680
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 accgtctcta gtggaggcgg aggatctggg ggcggtgggt ctggcgggcg aggctccgac 1860
 atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1920
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 accaaggtgg agatcaaacg t 2181

<210> 417
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 <212> PRT
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 <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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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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A-1937-WO-PCT_ST25

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 419

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 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

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
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 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
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 Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly

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

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

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

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
690 695 700

Ile Lys Arg
705

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<212>	DNA
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tgggtataatg	attatgcagt	ttctctgaaa	agtcgagtaa	ccatcagccc	agacacatcc		300
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tcctccaaga	gcacctctgg	gggcacagcg	gccctgggct	gcctgggtcaa	ggactacttc		540
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ctcatgatct	cccggacccc	tgaggtcaca	tgcgtgggtgg	tggacgtgag	ccacgaagac		900
cctgaggtca	agttcaactg	gtacgtggac	ggcgtggagg	tgcataatgc	caagacaaag		960
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A-1937-WO-PCT_ST25

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caagggacaa aagtcgagat caagcgt 2187

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<210> 421
 <211> 707
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 421

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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
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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

A-1937-WO-PCT_ST25

Gln Phe Ser Leu Lys₈₅ Leu Ser Ser Val Thr₉₀ Ala Ala Asp Thr Ala₉₅ Val

Tyr Tyr Cys Ala₁₀₀ Arg Glu Asp Gly Asp₁₀₅ Ser Tyr Tyr Arg Tyr₁₁₀ Gly Met

Asp Val Trp₁₁₅ Gly Gln Gly Thr Thr₁₂₀ Val Thr Val Ser Ser₁₂₅ Ala Ser Thr

Lys Gly₁₃₀ Pro Ser Val Phe Pro₁₃₅ Leu Ala Pro Ser Ser₁₄₀ Lys Ser Thr Ser

Gly₁₄₅ Gly Thr Ala Ala Leu₁₅₀ Gly Cys Leu Val Lys₁₅₅ Asp Tyr Phe Pro Glu₁₆₀

Pro Val Thr Val Ser₁₆₅ Trp Asn Ser Gly Ala₁₇₀ Leu Thr Ser Gly Val₁₇₅ His

Thr Phe Pro Ala₁₈₀ Val Leu Gln Ser Ser₁₈₅ Gly Leu Tyr Ser Leu₁₉₀ Ser Ser

Val Val Thr₁₉₅ Val Pro Ser Ser Ser₂₀₀ Leu Gly Thr Gln Thr₂₀₅ Tyr Ile Cys

Asn Val₂₁₀ Asn His Lys Pro Ser₂₁₅ Asn Thr Lys Val Asp₂₂₀ Lys Lys Val Glu

Pro₂₂₅ Lys Ser Cys Asp Lys₂₃₀ Thr His Thr Cys Pro₂₃₅ Pro Cys Pro Ala₂₄₀ Pro

Glu Leu Leu Gly Gly₂₄₅ Pro Ser Val Phe Leu₂₅₀ Phe Pro Pro Lys Pro₂₅₅ Lys

Asp Thr Leu Met₂₆₀ Ile Ser Arg Thr Pro₂₆₅ Glu Val Thr Cys Val₂₇₀ Val Val

Asp Val Ser₂₇₅ His Glu Asp Pro Glu₂₈₀ Val Lys Phe Asn Trp₂₈₅ Tyr Val Asp

Gly Val₂₉₀ Glu Val His Asn Ala₂₉₅ Lys Thr Lys Pro Cys₃₀₀ Glu Glu Gln Tyr

Gly₃₀₅ Ser Thr Tyr Arg Cys₃₁₀ Val Ser Val Leu Thr₃₁₅ Val Leu His Gln Asp₃₂₀

Trp Leu Asn Gly Lys₃₂₅ Glu Tyr Lys Cys Lys₃₃₀ Val Ser Asn Lys Ala₃₃₅ Leu

Pro Ala Pro Ile₃₄₀ Glu Lys Thr Ile Ser₃₄₅ Lys Ala Lys Gly Gln₃₅₀ Pro Arg

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

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

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

Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
690 695 700

Ile Lys Arg
705

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<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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attaggcagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 240
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A-1937-WO-PCT_ST25

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<210> 423
 <211> 707
 <212> PRT
 <213> Artificial Sequence
 <220>
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 <400> 423

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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
 Page 333

65				70				75				80			
Gln	Phe	Ser	Leu	Lys 85	Leu	Ser	Ser	Val	Thr 90	Ala	Ala	Asp	Thr	Ala 95	Val
Tyr	Tyr	Cys	Ala 100	Arg	Glu	Asp	Gly	Asp 105	Ser	Tyr	Tyr	Arg	Tyr 110	Gly	Met
Asp	Val	Trp 115	Gly	Gln	Gly	Thr	Thr 120	Val	Thr	Val	Ser	Ser 125	Ala	Ser	Thr
Lys	Gly 130	Pro	Ser	Val	Phe	Pro 135	Leu	Ala	Pro	Ser	Ser 140	Lys	Ser	Thr	Ser
Gly 145	Gly	Thr	Ala	Ala	Leu 150	Gly	Cys	Leu	Val	Lys 155	Asp	Tyr	Phe	Pro	Glu 160
Pro	Val	Thr	Val	Ser 165	Trp	Asn	Ser	Gly	Ala 170	Leu	Thr	Ser	Gly	Val 175	His
Thr	Phe	Pro	Ala 180	Val	Leu	Gln	Ser	Ser 185	Gly	Leu	Tyr	Ser	Leu 190	Ser	Ser
Val	Val	Thr 195	Val	Pro	Ser	Ser	Ser 200	Leu	Gly	Thr	Gln	Thr 205	Tyr	Ile	Cys
Asn	Val 210	Asn	His	Lys	Pro	Ser 215	Asn	Thr	Lys	Val	Asp 220	Lys	Lys	Val	Glu
Pro 225	Lys	Ser	Cys	Asp	Lys 230	Thr	His	Thr	Cys	Pro 235	Pro	Cys	Pro	Ala	Pro 240
Glu	Leu	Leu	Gly	Gly 245	Pro	Ser	Val	Phe	Leu 250	Phe	Pro	Pro	Lys	Pro 255	Lys
Asp	Thr	Leu	Met 260	Ile	Ser	Arg	Thr	Pro 265	Glu	Val	Thr	Cys	Val 270	Val	Val
Asp	Val	Ser 275	His	Glu	Asp	Pro	Glu 280	Val	Lys	Phe	Asn	Trp 285	Tyr	Val	Asp
Gly	Val 290	Glu	Val	His	Asn	Ala 295	Lys	Thr	Lys	Pro	Cys 300	Glu	Glu	Gln	Tyr
Gly 305	Ser	Thr	Tyr	Arg	Cys 310	Val	Ser	Val	Leu	Thr 315	Val	Leu	His	Gln	Asp 320
Trp	Leu	Asn	Gly	Lys 325	Glu	Tyr	Lys	Cys	Lys 330	Val	Ser	Asn	Lys	Ala 335	Leu
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
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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
 Page 335

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

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

<220>
 <223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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 <212> PRT
 <213> Artificial Sequence

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<400> 425

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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

A-1937-WO-PCT_ST25

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn
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 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met
 100 105 110
 Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135 140
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 165 170 175
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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

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<211> 2151
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

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A-1937-WO-PCT_ST25

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

<220>
<223> Synthetic polynucleotide

<400> 427

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Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
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 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
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 465 470 475 480
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 485 490 495
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 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
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 580 585 590
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 595 600 605

A-1937-WO-PCT_ST25

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
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Thr Lys Leu Glu Ile Lys Arg
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<210> 428
<211> 2151
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A-1937-WO-PCT_ST25

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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

A-1937-WO-PCT_ST25

Leu Gln Trp Ser Ser₈₅ Leu Lys Ala Ser Asp₉₀ Thr Ala Met Tyr Tyr₉₅ Cys
 Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val
 Thr Val Ser₁₁₅ Ser Ala Ser Thr Lys₁₂₀ Gly Pro Ser Val Phe₁₂₅ Pro Leu Ala
 Pro Ser₁₃₀ Ser Lys Ser Thr Ser₁₃₅ Gly Gly Thr Ala Ala₁₄₀ Leu Gly Cys Leu
 Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀
 Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser
 Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Cys Glu Glu Gln Tyr₂₉₅ Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val
 Leu Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro

A-1937-WO-PCT_ST25

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln 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

A-1937-WO-PCT_ST25

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
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Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly
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Thr Lys Leu Glu Ile Lys Arg
690 695

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A-1937-WO-PCT_ST25

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 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
 Page 349

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
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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
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Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
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Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
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Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
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Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
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Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn

355

360

365

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

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

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
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Ser Leu Ser Pro Gly Gly Gly Ser 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
 Page 351

Thr Pro Arg Thr Phe Gly **Gln** Gly Thr Lys Leu **Glu** Ile Lys Arg
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<213>	Artificial Sequence

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A-1937-WO-PCT_ST25

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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
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A-1937-WO-PCT_ST25

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp
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Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
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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
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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
355 360 365

A-1937-WO-PCT_ST25

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
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Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile Gly Tyr
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Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys Ser Arg
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Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu
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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
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A-1937-WO-PCT_ST25

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Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
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A-1937-WO-PCT_ST25

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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
 Page 357

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
 Page 358

370

375

380

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

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

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

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

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

Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu
 465 470 475 480

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

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

Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 515 520 525

Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu Thr Leu
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Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
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Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
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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
 Page 359

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A-1937-WO-PCT_ST25

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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

A-1937-WO-PCT_ST25

Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp
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Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
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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
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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

A-1937-WO-PCT_ST25

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

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

A-1937-WO-PCT_ST25

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
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Arg
705

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<213> Artificial Sequence

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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
 Page 365

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
Page 366

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

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

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

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

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

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

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
 Page 367

625 630 635 640
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 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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A-1937-WO-PCT_ST25

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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

A-1937-WO-PCT_ST25

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

Gln Gly Thr Leu Val Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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caagcgcctg gaaaagggtc cgagtgggtt tccgccatta cgtggaatag cggacacatc 240
gattatgcag acgctgtgga gggcagattc acaatctcac gagacaatgc taagaacagc 300
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 660
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ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag 960
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agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260

A-1937-WO-PCT_ST25

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 ctcacctgcg ctgtccatgg tgggtccttc agtgggttact actggaactg gattcgccag 1560
 ccaccaggga aggggctaga gtggattggg gaaatcaatc atgctggaaa caccaactac 1620
 aaccctgtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc 1680
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 tcaggaggcg gaggatctgg tggcggtggt tctggcggcg gaggctccga aattgtgttg 1860
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 gccagtcaga gtgttagaag cagtactta gcctggtacc agcagaaacc tggccaggct 1980
 cccaggctcc tcatttatgg tgcattcagc agggccactg gcatcccaga caggttcagt 2040
 ggcagtgggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt 2100
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 gagattaaac ga 2172

<210> 443
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 443

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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 Thr₁₁₅ Leu Val Thr Val Ser₁₂₀ Ser Ala Ser Thr Lys₁₂₅ Gly Pro Ser
 Val Phe₁₃₀ Pro Leu Ala Pro Ser₁₃₅ Ser Lys Ser Thr Ser₁₄₀ Gly Gly Thr Ala
 Ala₁₄₅ Leu Gly Cys Leu Val₁₅₀ Lys Asp Tyr Phe Pro₁₅₅ Glu Pro Val Thr Val₁₆₀
 Ser Trp Asn Ser Gly₁₆₅ Ala Leu Thr Ser Gly₁₇₀ Val His Thr Phe Pro₁₇₅ Ala
 Val Leu Gln Ser₁₈₀ Ser Gly Leu Tyr Ser₁₈₅ Leu Ser Ser Val Val₁₉₀ Thr Val
 Pro Ser Ser₁₉₅ Ser Leu Gly Thr Gln₂₀₀ Thr Tyr Ile Cys Asn₂₀₅ Val Asn His
 Lys Pro₂₁₀ Ser Asn Thr Lys Val₂₁₅ Asp Lys Lys Val Glu₂₂₀ Pro Lys Ser Cys
 Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀
 Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
 Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg₃₀₅ Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 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
 Page 375

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
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 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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 ttcaactggg acgtggacgg cgtggagggt cataatgcca agacaaagcc gtgtgaggag 960
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 1020
 aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1140
 cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1200
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260
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A-1937-WO-PCT_ST25

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 ctcacctgcg ctgtccatgg tgggtccttc agtgggttact actggaactg gattcgccag 1560
 ccaccagggga agtgtctaga gtggattggg gaaatcaatc atgctggaaa caccaactac 1620
 aacccgtccc tcaagagtcg agtcaccata tcattagaca cgtccaagaa ccagttctcc 1680
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 cccaggctcc tcatttatgg tgcattcagc agggccactg gcatcccaga caggttcagt 2040
 ggagtggtg ctgggacaga cttactctc accatcagca gactggagcc tgaagatttt 2100
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 gagattaaac ga 2172

<210> 445
 <211> 702
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 445

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
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 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 450 455 460
 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

A-1937-WO-PCT_ST25

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

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

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gtcaccatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
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ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgccgt cacaagagc ttcaacaggg gagagtgt 708

<210> 447
<211> 236
<212> PRT
<213> Homo sapiens

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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
Page 380

A-1937-WO-PCT_ST25															
65				70				75				80			
Pro	Ser	Arg	Phe	Ser ₈₅	Gly	Ser	Gly	Ser	Gly ₉₀	Thr	Asp	Phe	Thr	Leu ₉₅	Thr
Ile	Ser	Ser	Leu ₁₀₀	Gln	Pro	Glu	Asp	Phe ₁₀₅	Ala	Thr	Tyr	Tyr	Cys ₁₁₀	Gln	Gln
Ser	Tyr	Ser ₁₁₅	Thr	Pro	Arg	Thr	Phe ₁₂₀	Gly	Gln	Gly	Thr	Lys ₁₂₅	Leu	Glu	Ile
Lys	Arg ₁₃₀	Thr	Val	Ala	Ala	Pro ₁₃₅	Ser	Val	Phe	Ile	Phe ₁₄₀	Pro	Pro	Ser	Asp
Glu ₁₄₅	Gln	Leu	Lys	Ser	Gly ₁₅₀	Thr	Ala	Ser	Val	Val ₁₅₅	Cys	Leu	Leu	Asn	Asn ₁₆₀
Phe	Tyr	Pro	Arg	Glu ₁₆₅	Ala	Lys	Val	Gln	Trp ₁₇₀	Lys	Val	Asp	Asn	Ala ₁₇₅	Leu
Gln	Ser	Gly	Asn ₁₈₀	Ser	Gln	Glu	Ser	Val ₁₈₅	Thr	Glu	Gln	Asp	Ser ₁₉₀	Lys	Asp
Ser	Thr	Tyr ₁₉₅	Ser	Leu	Ser	Ser	Thr ₂₀₀	Leu	Thr	Leu	Ser	Lys ₂₀₅	Ala	Asp	Tyr
Glu	Lys ₂₁₀	His	Lys	Val	Tyr	Ala ₂₁₅	Cys	Glu	Val	Thr	His ₂₂₀	Gln	Gly	Leu	Ser
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<210> 448
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<212> DNA
<213> Homo sapiens
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<210> 449
<211> 217
<212> PRT
<213> Homo sapiens

<400> 449

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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

A-1937-WO-PCT_ST25

<210> 450
 <211> 708
 <212> DNA
 <213> Homo sapiens

<400> 450
 atggacatga ggggtgcccgc tcagctcctg gggctcctgc tgctgtggct gagaggtgcg 60
 cgctgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
 gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcagcag 180
 aaaccaggga aagcccctaa gctcctgata tatgtgtcgt ccagtttgca aagtgggggtc 240
 ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300
 cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc 360
 ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 420
 ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
 ctgacgctga gcaaagcaga ctacagaaaa cacaaagtct acgcctgcga agtcacccat 660
 cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 708

<210> 451
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 451
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 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 A-1937-WO-PCT_ST25 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 acctcgcatg gtatcagcaa 180
aaacccggaa aagcaccgaa gctcctgatc tatgccgcct cgactcttca gagtgggtgtg 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 cacaagctct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaagagc 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

A-1937-WO-PCT_ST25

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
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ctctcctgca gggccagtca gagtgtaaga agcagctact tagcctggta ccagcagaga 120
gctggccagg ctcccaggct cctcatctat ggtgcatcca gccgggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctctcctac cttcggccaa 300

A-1937-WO-PCT_ST25

gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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

Phe Asn Arg Gly Glu Cys
210

<210> 456
<211> 1350
<212> DNA
<213> Homo sapiens

<400> 456
caggtgcagt tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgatg tctatggtgg gtccttcagt ggttactact ggaactggat ccgccagccc 120
ccaggggaagg ggctggagtg gattggggaa atcaatcata gtggaattac caactacaac 180
ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc cgcgacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
aaatcttgtg aaaaaactca cacatgccc aacgtgcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagga gcagtacggc 900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320
cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 457
<211> 450
<212> PRT
<213> Homo sapiens

<400> 457

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gactgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcttctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagcaatg atttagcctg gtatcagcag 180
aaaccagggg aagcccctaa ggcctgatc tttgctgcat ccagtttgca aagtgggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctccagcata atagttaccc tcccactttc 360
ggcggagggg ccaaggtgga gatcaaacga acgggtggctg caccatctgt cttcatcttc 420

A-1937-WO-PCT_ST25

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
 ctgacgctga gcaaagcaga ctacgagaaa cacaagtctt acgcctgcga agtcacccat 660
 cagggcctga gctcgcccggt cacaagagc 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

A-1937-WO-PCT_ST25
200 205Phe Asn Arg Gly Glu Cys
210<210> 460
<211> 1425
<212> DNA
<213> Homo sapiens

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<400> 460
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc      60
agatgccagg tgcagctggt ggagtctggg ggaggcgctg tccagcctgg gaggtccctg      120
agactctcct gtgcagcctc tggattcacc ctcagtagct 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
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct      780
gaactcctgg ggggaccgtc agtcttctc tttcccccaa aaccaagga 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 caagtgaag gtctccaaca aagccctccc agccccatc     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

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<210> 461
<211> 453
<212> PRT
<213> Homo sapiens

<400> 461

A-1937-WO-PCT_ST25

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr 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

A-1937-WO-PCT_ST25

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	
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agatgcgaca tccagatgac ccagtctcca agctccctgt ctgctgtctgt gggcgatagg	120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gtcctaaca taagaactac	180
ttagtttggt accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct	240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact	300

A-1937-WO-PCT_ST25

ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360
aagactcctc tcactttcgg cggagggacc aaagaaacca ggaaagggttc ctaaactgct 420
catttactgg gcatctaccc gggaatccgg ggtccctagt cgattcagtg gcagcgggctc 480
tgggacagat ttactctca ccatcagcag cctgcagcct gaagatgtgg caacttatta 540
ctgtcagcaa tattataaga ctctctcac tttcggcgga gggaccaaca aggacagcac 600
ctacagcctc aagagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta 660
cgcctgcgaa gtcacccatc agggcctgag ctcgccgctc 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
Page 395

<210> 464
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 464
 gacattcaaa tgaccagag cccatccagc ctgagcgcac 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
 ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

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

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

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

<210> 466
<211> 36
<212> DNA
<213> Homo sapiens

<400> 466
agggccagtc agagtgttaag aagcagctac ttagcc 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

<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

21

<210> 473
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 473

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

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

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

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

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

A-1937-WO-PCT_ST25

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

Phe Asn Arg Gly Glu Cys
210

<210> 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
Page 401

165

170

175

Ser Thr Leu Glu₁₈₀ Leu Ser Lys Ala Asp₁₈₅ Tyr Glu Lys His Lys₁₉₀ Val Tyr

Ala Cys Glu₁₉₅ Val Thr His Gln Gly₂₀₀ Leu Ser Ser Pro Val₂₀₅ Thr Lys Ser

Phe Asn₂₁₀ Arg Gly Glu Cys

<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 Leu₅ Val Glu Ser Gly Gly₁₀ Leu Val Gln Pro Gly₁₅ Gly

Ser Leu Arg Leu₂₀ Ser Cys Ala Ala Ser₂₅ Gly Tyr Val Phe Thr₃₀ Asp Tyr

Gly Met Asn₃₅ Trp Val Arg Gln Ala₄₀ Pro Gly Lys Gly₄₅ Leu Glu Trp Met

Gly Trp₅₀ Ile Asn Thr Tyr Ile₅₅ Gly Glu Pro Ile Tyr₆₀ Ala Asp Ala Val

Lys Gly Arg Phe Thr Phe₇₀ Ser Arg Asp Thr Ser₇₅ Lys Ser Thr Ala Tyr₈₀

Leu Gln Met Asn₈₅ Ser Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Arg Gly Tyr₁₀₀ Arg Ser Tyr Ala Met₁₀₅ Asp Tyr Trp Gly Gln Gly Thr

Leu Val Thr₁₁₅ Val Ser Ser Ala Ser₁₂₀ Thr Lys Gly Pro Ser₁₂₅ Val Phe Pro

Leu Ala₁₃₀ Pro Ser Ser Lys Ser₁₃₅ Thr Ser Gly Gly Thr₁₄₀ Ala Ala Leu Gly

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly 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

A-1937-WO-PCT_ST25

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 480
<211> 15
<212> DNA
<213> Homo sapiens

<400> 480
agctatggca tgcac

15

<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

A-1937-WO-PCT_ST25

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 atagtggaat 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
 Page 407

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 gggccagtc gagtgaaga 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

A-1937-WO-PCT_ST25

<210> 492
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 492
 gacatccaga tgaccagtc tccatcctcc ctgtctgctt ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattagc aatgatttag cctgggtatca gcagaaacca 120
 gggaaagccc ctaagcgctt gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtctccag cataatagtt accctcccac 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 gggtactact ggaactggat ccgccagccc 120
 ccagggaagg ggctggagtg gattggggaa atcaatcata gtggaattac caactacaac 180
 ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

A-1937-WO-PCT_ST25

aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag 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 tggtggagtc tgggggaggc gtggtccagc ctgggaggtc 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 ctacggtatt gacgtctggg gccaaaggac cacggtcacc 360
gtctcctca 369

<210> 497
<211> 123

A-1937-WO-PCT_ST25

<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

atggaaacc cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccgga 60

A-1937-WO-PCT_ST25

<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

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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 gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc      480
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      540
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      600
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac      660
atctgcaacg tgaatcaciaa gccagcaac accaaggtgg acaagaaagt tgagcccaaa      720
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg      780
tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctcccg gacccttgag      840
gtcacatgcy tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac      900
gtggacggcg tggaggtgca taatgccaag acaaagccgt gcgaggagca gtacggcagc      960
acgtaccgtt gcgtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag     1020
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gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg gaaggagatg     1140
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc     1200

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A-1937-WO-PCT_ST25

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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

A-1937-WO-PCT_ST25

Ser Ser Ser₁₉₅ Leu Gly Thr Gln Thr₂₀₀ Tyr Ile Cys Asn Val₂₀₅ Asn His Lys

Pro Ser₂₁₀ Asn Thr Lys Val₂₁₅ Asp Lys Lys Val Glu Pro₂₂₀ Lys Ser Cys Asp

Lys₂₂₅ Thr His Thr Cys Pro₂₃₀ Pro Cys Pro Ala Pro₂₃₅ Glu Leu Leu Gly Gly₂₄₀

Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys Pro₂₅₀ Lys Asp Thr Leu Met₂₅₅ Ile

Ser Arg Thr Pro₂₆₀ Glu Val Thr Cys Val₂₆₅ Val Val Asp Val Ser₂₇₀ His Glu

Asp Pro Glu₂₇₅ Val Lys Phe Asn Trp₂₈₀ Tyr Val Asp Gly Val₂₈₅ Glu Val His

Asn Ala₂₉₀ Lys Thr Lys Pro Cys₂₉₅ Glu Glu Gln Tyr Gly₃₀₀ Ser Thr Tyr Arg

Cys₃₀₅ Val Ser Val Leu Thr₃₁₀ Val Leu His Gln Asp₃₁₅ Trp Leu Asn Gly Lys₃₂₀

Glu Tyr Lys Cys Lys₃₂₅ Val Ser Asn Lys Ala₃₃₀ Leu Pro Ala Pro Ile₃₃₅ Glu

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr

Thr Leu Pro₃₅₅ Pro Ser Arg Lys Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu

Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp

Glu₃₈₅ Ser Asn Gly Gln Pro₃₉₀ Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀

Leu Lys Ser Asp Gly₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp

Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His

Glu Ala₄₃₅ Leu His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro

Gly Lys₄₅₀

<210> 509
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 509
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 agatgtgaca ttcaaagac ccagagccca tccagcctga gcgcatctgt aggagaccgg 120
 gtcacatca cttgtaaagc cagtcagaac gtaggtacta acgtagcctg gtatcaggaa 180
 aaaccaggta aagccccaaa agccctcatc tacagtgcct ctttcctcta tagtggtgta 240
 ccatacaggt tcagcggatc cggtagtggc actgatttca ccctcacgat cagtagcctc 300
 cagccagaag atttcgccac ttattactgt caacagtata acatctaccc actcacattc 360
 ggtcagggtg ctaaagtaga aatcaaactg acggtagcgg ccccatctgt cttcatcttc 420
 ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
 ttctatccca gagaggccaa agtacagtgg aagggtgata acgccctcca atcgggtaac 540
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cgagagcacc 600
 ctgacgctga gcaaagcaga ctacagaaaa cacaagtctt acgcctgcga agtcacccat 660
 cagggcctga gtcaccagt 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

A-1937-WO-PCT_ST25

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 cagcgagct tctcttctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgttaga 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 gctgcacat ctgtcttcat cttcccgcca 420
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 480
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 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
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 agatgcgagg ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120
 agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180
 aaggccccgg 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 ccgaaccggt gacggtgtcg 540
 tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 600
 ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
 aaatcttgtg acaaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840
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 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
 agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
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 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380
 cagaagagcc tctccctgtc tccgggtaaa 1410

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

<220>
 <223> Synthetic polypeptide

<400> 514

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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agatgcgagg ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120
agattgtcct gtgctgcatc tggttacacc ttcacagact atggaatgaa ttggggttaga 180
aaggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240

A-1937-WO-PCT_ST25

atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360
ggatacagat cttatgccat ggactactgg ggccagggta ccctagtcac cgtctctagt 420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
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tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 600
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tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttctg acaaaaactca cacatgccc aagtgcccag cacctgaact cctgggggga 780
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gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
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gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200
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ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 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 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 Thr Phe Thr Asp Tyr Gly Met Asn Trp Val Arg Lys Ala Pro Gly
50 55 60

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gcgcctgac tatgctgcgt ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg ccagaattca ctctcacaat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gtcactttc 360
ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 420
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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
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A-1937-WO-PCT_ST25

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 519
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<213> Artificial Sequence

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<210> 520
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<213> Artificial Sequence

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<223> Synthetic polypeptide

<400> 520

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 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
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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
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Phe Asn Arg Gly Glu Cys
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<212> DNA

<213> Artificial Sequence

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A-1937-WO-PCT_ST25

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<213> Artificial Sequence

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20 25 30

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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<210> 523
<211> 234
<212> PRT
<213> Homo sapiens

<400> 523

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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
Page 431

A-1937-WO-PCT_ST25															
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Gly	Ser	Ser ₁₁₅	Pro	Thr	Phe	Gly	Gln ₁₂₀	Gly	Thr	Arg	Leu	Glu ₁₂₅	Ile	Lys	Arg
Thr	Val ₁₃₀	Ala	Ala	Pro	Ser	Val ₁₃₅	Phe	Ile	Phe	Pro	Pro ₁₄₀	Ser	Asp	Glu	Gln
Leu ₁₄₅	Lys	Ser	Gly	Thr	Ala ₁₅₀	Ser	Val	Val	Cys	Leu ₁₅₅	Leu	Asn	Asn	Phe	Tyr ₁₆₀
Pro	Arg	Glu	Ala	Lys ₁₆₅	Val	Gln	Trp	Lys	Val ₁₇₀	Asp	Asn	Ala	Leu	Gln ₁₇₅	Ser
Gly	Asn	Ser	Gln ₁₈₀	Glu	Ser	Val	Thr	Glu ₁₈₅	Gln	Asp	Ser	Lys	Asp ₁₉₀	Ser	Thr
Tyr	Ser	Leu ₁₉₅	Ser	Ser	Thr	Leu	Thr ₂₀₀	Leu	Ser	Lys	Ala	Asp ₂₀₅	Tyr	Glu	Lys
His	Lys ₂₁₀	Val	Tyr	Ala	Cys	Glu ₂₁₅	Val	Thr	His	Gln	Gly ₂₂₀	Leu	Ser	Ser	Pro
Val ₂₂₅	Thr	Lys	Ser	Phe	Asn ₂₃₀	Arg	Gly	Glu	Cys						

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<212> DNA
<213> Homo sapiens
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<212> DNA
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A-1937-WO-PCT_ST25

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<220>
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ccgccagcca	
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ggctagagt	gattggggaa
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ctgaggtcaa	gttcaactgg
900	
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gcataatgcc	aagacaaagc
cgtgcgagga	gcagtacggc
960	
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cgtcctcacc	gtcctgcacc
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caacaaagcc	ctcccagccc
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ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg	1260
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<220>
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtt ttactgtcag cagtattggt gctcacctac cttcggccaa	300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca	360
tctgatgagc agttgaaatc tggaactgcc aaagttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg	540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc	600
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<210> 531
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca	120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac	180
aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca	240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcgggtcag	300
ggtactaaag tagaaatcaa acgtacggtg gcggcccat ctgtcttcat cttcccgcca	360
tctgatgagc agttgaaatc tggaactgcc gaagttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag	480

A-1937-WO-PCT_ST25

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

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agattgtcct	gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180
caggcccccg	gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240
atttatgctg	acgccgtcaa gggcagattc acgttctctc gagacacatc caagtcaaca 300
gcatacctcc	aatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga 360
ggatacagat	cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt 420
gcctccacca	agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
ggcacagcgg	ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
tggaactcag	gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact	ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
tacatctgca	acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg	acaaaactca cacatgccc aacgtgcccag cacctgaact cctgggggga 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	gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaag	ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140
atgaccaaga	accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1200
gccgtggagt	gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
ctggactccg	acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320
cagcagggga	acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380
cagaagagcc	tctccctgtc tccgggtaaa 1410

<210> 533
 <211> 642
 <212> DNA

<213> Artificial Sequence

<220>

<223> Artificial polynucleotide

<400> 533

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ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc      180
aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca      240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag      300
ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc gaagtttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
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<210> 534

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 534

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ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc      180
aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca      240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag      300
ggtactaaag tagaaatcaa acgtacggta gcggcccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctggag      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc      600
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<210> 535

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

A-1937-WO-PCT_ST25

<400> 535

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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

A-1937-WO-PCT_ST25

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
Page 441

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

A-1937-WO-PCT_ST25

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
Page 443

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

A-1937-WO-PCT_ST25

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
Page 445

A-1937-WO-PCT_ST25

Protein Sequence: C-STE5															
65				70				75				80			
Glu	Asp	Phe	Ala	Thr ₈₅	Tyr	Phe	Cys	Gln	Gln ₉₀	Ser	Tyr	Ser	Thr	Pro ₉₅	Arg
Thr	Phe	Gly	Gln ₁₀₀	Gly	Thr	Lys	Val	Glu ₁₀₅	Ile	Lys	Arg	Thr	Val ₁₁₀	Ala	Ala
Pro	Ser	Val ₁₁₅	Phe	Ile	Phe	Pro	Pro ₁₂₀	Ser	Asp	Glu	Gln	Leu ₁₂₅	Lys	Ser	Gly
Thr	Ala ₁₃₀	Ser	Val	Val	Cys	Leu ₁₃₅	Leu	Asn	Asn	Phe	Tyr ₁₄₀	Pro	Arg	Glu	Ala
Lys ₁₄₅	Val	Gln	Trp	Lys	Val ₁₅₀	Asp	Asn	Ala	Leu	Gln ₁₅₅	Ser	Gly	Asn	Ser	Gln ₁₆₀
Glu	Ser	Val	Thr	Glu ₁₆₅	Gln	Asp	Ser	Lys	Asp ₁₇₀	Ser	Thr	Tyr	Ser	Leu ₁₇₅	Lys
Ser	Thr	Leu	Thr ₁₈₀	Leu	Ser	Lys	Ala	Asp ₁₈₅	Tyr	Glu	Lys	His	Lys ₁₉₀	Val	Tyr
Ala	Cys	Glu ₁₉₅	Val	Thr	His	Gln	Gly ₂₀₀	Leu	Ser	Ser	Pro	Val ₂₀₅	Thr	Lys	Ser
Phe	Asn ₂₁₀	Arg	Gly	Glu	Cys										

<210>	542
<211>	217
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 542

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
Page 449

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

A-1937-WO-PCT_ST25

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
Page 451

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

A-1937-WO-PCT_ST25

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

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
Page 453

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

A-1937-WO-PCT_ST25

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
Page 455

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 553
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 553
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cgctgtgagg tgcagctggt gcagctctgga gcagaggtga aaaagcccgg ggagtctctg 120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc 180
aagatgcccc 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 catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 480
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 540
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 600
tactccctca agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc 720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900
gacggcgtgg aggtgcataa tgccaagaca aagccgtgcg aggagcagta cggcagcacg 960
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1020
aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaagacc 1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1140
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1200
gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac 1260

A-1937-WO-PCT_ST25

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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	
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ccaggggaagg 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 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 aaaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga	720
ccgtcagctt tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc	900
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc 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 gagcaggtgg	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 Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

Thr Leu Pro Pro Ser Arg Lys 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

A-1937-WO-PCT_ST25

aaaccagggga aagcccctaa gctcctgatc tatgctacat ccagtttgca aagtgggggtc	240
ccatcaaggt tcagtggcag tggatctggg acagatttct ctctcaccat cagcagtctg	300
caacctgaag attttgcaac ttactttctgt caacagagtt acagtacccc tcggacgttc	360
ggccaagggga 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> 557

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 557

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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 ccccctggca ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac	480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctacaggactc	540
tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattct	660
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttcctct tcccccaaa 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 ctccaagacc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggaa ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag	1200

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

Pro Pro Ser Arg 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

A-1937-WO-PCT_ST25

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gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180
ttagtttggg accagaagaa accaggaaag gttcctaaac tgctcattta ctgggcatct 240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctggggac agatttcact 300
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat 360
aagactcctc tcactttcgg cggagggacc aaggtggaga tcaaacgaac ggtggctgca 420
ccatctgtct tcattctccc gccatctgat gagcagttga aatctggtac cgcctctggt 480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc 600
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac 660
gcctgcaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 720
gagtggt 726

<210> 560
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 560
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atcacttgta aagccagtca gaacgtaggt actaacgtag cctgggtatca ggaaaaacca 120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatcc 180
aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240
gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300
ggtactaaag tagaaatcaa acgtacggtg 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> 561
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

A-1937-WO-PCT_ST25

<400> 561
atgaaacatc tgtggttctt cctgctgttg gtggcagccc ccagatgggt gctgagccag 60
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc 120
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gatcagggag 180
cccccaggga aaggccttga gtggatagga aggacatact acaggtccaa gtggtataat 240
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 300
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 360
gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacggtc 420
accgtctcta gtgcctccac caagggccca tcggctcttc ccctggcacc ctctccaag 480
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt cccgaaccg 540
gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 600
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 660
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 720
aaagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa 780
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 840
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 900
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgagag 960
gagcagtacg gcagcacgta ccgttgctgc 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 ttcttctct atagcaagct caccgtggac 1320
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380
aaccactaca cgagaagag 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 ggggtgccgc ccagctcctc ggtcttctgt tgctctggct ccgtgggtgcc 60
cgctgtgaca tccagatgac ccagctctcca agctccctgt ctgcgtctgt gggcgatagg 120
gtcaccatca cttgcaggtc cagccagagt gtgttataca gctccaacaa taagaactac 180
ttagtttggt accagaagaa accaggaaag 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 tcattttccc gccatctgat gagcagttga aatctggtac cgcctctggt 480
gtgtgcctgc tgaataactt ctatccaga gaggccaaag tacagtggaa ggtggataac 540

A-1937-WO-PCT_ST25

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	
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc	60
agatgcgagg tacagttgct ggagtcaggt ggaggactgg tgcagcccgg ggggagcctc	120
cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg	180
atcagggagg ccccagggaa 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 aagggcccat cgggtcttccc cctggcaccc	480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	540
cccgaaccgg tgacgggtgc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	600
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc	660
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	720
gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccc	780
gcacctgaac tcctgggggg accgtcagtc ttctcttccc ccccaaaacc caaggacacc	840
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac	900
cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	960
ccgtgcgagg agcagtacgg cagcacgtac cgttgcgta gcgtcctcac cgtcctgcac	1020
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc	1080
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc	1140
ctgcccccat cccggaagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa	1200
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac	1260
tacaagacca cgctcccgt gctgaagtcc gacggctcct tcttctctta tagcaagctc	1320
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1380
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a	1431

<210> 565

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

<220>
 <223> Synthetic polypeptide

<400> 565

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys 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
atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc

A-1937-WO-PCT_ST25

agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga	120
gtcaccatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagaag	180
aaaccagggg aagcccctaa gctcctgatc tatgatgcat ccagtttgca aagtgggggtc	240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacagcata atagttaccc tccgacgttc	360
ggccaagggg 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 cacaaagtct 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 gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc	60
agatgccagg tgcagctggt ggagtctggg ggaggcgctg 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 ccatcggtct tccccctggc accctcctcc	480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct	600
gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc	660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	720
aagaaagttg agcccaaatt ttgtgacaaa actcacacat gccaccgtg cccagcacct	780
gaactcctgg ggggaccgtc agtcttctc tttcccccaa 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

A-1937-WO-PCT_ST25

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140
ccatcccgga 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
 atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
 agatgcgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
 gtcacatca cttgccggac aagtcaggac attagagatg atttaggctg gtatcagaag 180
 aaaccaggga aagcccctaa ggcctgatc tatgatgcat ccagtttgca aagtggggctc 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 gtcgccccgt cacaaagagc ttcaacaggg gagagtgt 708

<210> 570
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 570
 atggacatga ggggtcccg ctcagctcctg gggctcctgc tgctgtggct gagagggtgcg 60
 cgctgtcagt ctgtgctgac gcagccgccc tcagtgtctg gggccccagg gcagaggggtc 120
 accatctcct gcactgggag cagttccaac atcggggcag gttatgatgt aactggtac 180
 caggagtttc caggaacagc ccccaaactc ctcatccaag gtaacagcaa tcggccctca 240
 ggggtccctg accgattctc tggctccaag tctggcacct cagcctccct ggccatcact 300
 ggggtccagg ctgaggatga ggctgattat tactgccagt cctatgacag cagcctgagt 360
 gggtcggtgt 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
 gccgagagct atctgagcct gacgcctgag cagtgggaagt cccacagaag ctacagctgc 660

caggtcacgc atgaaggag 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

Gln Pro Glu Asn Asn Tyr 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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A-1937-WO-PCT_ST25

agatgcgagg ttcagctggt 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 ccgaaccggg gacggtgtcg 540
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ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 660
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tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
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gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
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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
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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 Lys Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggcaaa 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggt 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> 575
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 575

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ccaggaagg agctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac      180
ccgtcccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg      240
aagctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt      300
agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctctagt      360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg      480
tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca      540
ggactctact ccctcgagag cgtggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
aaatcttgtg acaaaaactca cacatgcca ccgtgccag cacctgaact cctgggggga      720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct      780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc      900
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gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                1350

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<210> 576

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 576

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atcacttgta aagccagtca gaacgtaggt actaacgtag cctggatatca gcaaaaacca      120
ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac      180

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A-1937-WO-PCT_ST25

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ggtactaaag tagaaatcaa acgtacggtg gcggcccat ctgtcttcat cttcccgcca	360
tctgatgagc agttgaaatc tggaactgcc 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
ctgagctcac cagtaacaaa aagctttaat agaggagagt gt	642

<210> 577
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 577	
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agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga	180
caggccccgg gaaagaagct ggaatggatg ggttgatta atacttacat tggagagcct	240
atttatgctg acagcgtaaa gggcagattc acgttctctc tagacacatc caagtcaaca	300
gcatacctcc aaatgaatag cctgagagca gaggacaccg cagtgtacta ttgtgctaga	360
ggatacagat cttatgccat ggactactgg ggccagggtg ccctagtcac cgtctctagt	420
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ggactctact ccctcaagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga	780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag	1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg	1260

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

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

Asn Gly Gln Pro Glu Asn Asn Tyr 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

A-1937-WO-PCT_ST25

<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
Page 484

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
 gtcacatca cttgccgggc aagtcagagc attaacaact atttaaattg gtatcagcag 180
 aaaccaggga aagcccctaa gctcctgatc tatgctacat ccagtttgca aagtggggtc 240

A-1937-WO-PCT_ST25

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caacctgaag	attttgcaac	ttactttctgt	caacagagtt	acagtacccc	tcggacgttc	360
ggcaaaggga	ccaaggtgga	gatcaaacga	acggtggctg	caccatctgt	cttcattctt	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

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cttcggagac	
cctgtccctc	
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tctctggtgg	
ctccatcagt	
agttacttct	
ggagctggat	
ccggcagccc	
ccagggaagg	180
aactggagtg	
gattgggtat	
atctattaca	
gtgggagcac	
caactacaac	
ccctccctca	240
agagtcgagt	
caccatgtca	
atagacacgt	
ccaagaacca	
gttctccctg	
aagctgagct	300
ctgtgaccgc	
tgcgacacgc	
gccgtgtatt	
actgtgagag	
agaaattggg	
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ggaaccctgg	
tcaccgtctc	
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tccagcagct	
tgggcacca	
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aactcctggg	
gggaccgtca	
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accctcatga	
tctcccgga	
ccctgaggtc	
acatgcgtgg	840
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gagccacgaa	
gaccctgagg	
tcaagttcaa	
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tgccaagaca	
aagccgtgcg	
aggagcagta	
cggcagcacg	
taccgttgcg	960
tcagcgtcct	
caccgtcctg	
caccaggact	
ggctgaatgg	
caaggagtac	
aagtgcgaag	1020
tctccaacaa	
agccctccca	
gccccatcg	
agaaaaccat	
ctccaaagcc	
aaagggcagc	1080
cccgagaacc	
acaggtgtac	
accctgcccc	
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ggagatgacc	
aagaaccagg	1140
tcagcctgac	
ctgcctggtc	
aaaggcttct	
atcccagcga	
catcgccgtg	
gagtgaggaga	1200
gcaatgggca	
gccggagaa	
aactacaaga	
ccacgcctcc	
cgtgctgaag	
tccgacggct	1260
ccttcttcct	
ctatagcaag	
ctcaccgtgg	
acaagagcag	
gtggcagcag	

A-1937-WO-PCT_ST25

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
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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 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
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 583

A-1937-WO-PCT_ST25

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ttagtttggg accagcagaa accaggaaag gttcctaaac tgctcattta ctgggcatct	240
acccgggaat ccgggggtccc tagtcgattc agtggcagcg ggtctgggac agatttcact	300
ctcaccatca gcagcctgca gcctgaagat gtggcaactt attactgtca gcaatattat	360
aagactcctc tcactttcgg caaagggacc aaggtggaga tcaaacgaac ggtggctgca	420
ccatctgtct tcactttccc gccatctgat gaggcagttga aatctggtac cgcctctggt	480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac	540
gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc	600
tacagcctca agagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac	660
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga	720
gagtgt	726

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 <212> DNA
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tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gatcaggcag	180
ccccaggga aagagcttga gtggatagga aggacatact acaggtccaa gtggtataat	240
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag	300
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A-1937-WO-PCT_ST25

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 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380
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<210> 585
 <211> 455
 <212> PRT
 <213> Artificial Sequence
 <220>
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 <400> 585

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 20 25 30

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 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
 Page 490

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25
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450 455<210> 586
<211> 1431
<212> DNA
<213> Artificial Sequence<220>
<223> Synthetic polynucleotide

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cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg      180
atcaggcagg cccagggaa agagcttgag tgggtgagca ggacatacta caggtccaag      240
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aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac      360
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tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc      540
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agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag      720
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ctgcccccat cccggaagga gatgaccaag aaccaggcca gcctgacctg cctgggtcaaa     1200
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accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag     1380
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<210> 587
<211> 726
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 587

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ttagtttggt accagcagaa accaggaaag 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 tcattctccc gccatctgat gaggcctgga aatctgggtac cgcctctgtt      480
gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac      540
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<210> 588

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 588

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Ser Val Ala Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Glu Leu Glu
35     40     45
Trp Val Ser Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50     55     60
Val Ser Val Lys Gly Arg Phe Thr Ile Ser Pro Asp Thr Ser Lys Asn
65     70     75     80
Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
85     90     95
Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met

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100

105

110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135 140
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 165 170 175
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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
 Page 494

370

375

380

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 450 455

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

<220>
 <223> Synthetic polynucleotide

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 gtcctacagt cctcaggact ctactccctc gagagcgtgg tgaccgtgcc ctccagcagc 660
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
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 gaggagcagt acggcagcac gtaccgttgc gtcagcgtcc tcaccgtcct gcaccaggac 1020
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A-1937-WO-PCT_ST25

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 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
 cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

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 <212> DNA
 <213> Artificial Sequence

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 <223> Synthetic polynucleotide

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 ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
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<210> 591
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

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 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val
 35 40 45

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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Leu Ser Pro Gly Lys
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 ctgacgctga gcaaagcaga ctacagagaa cacaaagtct acgcctgcga agtcacccat 660
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<210> 594
 <211> 1428
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 594
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 cgctgtcagg tgcagttggt ggagtctggg ggaggcgtgg tccagcctgg gaggtccctg 120
 agactctcct gtgcagcctc tggattcacc ttcagtagct atgacatgca ctgggtccgc 180
 caggctccag gcaagaagct ggagtgggtg gcagttatat catatgatgg aagtattaaa 240
 tactatgcag actccgtgaa gggccgattc accatctcca gagacaattc caagaacacg 300
 ctgtatctgc aagtgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360
 gaggtccgta gtgggagcta ctactattac tacagtatgg acgtctgggg ccaagggacc 420
 acggtcaccg tctctagtgc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 480
 tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 540
 gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600
 gctgtcctac agtcctcagg actctactcc ctcaagagcg tgggtgaccgt gccctccagc 660

A-1937-WO-PCT_ST25

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 840
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atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140
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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

A-1937-WO-PCT_ST25

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 165 170 175
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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

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

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

Ser Leu Ser Pro Gly Lys
450

<210> 596
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 596
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ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaatcac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
aagctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
aaatcttgtg acaaaaactca cacatgccc cctgtcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
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agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
aaagccaaag ggagccccg agaaccacag gtgtacaccc tgccccatc ccggaagaag 1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
ctgaagtccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

A-1937-WO-PCT_ST25

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 gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60
agatgcgagg ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120
agattgtcct gtgctgcatc tggttacgtc ttcacagact atggaatgaa ttgggttaga 180
caggcccccg gaaagggcct ggaatggatg ggttgatta atacttacat tggagagcct 240
atttatgctg acagcgtaaa 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 cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc 960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140
atgaccaaga accaggtcag cctgacctgc ctggtcgatg gcttctatcc cagcgacatc 1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380
cagaagagcc tctccctgtc tccgggtaaa 1410

<210> 598
<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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

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

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

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
Page 505

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
 Page 506

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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 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
 ccctccctca agatcgagt 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
 tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctcg agagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600

A-1937-WO-PCT_ST25

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tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
gtcttcctct 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 acaggtgtac accctgcccc catcccggaa gaagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctgaag	1200
tccgacggct ctttcttcct ctatagcaag ctaccgtgg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly 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 acaggtccaa gtggtataat 240
gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 300
ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 360
gaggatgggg atagctacta ccgctacggg atggacgtct ggggccaagg gaccacgggtc 420
accgtctcta gtgcctccac caagggccca tcgggtcttc ccctggcacc ctctccaag 480
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ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 840
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgag 960
gagcagtacg gcagcacgta ccgttgctgc agcgtcctca ccgtcctgca ccaggactgg 1020
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acgcctcccg tgctgaagtc cgacggctcc ttcttctct atagcaagct caccgtggac 1320
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1380

aaccactaca cgcagaagag cctctccctg tctccgggta aa

1422

<210> 603
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 603

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

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

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<400> 604
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cgactcagct gtgccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 180
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tgggtataatg attatgcagt ttctgtgaaa ggtcgattca ctatcagccc agacacatcc 300
aagaacacgt tctacctgca gatgaactct ctgagagccg aggacacggc tgtgtattac 360
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 420
accacgggtca ccgtctctag tgcctccacc aaggggccat cgggtcttccc cctggcaccc 480
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 540
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc 660
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gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 840
ctcatgatct cccggacccc tgaggtcaca tgcgtgggtg tggacgtgag ccacgaagac 900
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ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260
tacaagacca cgcctcccggt gctgaagtcc gacggctcct tcttcctcta tagcaagctc 1320
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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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agactctcct gtgcagcctc tggattcacc ttcagtagct atggcatgca ctgggtccgc 180
caggctccag gcaaggggct ggagtgggtg gcagtcatat catatgatgg aaataataaa 240
ctctatacag actccgtgaa gggccgattc accatctcca gagacgattc caagagcacg 300
ctgtatctgc aaatgaacag cctgagagct gaggacacgg ctgtgtatta ctgtgcgaga 360
gatccaacag taactctcta ctactactac ggtatggacg tctggggcca agggaccacg 420
gtcaccgtct ctagtgcctc caccaagggc ccatcggctt tccccctggc accctcctcc 480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540

A-1937-WO-PCT_ST25

ccggtgacgg tgtcgtggaa ctgaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600
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 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
 aagaaagttg agcccaaatc 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
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 tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260
 accacgcctc ccgtgctgaa gtccgacggc tccttcttcc tctatagcaa gctcaccgtg 1320
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
 cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaa 1425

<210> 607
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 607

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

A-1937-WO-PCT_ST25

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 225 230 235 240
 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser
 290 295 300
 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

A-1937-WO-PCT_ST25

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 tgcagctggt gcagctctgga gcagaggtga aaaagcccgg ggagtctctg	120
aagatctcct gtaagacttc tgaatacagc tttaccagct actggatcgg ctgggtgcgc	180
cagatgcccg ggaaaggcct ggagtggatg gggatcatct atcttggtga ctcagatacc	240
agatacagcc cgtccttcca aggccaggtc accatctcag ccgacaagtc catcagtacc	300
gcctacctgc agtggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgaga	360
agtaactggg gtcttgacta ctggggccag ggaaccctgg tcaccgtctc tagtgcctcc	420
accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca	480
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tactccctca agagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattct	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 aagccgtgcg aggagcagta cggcagcacg	960
taccgttgcg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1020
aagtgcaagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc	1080
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1140

A-1937-WO-PCT_ST25

aagaaccagg tcagcctgac ctgcctgggc gatggcttct atcccagcga catcgccgtg 1200
gagtgggaga gcaatgggca gccggagaac aactacgaca ccacgcctcc cgtgctggac 1260
tccgacggct ctttcttctt ctatagcgac ctcaccgtgg acaagagcag gtggcagcag 1320
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1380
agcctctccc tgtctccggg taaa 1404

<210> 609
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide
<400> 609

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

A-1937-WO-PCT_ST25

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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ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      540
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ggactctact ccctcaagag cgtggtgacc gtgccctcca gcagcttggg caccagacc      660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      720
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ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      840
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      900
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gagtacaagt gcaaggctct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1080
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg     1260
ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg     1380
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<210> 611

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 611

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A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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agattgtcct gtgctgcatc tggttacacc ttcacagact atggaatgaa ttgggttaga 180
caggccccgg gaaagggcct ggaatggatg ggttggatta atacttacat tggagagcct 240
atttatgctg acagcgtcaa gggcagattc acgatctctc gagacacatc caagtcaaca 300
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ggatacagat cttatgccat ggactactgg ggccagggtta ccctagtcac cgtctctagt 420
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

A-1937-WO-PCT_ST25

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 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
 aaatcttgtg acaaaactca cacatgccc aagtgcccag cacctgaact cctgggggga 780
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840
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 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc 960
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 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140
 atgaccaaga accaggtcag cctgacctgc ctggtcgatg gcttctatcc cagcgacatc 1200
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acgacaccac gcctcccgtg 1260
 ctggactccg acggctcctt cttcctctat agcgacctca ccgtggacaa gagcaggtgg 1320
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380
 cagaagagcc tctccctgtc tccgggtaaa 1410

<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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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 tgggtcaagga ctacttcccc 540
gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600
gctgtcctac agtcctcagg actctactcc ctcaagagcg tggtgaccgt gccctccagc 660
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 720
gacaagaaag ttgagccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 840
atgatctccc ggaccctga ggtcacatgc gtgggtggtg acgtgagcca cgaagaccct 900
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 960
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cccccatccc gggaggagat gaccaagaac caggtcagcc tgacctgcct ggtcgatggc 1200
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1260

A-1937-WO-PCT_ST25

gacaccacgc ctcccggtgct ggactccgac ggctccttct tcctctatag cgacctcacc 1320
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa 1428

<210> 615
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 615

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

A-1937-WO-PCT_ST25

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
 Page 529

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

atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc 60

agatgcgagg ttcagctggt cgagtcagga ggcggtctcg tgcagcctgg cggatcactg 120

agattgtcct gtgctgcac tggttacgtc ttcacagact atggaatgaa ttggggttaga 180

aaggccccgg gaaagggcct ggaatggatg gggttgatta atacttacat tggagagcct 240

A-1937-WO-PCT_ST25

atttatgctg	acgccgtcaa	gggcagattc	acgttctctc	gagacacatc	caagtcaaca	300
gcatactcc	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	gacggtgtcg	540
tggaactcag	gcgccctgac	cagcggcgctg	cacaccttcc	cggctgtcct	acagtcctca	600
ggactctact	ccctcaagag	cgtggtgacc	gtgccctcca	gcagcttggg	caccagacc	660
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	720
aaatcttgtg	acaaaactca	cacatgccca	ccgtgcccag	cacctgaact	cctgggggga	780
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcattgatctc	ccggaccct	840
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgagggtcaa	gttcaactgg	900
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgtgcgagga	gcagtacggc	960
agcacgtacc	gttgcgtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	1020
gagtacaagt	gcaagggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1080
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgccccatc	ccgggaggag	1140
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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> 618

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 618

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acctgcgctg	tccatggtgg	gtccttcagt	ggttactact	ggaactggat	ccgcgagcca	120
ccagggaagg	ggctagagtg	gattggggaa	atcaatcatg	ctggaaacac	caactacaac	180
ccgtcccctca	agatcgagtc	caccatatca	ttagacacgt	ccaagaacca	gttctccctg	240
acgctgacct	ctgtgaccgc	cgcgacacg	gctgtgtatt	actgtgagag	aggatattgt	300
agaagtacca	cctgctactt	tgactactgg	ggccagggaa	ccctagtcac	cgtctctagt	360
gcctccacca	agggcccatc	ggtcttcccc	ctggcaccct	cctccaagag	cacctctggg	420
ggcacagcgg	ccctgggctg	cctgggtcaag	gactacttcc	ccgaaccggt	gacggtgtcg	480
tggaactcag	gcgccctgac	cagcggcgctg	cacaccttcc	cggctgtcct	acagtcctca	540

A-1937-WO-PCT_ST25

ggactctact	ccctcgagag	cgtggtgacc	gtgccctcca	gcagcttggg	cacccagacc	600
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	660
aaatcttgtg	acaaaaactca	cacatgccc	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcatgatctc	ccggaccctt	780
gaggtcacat	gcgtggtggt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	840
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgtgcgagga	gcagtacggc	900
agcacgtacc	gttgcgtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	960
gagtacaagt	gcaagggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1020
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccggaaggag	1080
atgaccaaga	accaggtcag	cctgacctgc	ctggtcaaag	gcttctatcc	cagcgacatc	1140
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	1200
ctgaagtccg	acggctcctt	cttcctctat	agcaagctca	ccgtggacaa	gagcaggtgg	1260
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	1320
cagaagagcc	tctccctgtc	tccgggtaaa				1350

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

<220>
 <223> Synthetic polynucleotide

<400> 619	
atggacatga	gagtgcctgc acagctgctg ggcctgctgc 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
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gcctccacca	aggggccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
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ggactctact	ccctcaagag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660
tacatctgca	acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg	acaaaaactca cacatgccc
ccgtcagtct	tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 840
gaggtcacat	gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900

A-1937-WO-PCT_ST25

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgcgagga gcagtacggc	960
agcacgtacc gttgcgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaag ggcagccccc 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
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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

A-1937-WO-PCT_ST25

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

Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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

<210> 621
 <211> 1428
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 621
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 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 tgggtcaagga ctacttcccc 540
 gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 600
 gctgtcctac agtcctcagg actctactcc ctcaagagcg tgggtgaccgt gccctccagc 660
 agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaagggtg 720
 gacaagaaag ttgagccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 780
 cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 840
 atgatctccc ggaccctga ggtcacatgc gtgggtggtgg acgtgagcca cgaagaccct 900
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 tgcgaggagc agtacggcag cacgtaccgt tgcgtcagcg tcctcaccgt cctgcaccag 1020
 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc 1080
 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1140
 ccccatccc gggaggagat gaccaagaac caggctcagcc 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> 622
 <211> 708
 <212> DNA
 <213> Artificial Sequence

A-1937-WO-PCT_ST25

<220>

<223> Synthetic polynucleotide

<400> 622

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gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag	180
aaaccaggga aagcccctaa gctcctgatc tatgtgtcgt ccagtttgca aagtggggctc	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 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

A-1937-WO-PCT_ST25

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

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agactctcct	gtgcagcctc	tggattcacc	ttcagtagct	atgacatgca	ctgggtccgc		180
aaggctccag	gcaaggggct	ggagtggggtg	gcagttatat	catatgatgc	aagtattaaa		240
tactatgcag	aatccgtgaa	gggccgattc	accatctcca	gagacaattc	caagaacacg		300
ctgtatctgc	aagtgaacag	cctgagagct	gaggacacgg	ctgtgtatta	ctgtgcgaga		360
gaggtccgta	gtgggagcta	ctactattac	tacagtatgg	acgtctgggg	ccaagggacc		420
ttggtcaccg	tctctagtgc	ctccaccaag	ggcccatcgg	tcttccccct	ggcaccctcc		480
tccaagagca	cctctggggg	cacagcggcc	ctgggctgcc	tggtcaagga	ctacttcccc		540
gaaccggtga	cgggtgtcgtg	gaactcaggc	gccctgacca	gcggcgtgca	caccttccccg		600
gctgtcctac	agtcctcagg	actctactcc	ctcaagagcg	tggtgaccgt	gccctccagc		660
agcttgggca	cccagaccta	catctgcaac	gtgaatcaca	agcccagcaa	caccaagggtg		720
gacaagaaa	ttgagcccaa	atcttgtgac	aaaactcaca	catgcccacc	gtgcccagca		780
cctgaactcc	tggggggacc	gtcagtcttc	ctcttcccc	caaaacccaa	ggacaccctc		840
atgatctccc	ggaccctga	ggtcacatgc	gtggtgggtg	acgtgagcca	cgaagaccct		900
gaggtcaagt	tcaactggta	cgtggacggc	gtggagggtgc	ataatgcaa	gacaaagccg		960
tgcgaggagc	agtacggcag	cacgtaccgt	tgcgtcagcg	tcctcaccgt	cctgcaccag		1020
gactgggtga	atggcaagga	gtacaagtgc	aagggtctcca	acaaagccct	cccagcccc		1080
atcgagaaaa	ccatctccaa	agccaaaggg	cagccccgag	aaccacaggt	gtacaccctg		1140
cccccatccc	gggaggagat	gaccaagaac	caggtcagcc	tgacctgcct	ggtcaaaggc		1200

A-1937-WO-PCT_ST25

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac	1260
gacaccacgc ctcccgtgct ggactccgac ggctccttct tcctctatag cgacctcacc	1320
gtggacaaga gcaggtggca gcaggggaac gtctttctcat gctccgtgat gcatgaggct	1380
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	1428

<210> 625
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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gtcaccatca cttgccgggc aagtcaggac atcagaaatg atttaggctg gtatcaggag	180
aaaccaggga aagcccctaa gctcctgatc tatgctgcgt ccagtttgca aagtggggtc	240
ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcacaat cagcagcctg	300
cagcctgaag attttgcaac ttattactgt ctacaacata atagttatcc gctcactttc	360
ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc	420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac	480
ttctatccca gagaggccaa agtacagtgg 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> 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	
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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 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	

A-1937-WO-PCT_ST25

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Val Arg Ser Gly Ser Tyr Tyr Tyr Tyr Tyr Ser Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
450

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

<220>
<223> Synthetic polynucleotide

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc aaagtgtgtg gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 628
<211> 642
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 628

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

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<210> 629

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 629

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ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac      180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg      240
acgctgacct ctgtgaccgc gcgggacacg gctgtgtatt actgtgagag aggatattgt      300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctctagt      360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420
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ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
aaatcttggt acaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga      720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgagagga gcagtacggc      900

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A-1937-WO-PCT_ST25

agcacgtacc gttgcgtag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc 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> 630
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

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

<210> 631
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 631

Leu Gln His Gln Ser Tyr Pro Pro Thr
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<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
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<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

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<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>

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<220>

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<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>

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<222> (5)..(5)

<223> Xaa may be A, C, D, E, F, I, K, L, M, N, P, Q, R, V, W, or Y

<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

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<210> 640

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<221> MISC_FEATURE

<222> (1)..(2)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

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<222> (6)..(6)

<223> Each Xaa is independently M, G, A, V, I, or L

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Each Xaa is independently M, G, A, V, I, or L

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<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
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Xaa

<210> 641

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>
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 <223> Each Xaa is independently M, G, A, V, I, or L

<220>
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 <222> (5)..(5)
 <223> Each Xaa is independently M, G, A, V, I, or L

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 <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>
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<220>
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 <222> (2)..(2)
 <223> Each Xaa is independently M, G, A, V, I, or L

<220>
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 <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
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

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 <223> Each Xaa is independently M, G, A, V, I, or L

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 <222> (5)..(5)
 <223> Each Xaa is independently M, G, A, V, I, or L

<400> 643

Xaa Thr Ser Ser Xaa Gln Ser
1 5

<210> 644
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

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<221> MISC_FEATURE
<222> (2)..(2)
<223> Each Xaa is independently M, G, A, V, I, or L

<220>
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<222> (6)..(6)
<223> Each Xaa is independently M, G, A, V, I, or L

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

<400> 644

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

<210> 645
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<220>
<221> MISC_FEATURE
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<223> Each Xaa is independently M, G, A, V, I, or L

<220>
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<222> (7)..(7)
<223> Each Xaa is independently M, G, A, V, I, or L

<400> 645

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

<210> 646
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<220>
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 <222> (2)..(3)
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<400> 646

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

<210> 647
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<400> 647

Xaa Xaa Ser Ser Xaa Gln Ser
 1 5

<210> 648
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<400> 648

Tyr Xaa Tyr Tyr Ser Xaa Gln Thr Lys Tyr Asn Pro Ser Xaa Lys Ser
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<210> 649

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<400> 649

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<210> 650

<211> 10

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<400> 650

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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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<400> 652

Trp Xaa Ser Thr Arg Glu Ser
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<210> 653
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<400> 653

Gln Gln Tyr Tyr Lys Thr Pro Xaa Thr
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<400> 655

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A-1937-WO-PCT_ST25

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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
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 1 5 10 15

Xaa

<210> 659
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<400> 659

Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Xaa	Xaa	Ser	Xaa
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Lys Ser

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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

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<400> 661

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

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<400> 662

Xaa Xaa Ser Ser Arg Xaa Thr
 1 5

<210> 663
 <211> 8
 <212> PRT
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<400> 663

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 1 5

<210> 664
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<210> 665

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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

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A-1937-WO-PCT_ST25

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 1 5 10 15

<210> 667
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<400> 668

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 1 5 10

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A-1937-WO-PCT_ST25

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Xaa

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<400> 670

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

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<400> 673

Gly Gly Gly Ser Gly Gly Gly Ser
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<210> 674
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<400> 674

Leu Gln His Asn Ser Tyr Pro Leu Thr
 1 5

<210> 675
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Gly Thr Thr Gly Thr Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
 1 5 10

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<400> 676

Glu Asp Gly Asp Xaa Tyr Tyr Arg Tyr Gly Met Asp Val
 1 5 10

<210> 677
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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
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<400> 678

Val Ile Ser Tyr Glu Gly Asn Asn Lys Leu Tyr Thr Glu Ser Val Lys
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Gly

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<400> 679

Xaa	Xaa	Ser	Tyr	Glu	Xaa	Asn	Asn	Lys	Leu	Tyr	Thr	Glu	Ser	Xaa	Lys
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Xaa

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A-1937-WO-PCT_ST25

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Glu Glu Xaa Glu Ser Tyr Tyr Arg Tyr Xaa Xaa Asp Xaa
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<400> 682
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48

<210> 683
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<400> 683
 Arg Ser Ser Gln Ser Leu Leu Tyr Ser Asn Gly Tyr Asn Tyr Leu Asp
 1 5 10 15

<210> 684
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 <212> DNA
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<400> 684
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21

<210> 685
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<400> 685
 Leu Gly Ser Ser Arg Ala Ser
 1 5

<210> 686
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<400> 686
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27

<210> 687
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<400> 687
 Met Gln Pro Leu Gln Thr Pro Leu Thr
 1 5

<210> 688
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<210> 689
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<400> 689
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Ala

<210> 690
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Gly

<210> 692
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<400> 692
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<210> 693
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<400> 693
Gln Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

<210> 694
<211> 51
<212> DNA
<213> Homo sapiens

<400> 694
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<210> 695
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1 5 10

<210> 696
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<400> 696
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<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
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<212> DNA
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<400> 698
ggtaacaaca atcgccctc a 21

<210> 699
 <211> 7
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<400> 699

Gly Asn Asn Asn Arg Pro Ser
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<210> 700
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<400> 701

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val
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<210> 704
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21

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Gly Asn Ser His Arg Pro Ser
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<210> 706

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<211> 11

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<210> 708

<211> 42

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42

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<211> 14

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A-1937-WO-PCT_ST25

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A-1937-WO-PCT_ST25

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A-1937-WO-PCT_ST25

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<400> 844

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<210> 845

<211> 10

<212> PRT

<213> Homo sapiens

<400> 845

Asp Asn Gly Trp His Tyr Ala Phe Asp Ile
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<210> 846

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<400> 846

gcctactata tgcac

15

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<211> 5

<212> PRT

<213> Homo sapiens

<400> 847

Ala Tyr Tyr Met His
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<210> 848

<211> 51

<212> DNA

<213> Homo sapiens

<400> 848

tggatcaacc ctaacagtgg tggcacaaac tatgcacaga agtttcgggg c

51

<210> 849

<211> 17

<212> PRT

<213> Homo sapiens

<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
Page 589

1

5

10

15

Gly

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

<400> 854
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24

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

<400> 855

Glu Val Ala Gly Ala Phe Asp Ile
 1 5

<210> 856
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<400> 856
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15

<210> 857
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<400> 857

Gly Tyr Tyr Met His
 1 5

<210> 858
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<400> 858
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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
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 <212> DNA
 <213> Homo sapiens

<400> 860
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<210> 861
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 <212> PRT
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<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
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<210> 864
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 <212> PRT
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<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

A-1937-WO-PCT_ST25

tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgggggtt tattactgca tgcaacctct acaaactccg 300
ctcacttttcg gcggaggggac 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
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<400> 867

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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 cctca 375

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

A-1937-WO-PCT_ST25

<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 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

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tggtaccagc agaaaccagg acagcctcct agcctgctca tttactgggc atctaccgg	180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc	240
ctcagcagcc tgcaggctga agatgtggca gtttatttct gtcaacaata ttatagtatt	300
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<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

A-1937-WO-PCT_ST25

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

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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

<210> 872
<211> 122
<212> PRT
<213> Homo sapiens

<400> 872
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

A-1937-WO-PCT_ST25

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

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

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

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 873
<211> 342
<212> DNA
<213> Homo sapiens

<400> 873
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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 gaccaagggtg gaaatcaaac ga 342

<210> 874
<211> 113
<212> PRT
<213> Homo sapiens

<400> 874
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

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

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

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

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

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

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

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

<400> 875
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 tcctgtgcag cgtctggatt catcttcagt agttatggca tgcactgggt ccgccagggt 120
 ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa taaagactat 180
 gcagactccg tgaagggccg attcaccgtc tccagagaca attccaggga cacgtttgtat 240
 ctgcaaataa 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
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 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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Homo sapiens

<400> 877
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 cttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcagggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggactc 240
 cagactgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttg 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
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 ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggtggt 300

A-1937-WO-PCT_ST25

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 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

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tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
cttccaggaa cagccccaa actcctcatc tatggtaaca gccatcggcc ctcaagggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300
gtcttcggaa ctgggaccaa ggtcaccgtc ctaggt 336

<210> 882
<211> 111
<212> PRT
<213> Homo sapiens

A-1937-WO-PCT_ST25

<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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tcctgtgcag cctctggatt cacctttagc aactatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctgcagtg ggtctcagtt attagtggta gaggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca actccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagacggg	300
tatagcagtg cctggtactt tgactactgg ggccagggaa ccctggtcac cgtctcctca	360

<210> 884

<211> 120

<212> PRT

<213> Homo sapiens

<400> 884

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

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

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

A-1937-W0-PCT_ST25

Ser Val Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<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 gtcatcggcc ctcagggatc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 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

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 ccaggaagg ggctggagt ggtctcagtc attagtggtc gtggtggtag tacatactat 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaggaa cacgctgtat 240
 ctgcaaata acagcctgag agccgaggac acggccatat attactgtgc gaaagacggg 300
 tatagcagt cctggttctt tgactactgg ggccaggga ccctgatcac cgtctcctca 360

<210> 888
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 888
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 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

A-1937-WO-PCT_ST25

<400> 889
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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
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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
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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 cctggtcacc 360

gtctcctca

<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

gacatccaga tgaccagtc 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

gaagattttg caacttactt ctgtcaacag agttacagta cccctcgcag ttttggccag 300

gggaccaagc tggagatcaa acga 324

<210> 894
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 894

A-1937-WO-PCT_ST25

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

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

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

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

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

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

Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 895
<211> 369
<212> DNA
<213> Homo sapiens

<400> 895
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgagac cctctcactc 60
acctgtgcca tctccgggga cagtgtctct agcaacagtg ctacttgga ctggatcagg 120
cagtcacccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagttgtat 180
aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240
cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggtgtgta ttactgtgca 300
agagaagtag tggctggccc gaggtggttc gaccctggg gccaggggaac 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

A-1937-W0-PCT_ST25

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 aggagtcctt 180
gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
tctgaggatg aggctgatta ttactgtgca acatgggatg acaacctcaa tgggtccgcta 300
ttcggcggag ggaccaagct gaccgtccta ggt 333

<210> 898
<211> 110
<212> PRT
<213> Homo sapiens

<400> 898
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

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

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

Ile Tyr Ser Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

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

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Asn Leu
85 90 95

A-1937-WO-PCT_ST25

Asn Gly Pro Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 899
<211> 354
<212> DNA
<213> Homo sapiens

<400> 899
caggtgcaac tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaggggc 60
tcctgcaagg cttctggata caccttcacc ggcttctata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagt gatgggatgg atcaaccctg acagtgggtg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagttga gtaggctgag atctgacgac acggccgtat attactgtgc gagagagggg 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

A-1937-WO-PCT_ST25

<400> 901
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatggt gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca 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 tacagcagt gggcgagga ctgttgaagc cttcgagac cctgtccctc 60
acctgcgctg tctatggtgg gtccttcagt gggtactact ggagctggat ccgccagccc 120
ccagggaagg ggctggagt gattggggaa atcaatcata gtggaagaac caactacaac 180
ccgtccctca agatcgagt caccatatca gtggacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag ggacagtggc 300
tggcactttt cttttgatat ctgggaccaa gggacaatgg tcaccgtctc ttca 354

A-1937-WO-PCT_ST25

<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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc gggcaagtca gggcattaga aatgacttag gctggtatca ggagaaacca	120
gggaaagccc ctaagcgcct gatctatgct gcatccggtt tacaagggtg 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

A-1937-WO-PCT_ST25

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
caggtgcagc tgggtggagtc cggggcaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggcatgg ggctggagtg ggtggcagtt atatggtttg atggaagtaa tgaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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

A-1937-WO-PCT_ST25

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
gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg 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

A-1937-WO-PCT_ST25

<210> 911
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 911
 gaggtgcacc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttttagc agctatgccca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcaggt attagtgggtg gtggtggttag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgagaac acggccgtat attactgtgc gatagaaatg 300
 gctggggcctt ttgatattctg 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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

A-1937-WO-PCT_ST25

atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagagacca 120
 gggaaagccc ctaacctcct gctctttact gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggtatc tgggacagat ttcactctca 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

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tctatggtgg gtccttcagt ggttactact ggagctggat ccgccagcct 120
 ccaggaagg ggctggagtg gattggggaa atcaatcctg ttggaagaac caactacaaa 180
 ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
 aagctgagtt ctgtgaccgc cgcgacacg gctctgtatt actgtgagag ggacaatggg 300
 tggcactatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> 916
 <211> 118
 <212> PRT

<213> Homo sapiens

<400> 916

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

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

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

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

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

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

Arg Asp Asn Gly Trp His Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser
115

<210> 917

<211> 333

<212> DNA

<213> Homo sapiens

<400> 917

gatgttgta tgactcagtc tccactctcc ctgcccgtca cccttgga gacgccctcc 60
atctcctgca ggtctagtca aagcctcgta tacagtgacg gaaacaccta cttgaattgg 120
tttcagcaga ggccaggccg atctccaagg cgcttaattt ataaggtttc taactgggac 180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgattccac actgataatc 240
agcaggggtgg aggctgagga tgttgggggtt tattactaca tgcaagggtac 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

A-1937-WO-PCT_ST25

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 agtgaaggctc 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcgctc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca 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

A-1937-WO-PCT_ST25

<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 ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agtttcagta ccatcacctt cggccaaggg 300
acacgactgg agattaaacg a 321

<210> 924
<211> 106
<212> PRT
<213> Homo sapiens

<400> 924
Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45
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 tggttgagtc tgggggagggc 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 gcatcccgtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagactttg caacttacta ctgtcaacag agtgacacta ccccgatcac cttcggccaa 300

gggacacgac tggagattaa acga 324

<210> 928
 <211> 107
 <212> PRT
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<400> 928

A-1937-WO-PCT_ST25

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 929
<211> 354
<212> DNA
<213> Homo sapiens

<400> 929
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tcctgcaagg cttctggata caccttcacc ggctactata tgcactggat tcgacaggcc 120
cctgggcaag ggcttgagt gctgggatgg atcatcccta acagtgggtg cacaattat 180
gccagaagt ttcagggcag ggtcaccatg accagggaca 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

A-1937-WO-PCT_ST25

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

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gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc cactatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagttcct gatctatgct gcatccagtt taaaaagtgg ggtcccatca 180
aggttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agtttcagta gcatcacctt cggccaaggg 300
acacgactgg agattaaacg a 321

<210> 932
<211> 106
<212> PRT
<213> Homo sapiens

<400> 932
Asp Ile Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

A-1937-WO-PCT_ST25

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 933
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<212> DNA
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<400> 933
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tcttgtgcag cctctggatt cacctttagc agttatgcca tgagttgggt ccgccaggtt 120
ccaggggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaattg acagcctgag agccgaggac acggccgtat ataactgtgc gatagaagtg 300
gctggggcctt ttgatattctg gggccaaggg acaatggtca 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
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<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
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<220>
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<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
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<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
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<400> 940

Xaa Gln Pro Xaa Gln Thr Pro Xaa Thr
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<210> 941
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<220>
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<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

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<400> 942

Gln Gln Ser Tyr Ser Thr Pro Ile Thr
 1 5

<210> 943
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<400> 943

Lys Val Ser Asn Arg Asp Ser
 1 5

<210> 944
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 <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

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<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
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<210> 946

<211> 9

<212> PRT

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<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

A-1937-WO-PCT_ST25

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

<210> 950
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<400> 950

Ser Tyr Ser Met Asn
1 5

<210> 951
<211> 17
<212> PRT
<213> Homo sapiens
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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
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Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 954
<211> 15
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<400> 954

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

<210> 955
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<400> 955

Thr Tyr Tyr Xaa Ser
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<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
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<400> 957
 cgcgcggtccc agggaatccg gaattacctc gca

33

<210> 958
 <211> 10
 <212> PRT
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<400> 958

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

<210> 959
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21

<210> 960
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 <212> DNA
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<400> 960
 cagagataca accgagcgcc ttacaca 27

<210> 961
 <211> 11
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<400> 961
 Gly Ile Ala Val Ala Gly Asn Trp Phe Asp Pro
 1 5 10

<210> 962
 <211> 42
 <212> DNA
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 Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
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Gly

<210> 964
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 Ser Ile Ala Ala Arg Ala Glu Tyr Phe Gln His
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<210> 965
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<400> 966

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

<210> 967
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Arg Trp Leu Gln Leu Tyr Phe Asp Tyr
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<210> 968
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Val Glu Met Ala Thr Ile Asp Ala Phe Asp Ile
 1 5 10

<210> 969
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Gly Tyr Ser Tyr Gly Tyr Tyr Phe Asp Tyr
 1 5 10

<210> 970
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<400> 970

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

<210> 971
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<400> 971

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 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>

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<222> (12)..(12)

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

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

Xaa

<210> 975
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<220>
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A-1937-WO-PCT_ST25

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<400> 975

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

Xaa

<210> 976
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 <212> PRT
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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
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<220>
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<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
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<400> 978

Gln Gln Tyr Tyr Ser Xaa Pro Trp Thr
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<210> 979
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<400> 979

Thr Tyr Xaa Xaa His
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<210> 980
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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>
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<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
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A-1937-WO-PCT_ST25

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<400> 982

Xaa	Xaa	Trp	Tyr	Asp	Xaa	Ser	Asn	Lys	Asp	Tyr	Xaa	Asp	Ser	Xaa	Lys
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Xaa

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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

<210> 985
 <211> 13
 <212> PRT
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<220>
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<400> 985

Glu Glu Arg Asp Ser Tyr Tyr His Tyr Xaa Xaa Asp Xaa
 1 5 10

<210> 986
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<220>
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 986

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

Xaa

<210> 987

<211> 14

<212> PRT

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<222> (13)..(13)

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

<210> 988

<211> 7

<212> PRT

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<220>

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Gln Ser Tyr Asp Xaa 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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<210> 995
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Gly

<210> 996

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1 5 10 15

Gly

<210> 997

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A-1937-WO-PCT_ST25

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<400> 997

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Xaa

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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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A-1937-WO-PCT_ST25

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 1 5

<210> 1003

<211> 7
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Gly Gln Ser His Arg Pro Ser
 1 5

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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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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
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Xaa

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1 5 10

<210> 1013

<211> 11

<212> PRT

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A-1937-WO-PCT_ST25

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Asn Tyr Xaa Xaa Asn
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 1 5 10

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Glu Gly Tyr Ser Ser Ala Trp Phe Phe Asp Tyr
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A-1937-WO-PCT_ST25

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Ser Gln Ser Ala Thr Trp Asn
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Lys Ser

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

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

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<210> 1032
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<220>
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<400> 1032

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 1 5 10

<210> 1033
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<210> 1034
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1034

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

<210> 1035

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1035

Ala Thr Trp Asp Asp Asn Leu Gln Gly Pro Leu
1 5 10

<210> 1036

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<221> MISC_FEATURE

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

<220>

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<222> (7)..(7)

<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>

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<222> (11)..(11)

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

<400> 1036

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

<210> 1037

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

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<220>

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

<220>

<221> MISC_FEATURE

<222> (4)..(4)

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

<400> 1037

Xaa Phe Tyr Xaa His
1 5

<210> 1038

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (6)..(6)

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

<400> 1038

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

Gly

<210> 1039

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1039

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

Gly

<210> 1040

<211> 17

<212> PRT

<213> Artificial Sequence

<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> (7)..(8)

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

<220>

<221> MISC_FEATURE

<222> (12)..(12)

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

<220>

<221> MISC_FEATURE

<222> (17)..(17)

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

<400> 1040

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

Xaa

<210> 1041

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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<220>

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<222> (2)..(2)

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

<220>

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<222> (6)..(8)

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

<220>

<221> MISC_FEATURE

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

<220>

<221> MISC_FEATURE

<222> (17)..(17)

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

<400> 1041

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

Xaa

<210> 1042

<211> 17

<212> PRT

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<220>

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<220>

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

<220>

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

<220>

<221> MISC_FEATURE

<222> (17)..(17)

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

<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

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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

<400> 1043

Glu Xaa Xaa Xaa Xaa Xaa Xaa Thr Tyr
 1 5

<210> 1044
 <211> 11
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<220>
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<220>
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<220>
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 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>
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 <222> (10)..(10)
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1044

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

<210> 1045
 <211> 5
 <212> PRT
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<220>
 <223> Synthetic polypeptide

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

<400> 1045

Xaa Tyr Tyr Trp Ser
 1 5

<210> 1046
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

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

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

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

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

<400> 1046

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

<210> 1047
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1047

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

<210> 1048
 <211> 16
 <212> PRT
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<220>
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<220>
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 <222> (14)..(14)
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1048

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

<210> 1049

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

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<222> (2)..(2)

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

<400> 1049

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

<210> 1050

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1050

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

<210> 1051

<211> 10

<212> PRT

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<220>

<223> Synthetic polypeptide

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<222> (3)..(3)

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<220>

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<222> (10)..(10)

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

<400> 1051

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

<210> 1052

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

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<220>

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<220>

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<222> (10)..(10)

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

<400> 1052

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

<210> 1053

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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

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<222> (11)..(11)

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

<400> 1053

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

<210> 1054

<211> 7

<212> PRT

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<220>

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A-1937-WO-PCT_ST25

<222> (4)..(5)
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1054

Xaa Xaa Ser Xaa Xaa Gln Xaa
1 5

<210> 1055
<211> 10
<212> PRT
<213> Artificial Sequence

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<223> Synthetic polypeptide

<220>
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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>
<223> Synthetic polypeptide

<400> 1056

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

<210> 1057
<211> 10
<212> PRT
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<220>
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<220>
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1057

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

<210> 1058
 <211> 17
 <212> PRT
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<220>
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<220>
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<400> 1058

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

Gly

<210> 1059
 <211> 17
 <212> PRT
 <213> Artificial Sequence

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

<220>
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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
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1061

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

Gly

<210> 1062

<211> 16

<212> PRT

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<220>

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<220>

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<222> (5)..(5)

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

<220>

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<220>

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<222> (16)..(16)

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

<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

<213> Artificial Sequence

<220>

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

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

<400> 1063

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

<210> 1064
 <211> 11
 <212> PRT
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<220>
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<400> 1064

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

<210> 1065
 <211> 8
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<400> 1065

Gln Gln Ser Tyr Ser Ser Xaa Thr
 1 5

<210> 1066
 <211> 17
 <212> PRT
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<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> 1066

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

Gly

<210> 1067

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1067

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

Gly

<210> 1068

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(2)

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

<220>

<221> MISC_FEATURE

<222> (4)..(7)

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

<220>

<221> MISC_FEATURE

<222> (12)..(12)

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<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> 1068

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

Xaa

<210> 1069

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

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<220>

<221> MISC_FEATURE

<222> (1)..(2)

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

<220>

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<222> (4)..(7)

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<221> MISC_FEATURE

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<220>

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<220>

<221> MISC_FEATURE

<222> (17)..(17)

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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

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<220>

<221> MISC_FEATURE

<222> (4)..(7)

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

<220>

<221> MISC_FEATURE

<222> (12)..(12)

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<220>

<221> MISC_FEATURE

<222> (15)..(15)

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

<220>

<221> MISC_FEATURE

<222> (17)..(17)

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

<400> 1070

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

Xaa

<210> 1071

<211> 8

<212> PRT

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<220>

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<220>

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

<220>

<221> MISC_FEATURE

<222> (8)..(8)

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

<400> 1071

Glu Xaa Xaa Xaa Xaa Phe Asp Xaa
1 5

<210> 1072

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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A-1937-WO-PCT_ST25

<222> (2)..(2)
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<220>
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1072

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

<210> 1073
<211> 7
<212> PRT
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<220>
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<220>
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

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

<400> 1073

Thr	Xaa	Ser	Ser	Xaa	Gln	Ser
1				5		

<210> 1074
<211> 16
<212> PRT
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<220>
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<220>
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<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>
<221> MISC_FEATURE
<222> (5)..(6)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1074

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

<210> 1075

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<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> (10)..(10)

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

<400> 1075

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

<210> 1076

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1076

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

<210> 1077

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<220>

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<222> (3)..(3)

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<220>

<221> MISC_FEATURE

<222> (7)..(7)

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

<400> 1077

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

<210> 1078
 <211> 16
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<220>
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<220>
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<220>
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 <222> (15)..(15)
 <223> Each Xaa is independently selected from M, G, A, V, I and L.

<400> 1078

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

<210> 1079
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1079

Arg Ser Ser Gln Ser Leu Val Tyr Ser Asp Gly Gln Thr Tyr Leu Asn
 1 5 10 15

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<400> 1080

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1 5 10 15

<210> 1081

<211> 7

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<400> 1081

Lys Val Ser Asn Trp Asp Xaa
1 5

<210> 1082

<211> 7

<212> PRT

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<220>

<223> Synthetic polypeptide

<400> 1082

Lys Val Ser Asn Trp Glu Ser
1 5

<210> 1083

<211> 7

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<400> 1083

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<400> 1084

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<210> 1085
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<400> 1085

Lys Xaa Ser Asn Trp Glu Ser
1 5

<210> 1086
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<400> 1086

Xaa Gln Xaa Thr His Trp Pro
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<210> 1087

<211> 5

<212> PRT

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<400> 1087

Xaa Tyr Tyr Xaa His
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<210> 1088

<211> 17

<212> PRT

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

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

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<222> (17)..(17)

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

<400> 1088

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1

5

10

15

Xaa

<210> 1089
 <211> 17
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 <400> 1089

Trp Ile Asn Pro Gln Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Arg
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Gly

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Xaa

<210> 1091
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<210> 1092
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<400> 1092

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 1 5

<210> 1093
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<400> 1093

Gln Gln Ser Asp Ser Thr Pro Xaa Thr
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<210> 1094
 <211> 8

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<400> 1094

Gln Gln Ser Phe Ser Thr Xaa Thr
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<210> 1095
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Gly

<210> 1096
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A-1937-WO-PCT_ST25

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<400> 1096

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Xaa

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<400> 1097

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1				5					10					15	

Xaa

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<210> 1099
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<400> 1099

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<210> 1100
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<400> 1100

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<400> 1101

Gln Gln Ser Asp Xaa Thr Pro Xaa Thr
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<210> 1102
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Trp Xaa Xaa Pro Asn Xaa Xaa Xaa Thr Asn Tyr Xaa Gln Lys Phe Gln
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Xaa

<210> 1103
 <211> 17
 <212> PRT
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<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
 <211> 17
 <212> PRT
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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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A-1937-WO-PCT_ST25

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<400> 1105

Xaa Ser Ser Trp Glu Xaa Phe Asp Tyr
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 1 5

<210> 1108
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<400> 1108

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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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

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1 5 10 15

Xaa

<210> 1113

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

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1 5 10 15

<210> 1114

<211> 17

<212> PRT

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<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
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 gggaaagccc ctaagcgctt gatctatgct gcatccggtt tacaaggtgg ggacccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
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 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

A-1937-WO-PCT_ST25

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

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195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

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A-1937-WO-PCT_ST25

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<210> 1118
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<400> 1118

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

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<212> PRT

<213> Homo sapiens

<400> 1120

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Ile Leu Tyr Ser
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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
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A-1937-WO-PCT_ST25

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
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<212> DNA
<213> Homo sapiens

<400> 1121
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A-1937-WO-PCT_ST25

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<210> 1122
<211> 448
<212> PRT
<213> Homo sapiens

<400> 1122

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

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

A-1937-WO-PCT_ST25

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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A-1937-WO-PCT_ST25

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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
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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 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

A-1937-WO-PCT_ST25

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

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<210> 1126
<211> 446

<212> PRT
 <213> Homo sapiens

<400> 1126

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 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

A-1937-WO-PCT_ST25

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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A-1937-WO-PCT_ST25

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<210> 1128
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<212> PRT
<213> Homo sapiens

<400> 1128

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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

A-1937-WO-PCT_ST25

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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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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atcacttgcc gggcaagtca gagcattagt tactatttaa attggtatca acagaaacca 120
gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggtttagtg 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 gaaggtgat aacgccctcc aatcgggtaa ctcccaggag 480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

A-1937-WO-PCT_ST25

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
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

A-1937-WO-PCT_ST25

<210> 1133
 <211> 1329
 <212> DNA
 <213> Homo sapiens

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 ccagggaagg ggctggagtg ggtctcaggt attagtgggt gtgggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
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 gctggggctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc 360
 aagggcccat cggctctccc cctggcgccc tgctctagaa gcacctccga gagcacagcg 420
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 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260
 tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1320
 ccgggtaaa 1329

<210> 1134
 <211> 443
 <212> PRT
 <213> Homo sapiens

<400> 1134
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

A-1937-WO-PCT_ST25

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

Ser Gly Ile Ser Gly 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

A-1937-WO-PCT_ST25

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 tgaccagtc 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 actgtggctg caccatctgt cttcatcttc 360
ccgccatctg atgagcagtt gaaatctgga actgctagcg ttgtgtgcct gctgaataac 420
ttctatcca gagaggcaa agtacagtgg aagggtgata acgccctcca atcgggtaac 480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540
ctgacgctga gcaaagcaga ctacagaaa cacaaagtct acgcctgcga agtcacccat 600
cagggcctga gtcgcccgt cacaaagagc ttcaacaggg gagagtgt 648

<210> 1136
<211> 216

A-1937-WO-PCT_ST25

<212> PRT
<213> Homo sapiens

<400> 1136

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

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

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

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

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

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

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

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc

60

A-1937-WO-PCT_ST25

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acctgcgctg tctatggtgg gtccttcagt ggggtactact ggagctggat ccgccagcct      120
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ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg      240
aagctgagtt ctgtgaccgc cgcggacacg gctctgtatt actgtgagag ggacaatggg      300
tggcactatg cttttgatat ctggggccaa gggacaatgg tcaccgtctc ttcagcctcc      360
accaagggcc catcgggtctt ccccctggcg ccctgctcta gaagcacctc cgagagcaca      420
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tctccgggta aa                                                                1332

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagctc caacatcggg gcaggttata atgttcactg gtaccagcag 120
cttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcagggggtc 180
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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

A-1937-WO-PCT_ST25

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

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ccagggaagg ggctggagt ggtctcagtt attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagac cagcgtgtat 240

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A-1937-WO-PCT_ST25

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<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

A-1937-WO-PCT_ST25

Ala Lys Gly Gly Thr Asn 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

A-1937-WO-PCT_ST25

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
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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

A-1937-WO-PCT_ST25

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 tggttgagtc 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
gctggggctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc 360
aagggcccat cggctcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg 420

A-1937-WO-PCT_ST25

gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
 ggcgctctga ccagcggcgt gcacaccttc ccagctgtcc tacagtcctc aggactctac 540
 tccctcagca gcgtgggtgac cgtgccctcc agcaacttcg gcacccagac ctacacatgc 600
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 gacgtgagcc acgaagacct cgaggtccag ttcaactggg acgtggacgg cgtggagggtg 840
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 gtcctcaccg ttgtgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 960
 aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg gcagccccga 1020
 gaaccacagg tgtacaccct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 1080
 ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat 1140
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 ttctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260
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 ccgggtaaa 1329

<210> 1146
 <211> 443
 <212> PRT
 <213> Homo sapiens

<400> 1146

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcgttacc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatact gcatccagtt tgcaaagtgg gatcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttactt ctgtcaacag agttacagta cccctcgcag ttttggccag 300
gggaccaagc tggagatcaa acgaactgtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgct agcgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1148
<211> 214
<212> PRT
<213> Homo sapiens

<400> 1148
Asp Ile Gln Met Thr Gln Ser 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60

acctgtgcca tctccgggga cagtgtctct agcaacagtg ctacttggaa ctggatcagg 120

cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagttgtat 180

aatgattatg cagtatctgt gaaaagtcga ataaccatca acccagacac atccaagaac 240

cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300

agagaagtag tggctggccc gaggtggttc gaccctggg gccaggggaac cctggtcacc 360

gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctctagaagc 420

acctccgaga gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 480

acgggtgtcgt ggaactcagg cgctctgacc agcggcgtgc acaccttccc agctgtccta 540

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag caacttcggc 600

acccagacct acacatgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca 660

A-1937-WO-PCT_ST25

gttgagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggcaggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccttgag 780
gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtccagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccac gggaggagca gttcaacagc 900
acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag 960
tacaagtgca aggtctccaa caaaggcctc ccagccccca tcgagaaaac catctccaaa 1020
accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaa 1347

<210> 1150
<211> 449
<212> PRT
<213> Homo sapiens

<400> 1150

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

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

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

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

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

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

Tyr Tyr Cys Ala Arg Glu Val Val Ala Gly Pro Arg Trp Phe Asp Pro
100 105 110

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

Lys

<210> 1151
<211> 648
<212> DNA
<213> Homo sapiens

<400> 1151
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agttatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgtt gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta atcctcagga gtgcagtttt 300
ggccagggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc 360
ccgccatctg atgagcagtt gaaatctgga actgctagcg ttgtgtgcct gctgaataac 420
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt 648

<210> 1152
<211> 216
<212> PRT
<213> Homo sapiens

<400> 1152
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

A-1937-WO-PCT_ST25

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 actgtgagag ggacagtggc 300
tggcactttt cttttgatat ctgggaccaa gggacaatgg tcaccgtctc ttcagcctcc 360
accaagggcc catcgggtctt ccccctggcg ccctgctcta gaagcacctc cgagagcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggg gaccgtgccc tccagcaact tcggcaccca gacctacaca 600
tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agacagttga gcgcaaatgt 660
tgtgtcgagt gccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc 720
ccccaaaac ccaaggacac cctcatgatc tcccggaacc ctgaggtcac gtgcgtgggtg 780

A-1937-WO-PCT_ST25

gtggacgtga gccacgaaga ccccgaggtc cagttcaact ggtacgtgga cggcgtggag	840
gtgcataatg ccaagacaaa gccacgggag gagcagttca acagcacgtt ccgtgtgggtc	900
agcgtcctca ccgttgtgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc	960
tccaacaaag gcctcccagc ccccatcgag aaaaccatct ccaaaaccaa agggcagccc	1020
cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc	1080
agcctgacct gcctgggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc	1140
aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc	1200
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc	1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg	1320
tctccgggta aa	1332

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

<400> 1154

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

A-1937-WO-PCT_ST25

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

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

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

A-1937-WO-PCT_ST25

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 ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttat 300
gtcttcggaa ctgggaccaa ggtcaccgtc ctaggtcagc ccaaggctgc cccctcggctc 360
actctgttcc cgccctctag cgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggctc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<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

A-1937-WO-PCT_ST25

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
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A-1937-WO-PCT_ST25

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<210> 1158
<211> 446
<212> PRT
<213> Homo sapiens

<400> 1158

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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

A-1937-WO-PCT_ST25

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
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 1159
<211> 651
<212> DNA

<213> Homo sapiens

<400> 1159

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<210> 1160

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1160

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

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

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

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

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

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130       135       140

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A-1937-WO-PCT_ST25

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

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala 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
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A-1937-WO-PCT_ST25

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<210> 1162
<211> 449
<212> PRT
<213> Homo sapiens

<400> 1162

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20 25 30

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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 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

A-1937-WO-PCT_ST25

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
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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
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Page 731

A-1937-WO-PCT_ST25

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 <211> 214
 <212> PRT
 <213> Homo sapiens
 <400> 1164

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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

A-1937-WO-PCT_ST25

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

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

<400> 1166

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 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
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 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
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 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
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 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

A-1937-WO-PCT_ST25

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

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<211> 648
<212> DNA
<213> Homo sapiens

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A-1937-WO-PCT_ST25

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<212> PRT
<213> Homo sapiens

<400> 1168

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Ala Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Phe Leu
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Ile Tyr Ser Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
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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

A-1937-WO-PCT_ST25

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

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tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1320
tctccgggta aa 1332

<210> 1170
<211> 444

A-1937-WO-PCT_ST25

<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

A-1937-WO-PCT_ST25

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

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

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

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

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

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

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

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

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

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

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

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

<210> 1171

<211> 660

<212> DNA

<213> Homo sapiens

<400> 1171

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tggtagcagc agaaaccagg acagcctcct agcctgctca ttactgggc 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 cgttgtgtgc 420

A-1937-WO-PCT_ST25

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 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1172
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 1172

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

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

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

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

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

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

Tyr Tyr Ser Ile Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

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

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

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

A-1937-WO-PCT_ST25

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 atttggtatg atggaagtaa taaagactat 180
gcagactccg tgaagggccg attcacgctc tccagagaca attccaggga cacgttgtat 240
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agggattcct actaccacta cggtatggac gtctggggcc aagggaaccac ggtcaccgtc 360
tcttcagcct ccaccaaggg cccatcggtc tttcccctgg cgccctgctc tagaagcacc 420
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cagacctaca catgcaacgt agatcacaag cccagcaaca ccaagggtgga caagacagtt 660
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agcctctccc tgtctccggg taaa 1344

<210> 1174
<211> 448
<212> PRT
<213> Homo sapiens

<400> 1174

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

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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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 gggaaagccc ctaagttcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
 aggttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agtttcagta gcatcacctt cggccaaggg 300
 acacgactgg agattaaacg aactgtggct gcaccatctg tcttcatctt cccgccatct 360
 gatgagcagt tgaaatctgg aactgctagc gttgtgtgcc tgctgaataa cttctatccc 420
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 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg 600
 agctcgccccg tcacaaagag cttcaacagg ggagagtgt 639

A-1937-WO-PCT_ST25

<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

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ccaggaagg ggctggagtg ggtctcaggt attagtggta gaggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgttat      240
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gctggggctt ttgatatctg gggccaaggg acaatgggtca ccgtctcttc agcctccacc      360
aagggcccat cggctcttccc cctggcgccc tgctctagaa gcacctccga gagcacagcg      420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca      480
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tccctcagca gcgtgggtgac cgtgccctcc agcaacttcg gcacccagac ctacacatgc      600
aacgtagatc acaagcccag caacaccaag gtggacaaga cagttgagcg caaatgttgt      660
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tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct     1320
ccgggtaaa                                     1329

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<210> 1178

<211> 443

<212> PRT

<213> Homo sapiens

<400> 1178

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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

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A-1937-WO-PCT_ST25

Ser Gly Ile Ser Gly Arg Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Ile Glu Val Ala Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

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

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

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

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

A-1937-WO-PCT_ST25

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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aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<210> 1180
<211> 214
<212> PRT
<213> Homo sapiens

<400> 1180

A-1937-WO-PCT_ST25

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

Asp Arg Val Thr Ile Thr Cys 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

<210> 1181

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 1181

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tcctgcaagg cttctggata caccttcacc ggctactata tgcactggat tcgacaggcc 120

cctgggcaag ggcttgagtg gctgggatgg atcatcccta acagtgggtg cacaaattat 180

A-1937-WO-PCT_ST25

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agctgggagg gatttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc      360
accaagggcc catcgggtctt cccctggcg ccctgtctta gaagcacctc cgagagcaca      420
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tctccgggta aa                                                                1332

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<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

A-1937-WO-PCT_ST25

Met Glu Leu Ser Arg₈₅ Leu Arg Ser Asp₉₀ Asp Thr Ala Val Tyr Tyr₉₅ Cys

Ala Thr Gly Ser₁₀₀ Ser Trp Glu Gly Phe₁₀₅ Asp Tyr Trp Gly Gln₁₁₀ Gly Thr

Leu Val Thr₁₁₅ Val Ser Ser Ala Ser₁₂₀ Thr Lys Gly Pro Ser₁₂₅ Val Phe Pro

Leu Ala Pro Cys Ser Arg Ser₁₃₅ Thr Ser Glu Ser Thr₁₄₀ Ala Ala Leu Gly

Cys₁₄₅ Leu Val Lys Asp Tyr₁₅₀ Phe Pro Glu Pro Val₁₅₅ Thr Val Ser Trp Asn₁₆₀

Ser Gly Ala Leu Thr₁₆₅ Ser Gly Val His Thr₁₇₀ Phe Pro Ala Val Leu₁₇₅ Gln

Ser Ser Gly Leu₁₈₀ Tyr Ser Leu Ser Ser₁₈₅ Val Val Thr Val Pro₁₉₀ Ser Ser

Asn Phe Gly₁₉₅ Thr Gln Thr Tyr Thr₂₀₀ Cys Asn Val Asp His₂₀₅ Lys Pro Ser

Asn Thr₂₁₀ Lys Val Asp Lys Thr₂₁₅ Val Glu Arg Lys Cys₂₂₀ Cys Val Glu Cys

Pro₂₂₅ Pro Cys Pro Ala Pro₂₃₀ Pro Val Ala Gly Pro₂₃₅ Ser Val Phe Leu Phe₂₄₀

Pro Pro Lys Pro Lys₂₄₅ Asp Thr Leu Met Ile₂₅₀ Ser Arg Thr Pro Glu₂₅₅ Val

Thr Cys Val Val₂₆₀ Val Asp Val Ser His₂₆₅ Glu Asp Pro Glu Val₂₇₀ Gln Phe

Asn Trp Tyr₂₇₅ Val Asp Gly Val Glu₂₈₀ Val His Asn Ala Lys₂₈₅ Thr Lys Pro

Arg Glu₂₉₀ Glu Gln Phe Asn Ser₂₉₅ Thr Phe Arg Val Val₃₀₀ Ser Val Leu Thr

Val₃₀₅ Val His Gln Asp Trp₃₁₀ Leu Asn Gly Lys Glu₃₁₅ Tyr Lys Cys Lys Val₃₂₀

Ser Asn Lys Gly Leu₃₂₅ Pro Ala Pro Ile Glu₃₃₀ Lys Thr Ile Ser Lys₃₃₅ Thr

Lys Gly Gln Pro₃₄₀ Arg Glu Pro Gln Val₃₄₅ Tyr Thr Leu Pro Pro₃₅₀ Ser Arg

A-1937-WO-PCT_ST25

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
gatgttgtaga tgactcagtc tccactctcc ctgcccgtca cccttgagaca gccggcctcc 60
atctcctgca ggtctagtaga aagcctcgta tacagttagc gaaacaccta cttgaattgg 120
tttcagcaga ggccaggccg atctccaagg cgcttaattt ataagggttc taactgggac 180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgattccac actgataatc 240
agcagggttg aggctgagga tggtaggggtt tattactaca tgcaaggtag acactggcct 300
ctcggcggag ggaccaaggt ggagatcaaa cgaactgtgg ctgcaccatc tgtcttcatc 360
ttcccgccat ctgatgagca gttgaaatct ggaactgcta gcgttgtagt cctgctgaat 420
aacttctatc ccagagaggc caaagtacag tggaaggtag 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

A-1937-WO-PCT_ST25

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 gatgggttg atcaacccta acagtgggtg cacaaactat 180
gcacagaagt ttcggggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gactggcggc 300
agctgggagg gttttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360
accaagggcc catcgggtctt ccccctggcg ccctgtctta gaagcacctc cgagagcaca 420

A-1937-WO-PCT_ST25

gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480
tcaggcgctc tgaccagcgg cgtgcacacc ttcccagctg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggt gaccgtgccc tccagcaact tcggcaccca gacctacaca 600
tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agacagttga gcgcaaattgt 660
tgtgtcgagt gcccaccgtg cccagcacca cctgtggcag gaccgtcagt cttcctcttc 720
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 780
gtggacgtga gccacgaaga ccccagagtc 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 gcctggtcaa aggccttctac cccagcgaca tcgccgtgga gtgggagagc 1140
aatgggcagc cggagaacaa ctacaagacc acacctcca tgctggactc cgacggctcc 1200
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1260
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1320
tctccgggta aa 1332

<210> 1186
<211> 444
<212> PRT
<213> Homo sapiens

<400> 1186

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

Ser Val Lys Val Ser Cys Gln Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Thr Gly Gly Ser Trp Glu Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcgctc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagttcct gatctatgct gcatccaggt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagtag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agtgacagta 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
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1188
<211> 214
<212> PRT
<213> Homo sapiens

<400> 1188
Asp Ile Gln Met Thr Gln Ser 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 1189
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 1189
cagtcctatg acagcagcct gagtggttcg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 acactttgct 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>		
<223>	Synthetic polynucleotide	
<400>	1203	
	caccatggaa tttgggctga gctgg	25
<210>	1204	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	Synthetic polynucleotide	
<400>	1204	
	caccatggag ttggggctgt gctg	24

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

 <220>
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 <400> 1205
 caccatggag tttgggctta gctgg 25

<210> 1206
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1206
 caccatggag ttttggctga gctgg 25

<210> 1207
 <211> 28
 <212> DNA
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 <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>
 <223> Synthetic polynucleotide

 <400> 1209
 caccatgaaa catctgtggt tcttccttct c 31

<210> 1210
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 1210
caccatgggg tcaaccgcca tcc 23

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

<220>
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<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
 <213> Artificial Sequence
 <220>
 <223> Synthetic polynucleotide
 <400> 1217
 caccatgagg ctccttgctc agcttc 26

<210> 1218
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic polynucleotide
 <400> 1218
 caccatggaa accccagcgc agc 23

<210> 1219
 <211> 22
 <212> DNA
 <213> Artificial Sequence
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 <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
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 <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
 caccatggtg tccccgttgc aattc 25

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

 <220>
 <223> Synthetic polynucleotide

 <400> 1226
 acccgattgg agggcggttat ccacc 25

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

 <220>
 <223> Synthetic polynucleotide

<400> 1227
caccatggcc tggccccctc tc 22

<210> 1228
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1228
caccatggcc tggctctcctc tcc 23

<210> 1229
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1229
caccatggcc agcttcctc tcc 23

<210> 1230
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1230
caccatggcc ggcttcctc tc 22

<210> 1231
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1231
caccatgacc tgctcccctc 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 tggaccctc 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	
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<210> 1239
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 1239
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<210> 1240
 <211> 23
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 <220>
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 <400> 1240
 caccatggcc tggatccctc tac 23

<210> 1241
 <211> 25
 <212> DNA
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 <220>
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 <400> 1241
 caccatggcc tgggtctcct tctac 25

<210> 1242
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 <220>
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<210> 1243
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 <400> 1243
 caccatggct tggacccac tcc 23

<210> 1244
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<400> 1244
caccatggcc tggactcctc tcc 23

<210> 1245
<211> 26
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<220>
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<400> 1245
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<210> 1246
<211> 26
<212> DNA
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<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
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<220>
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<400> 1249
caccatggcc tggatgatgc ttctcc 26

<210> 1250
<211> 22
<212> DNA
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<220>
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 <400> 1250
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<210> 1251
 <211> 22
 <212> DNA
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 <220>
 <223> Synthetic polynucleotide
 <400> 1251
 caccatgccc tgggctctgc tc 22

<210> 1252
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
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<220>
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 <400> 1252
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<210> 1253
 <211> 642
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic polynucleotide
 <400> 1253
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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 gcgtacggtg gctgcacat 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> 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
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 ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
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 gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac 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

A-1937-WO-PCT_ST25

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

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 agctgtgcgg catcggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
 cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcdc caaagtctcc 300
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
 agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag 600
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 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tgggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac 900

A-1937-WO-PCT_ST25

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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
tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggattcg ccagccacca      1500
gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaaccg      1560
tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg      1620
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tccaccaagg gcccatcggg cttccccctg gcaccctcct ccaagagcac ctctgggggc      1800
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      1860
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      1920
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac      1980
atctgcaacg tgaatcacia gccagcaac accaaggtgg acaagaaagt tgagcccaaa      2040
tcttgt                                           2046

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
610 615 620

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
625 630 635 640

Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
645 650 655

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
660 665 670

Val Asp Lys Lys Val Glu Pro Lys Ser Cys
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<210> 1259

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1259

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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 gcgtacggtg gctgcacat ctgtcttcat cttcccgcca	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> 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

A-1937-WO-PCT_ST25

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

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300

A-1937-WO-PCT_ST25

gggaccaagc tggaaatcaa acgaacggtg gctgcacccat ctgtcttcat cttccccgcca 360
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cccagagagg ccaaagtaca gtggaaggtg 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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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1262

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

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

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

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

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

Thr Phe Gly 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

A-1937-WO-PCT_ST25

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

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cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
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tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
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acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 1440

A-1937-WO-PCT_ST25

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tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag	1620
ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc	1680
tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc agcctccacc	1740
aagggcccat cggtcttccc 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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 gtggaaggtg 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggtcct aaactgctca ttactgggc atctaccggg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcatct tccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480
caatcgggta actcccagga gagtgtcaca gacgaggaca 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

A-1937-WO-PCT_ST25

<400> 1269

gaggtacaac 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
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa 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
atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag	1380
gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc	1440
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag	1500
ccccaggga aaggccttga gtggatagga aggacatact 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 ctcttccaag	1800
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg	1860
gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc	1920
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg	1980
ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag	2040

aaagttgagc ccaaattcttg t

<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gagtggttcg 300

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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 tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccaggaacc ctgggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

A-1937-WO-PCT_ST25

ctcaaaagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tgggggggacc	gtcagtcttc	720
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtggtggtgg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
gtggaggtgc	ataatgccaa	gacaaagccg	tgtgaggagc	agtacggcag	cacgtaccgt	900
tgtgtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	960
aaggtctcca	acaaagccct	cccagccccc	atcgagaaaa	ccatctccaa	agccaaaggg	1020
cagccccgag	aaccacaggt	gtacaccctg	cccccatccc	gggaggagat	gaccaagaac	1080
caggtcagcc	tgacctgcct	ggtcaaaggc	ttctatccca	gcgacatcgc	cgtggagtgg	1140
gagagcaatg	ggcagccgga	gaacaactac	aagaccacgc	ctcccgtgct	ggactccgac	1200
ggctccttct	tcctctatag	caagctcacc	gtggacaaga	gcaggtggca	gcaggggaac	1260
gtcttctcat	gctccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1320
tcctgtctc	cgggtggtgg	cggatcggga	ggtggcggat	cccaggtgca	gttacagcag	1380
tcgggcgag	gactgttgaa	gccttcggag	accctgtccc	tcacctgcgc	tgtccatggt	1440
gggtccttca	gtggttacta	ctggaactgg	attcgccagc	caccagggaa	ggggctagag	1500
tggattgggg	aaatcaatca	tgctggaaac	accaactaca	accgctccct	caagagtcga	1560
gtcaccatat	cattagacac	gtccaagaac	cagttctccc	tgacgctgac	ctctgtgacc	1620
gccgcggaca	cggctgtgta	ttactgtgcg	agaggatatt	gtagaagtac	cacctgctac	1680
tttgactact	ggggccaggg	aaccctagtc	accgtctcct	cagcctccac	caagggccca	1740
tcggtcttcc	ccctggcacc	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcctggtca	aggactactt	ccccgaaccg	gtgacggtgt	cgtggaactc	aggcgccctg	1860
accagcggcg	tgcacacctt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtggtga	ccgtgccctc	cagcagcttg	ggcaccacga	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		

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagccccaa 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 tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcacaca 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

A-1937-WO-PCT_ST25

<400> 1279
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 gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1280
<211> 214
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic polypeptide
<400> 1280

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
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

A-1937-WO-PCT_ST25

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc 720
cttttcccc 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
aaggtctcca acaaagccct ccagcccc atcgagaaaa ccatctcaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

A-1937-WO-PCT_ST25

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac 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 attcggcagc cccaggttaa gggactggag 1500
 tggattggct atatctatta cagtgggcag accaaatata acccctccct caagagtcga 1560
 gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc 1620
 gctgcggaca cggccgtgta ttactgtgcg agagaaactg ggagctacta cggctttgac 1680
 tactggggcc aggaaccct 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 ccaaggtgga caagaaagt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
660 665 670

Lys Ser Cys
675

<210> 1283
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1283
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcacctg 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

A-1937-WO-PCT_ST25

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

gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgcctc 480

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt

660

<210> 1286
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1286

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

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

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

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

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

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

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

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

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

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
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
 agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
 ctgcagtga gacgcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
 tggggctctg actactgggg ccagggaaacc 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 cccagacctt catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag 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
 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa 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 cgggtggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag 1380
 tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
 gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc 1500
 cttgagtga taggaaggac atactacagg tccaagtggg ataagtatta tgcagtttct 1560
 ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg 1620
 agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc 1680
 tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctctcagcc 1740

A-1937-WO-PCT_ST25

tccaccaagg gcccatcggt 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 gccagcaac 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

A-1937-WO-PCT_ST25

Gly Leu Tyr Ser₁₈₀ Leu Lys Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu

Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr

Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr

Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀

Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro

Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val

Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr

Lys Pro₂₉₀ Cys Glu Glu Gln Tyr₂₉₅ Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val

Leu Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀

Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser

Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro

Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val

Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly

Gln Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀

Gly Ser Phe Phe Leu₄₀₅ Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg₄₁₅ Trp

Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His

Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<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

A-1937-WO-PCT_ST25

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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 ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat 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

A-1937-WO-PCT_ST25

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

caggtgcagt 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

A-1937-WO-PCT_ST25

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	cagcggcggtg	cacaccttcc	cggctgtcct	acagtcctca	540
ggactctact	ccctcaaaag	cgtgggtgacc	gtgccctcca	gcagcttggg	caccagacc	600
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	660
aaatcttgtg	acaaaactca	cacatgccca	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcattgatctc	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
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	aatcaggtgg	aggtttgggtg	cagccgggga	gatcgctcag	gcttagctgt	1440
gcggcatcgg	ggtttacttt	cgatgattat	gcgatgcatt	gggtccggca	agcgcctgga	1500
aaagggctcg	agtgggtttc	cgccattacg	tggaatagcg	gacacatcga	ttatgcagac	1560
agtgtggagg	gcagattcac	aatctcacga	gacaatgcta	agaacagcct	gtaccttcag	1620
atgaactcac	ttcgcgcgga	agataccgcc	gtatactact	gcgccaaagt	ctcctacttg	1680
tctacagctt	cgtcgctcga	ctattggggg	caaggaacgt	tggtcaccgt	ctctagtgcc	1740
tccaccaagg	gcccacggtt	cttccccctg	gcacctctct	ccaagagcac	ctctgggggc	1800
acagcggccc	tgggctgcct	ggtcaaggac	tacttccccg	aaccggtgac	ggtgtcgtgg	1860
aactcaggcg	ccctgaccag	cggcgtgcac	accttcccgg	ctgtcctaca	gtcctcagga	1920
ctctactccc	tcgagagcgt	ggtgaccgtg	ccctccagca	gcttgggcac	ccagacctac	1980
atctgcaacg	tgaatcacia	gcccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

<210> 1294
 <211> 682
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1294

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

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

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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

Thr Leu Pro Pro Ser Arg 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

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctccaggggtc 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 cgcggccaaag 540
agctatctga gcctgacgcc tgagcagtg 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

A-1937-WO-PCT_ST25

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

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

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

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1299
<211> 2031
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1299
caggtgcagt 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 gcgggacacg gctgtgtatt actgtgagag 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 cggtgtcct acagtcctca 540
ggactctact ccctcaaaag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
aaatcttgatg acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga 720
ccgtcagctt tcctcttccc ccaaaaacc aaggacacc tcgatgctc ccggaccct 780

A-1937-WO-PCT_ST25

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg 1320
 cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggtg 1380
 cagctggtgc agtctggagc agaggtgaaa aagccccggg agtctctgaa gatctcctgt 1440
 aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgccccgg 1500
 aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg 1560
 tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag 1620
 tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggg 1680
 cttgactact ggggccaggg aaccctggtc accgtctcta gtgcctccac caagggccca 1740
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 1800
 tgcttggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 1860
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag 1920
 agcgtggtga ccgtgccctc cagcagcttg ggcaccacga cctacatctg caacgtgaat 1980
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr
 Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu
 Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp
 Glu₃₈₅ Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀
 Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp
 Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His
 Glu Ala Leu₄₃₅ His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro
 Gly Gly₄₅₀ Gly Gly Ser Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln
 Ser₄₆₅ Gly Ala Glu Val Lys₄₇₀ Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀
 Lys Thr Ser Glu Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg
 Gln Met Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly
 Asp Ser Asp₅₁₅ Thr Arg Tyr Ser Pro₅₂₀ Ser Phe Gln Gly Gln₅₂₅ Val Thr Ile
 Ser Ala Asp Lys Ser Ile Ser₅₃₅ Thr Ala Tyr Leu Gln₅₄₀ Trp Ser Ser Leu
 Lys Ala Ser Asp Thr Ala₅₅₀ Met Tyr Tyr Cys Ala₅₅₅ Arg Ser Asn Trp Gly₅₆₀
 Leu Asp Tyr Trp Gly₅₆₅ Gln Gly Thr Leu Val₅₇₀ Thr Val Ser Ser Ala₅₇₅ Ser
 Thr Lys Gly Pro₅₈₀ Ser Val Phe Pro Leu₅₈₅ Ala Pro Ser Ser Lys₅₉₀ Ser Thr
 Ser Gly Gly₅₉₅ Thr Ala Ala Leu Gly₆₀₀ Cys Leu Val Lys Asp₆₀₅ Tyr Phe Pro

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg 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 accatcgctcgt ctttcagcgt ctggtggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240

A-1937-WO-PCT_ST25

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgctttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Ser Thr Leu Thr₁₈₀ Leu Ser Lys Ala Asp₁₈₅ Tyr Glu Lys His Lys₁₉₀ Val Tyr

Ala Cys Glu₁₉₅ Val Thr His Gln₂₀₀ Gly Leu Ser Ser Pro Val₂₀₅ Thr Lys Ser

Phe Asn Arg Gly Glu Cys₂₁₀

<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 caaatataac 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 ttcccgaac cgggtgacggt gtcgtggaac 480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc 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
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgaggga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtacaactg 1380

A-1937-WO-PCT_ST25

gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca 1440
tcgggggttta ctttcgatga ttatgcatg cattgggtcc ggcaagcgcc tggaaaaggg 1500
ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg 1560
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac 1620
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680
gcttcgtcgc tcgactattg ggggtcaagga acgttggtca ccgtctctag tgcctccacc 1740
aagggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 1800
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1860
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 1980
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1306
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1306

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

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

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

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

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

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
580 585 590

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
595 600 605

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 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 gttcggccaa 300
 gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggtagcgcc tctgtttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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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 cgcggccaaag 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
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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> 1311

<211> 2025

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1311

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ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaataacaac	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
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcggcc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga 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
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc	1020
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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
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gggaacgtct tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacgcagaag	1320
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caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc	1620
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tactggggcc aggaaccct ggtcaccgtc tctagtgcct 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 ccaaggtgga caagaaagtt gagcccaaat 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Pro Gly Lys Gly₅₀₀ Leu Glu Trp Met Gly₅₀₅ Ile Ile Tyr Leu Gly₅₁₀ Asp Ser

Asp Thr Arg₅₁₅ Tyr Ser Pro Ser Phe₅₂₀ Gln Gly Gln Val Thr₅₂₅ Ile Ser Ala

Asp Lys₅₃₀ Ser Ile Ser Thr Ala₅₃₅ Tyr Leu Gln Trp Ser₅₄₀ Ser Leu Lys Ala

Ser₅₄₅ Asp Thr Ala Met Tyr₅₅₀ Tyr Cys Ala Arg Ser₅₅₅ Asn Trp Gly Leu Asp₅₆₀

Tyr Trp Gly Gln Gly₅₆₅ Thr Leu Val Thr Val₅₇₀ Ser Ser Ala Ser Thr₅₇₅ Lys

Gly Pro Ser Val₅₈₀ Phe Pro Leu Ala Pro₅₈₅ Ser Ser Lys Ser Thr₅₉₀ Ser Gly

Gly Thr Ala₅₉₅ Ala Leu Gly Cys Leu₆₀₀ Val Lys Asp Tyr Phe₆₀₅ Pro Glu Pro

Val Thr₆₁₀ Val Ser Trp Asn Ser₆₁₅ Gly Ala Leu Thr Ser₆₂₀ Gly Val His Thr

Phe₆₂₅ Pro Ala Val Leu Gln₆₃₀ Ser Ser Gly Leu Tyr₆₃₅ Ser Leu Glu Ser Val₆₄₀

Val Thr Val Pro₆₄₅ Ser Ser Ser Leu Gly Thr₆₅₀ Gln Thr Tyr Ile Cys₆₅₅ Asn

Val Asn His Lys₆₆₀ Pro Ser Asn Thr Lys₆₆₅ Val Asp Lys Lys Val₆₇₀ Glu Pro

Lys Ser Cys₆₇₅

<210> 1313

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1313

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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

A-1937-WO-PCT_ST25

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttggtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc 480
caatcgggta actcccagga gagtgtcaca gaggcaggaca gcaaggacag cacctacagc 540
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga 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

A-1937-WO-PCT_ST25

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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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 gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120
cagcccccag 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 ccatcggctt tccccctggc accctcctcc 420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540

A-1937-WO-PCT_ST25

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aagaaagtgt agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct      720
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aaccaagga caccctcatg      780
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag      840
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gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac      960
tggctgaatg gcaaggagta caagtgcagg gtctccaaca aagccctccc agccccatc     1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc     1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc     1140
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accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg     1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg     1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt     1380
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cggcaagcgc ctggaaaagg gctcgagtgg gtttccgcca ttacgtggaa tagcggacac     1560
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agcctgtacc ttcagatgaa ctacttcgc gcggaagata ccgccgtata ctactgcgcc     1680
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accgtctcta gtgcctccac caagggccca tcggtcttcc ccctggcacc ctctccaag     1800
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt cccgaaccg     1860
gtgacggtgt cgtggaactc aggcgcctg accagcggcg tgcacacctt cccggtgtc     1920
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg     1980
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag     2040
aaagttgagc ccaaattctg t                                     2061

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Val Ser Tyr Leu₅₆₅ Ser Thr Ala Ser₅₇₀ Ser Leu Asp Tyr Trp Gly₅₇₅ Gln

Gly Thr Leu Val₅₈₀ Thr Val Ser Ser Ala₅₈₅ Ser Thr Lys Gly Pro₅₉₀ Ser Val

Phe Pro Leu₅₉₅ Ala Pro Ser Ser Lys₆₀₀ Ser Thr Ser Gly Gly₆₀₅ Thr Ala Ala

Leu Gly₆₁₀ Cys Leu Val Lys Asp₆₁₅ Tyr Phe Pro Glu Pro₆₂₀ Val Thr Val Ser

Trp Asn Ser Gly Ala Leu₆₃₀ Thr Ser Gly Val His₆₃₅ Thr Phe Pro Ala Val₆₄₀

Leu Gln Ser Ser Gly₆₄₅ Leu Tyr Ser Leu Glu₆₅₀ Ser Val Val Thr Val₆₅₅ Pro

Ser Ser Ser Leu₆₆₀ Gly Thr Gln Thr Tyr₆₆₅ Ile Cys Asn Val Asn₆₇₀ His Lys

Pro Ser Asn₆₇₅ Thr Lys Val Asp Lys₆₈₀ Lys Val Glu Pro Lys₆₈₅ Ser Cys

<210> 1319

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1319

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tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgga	180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc	240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact	300
cctctcactt tcggcggagg gaccaagggt 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> 1320

<211> 220

<212> PRT

<213> Artificial Sequence

A-1937-WO-PCT_ST25

<220>

<223> Synthetic polypeptide

<400> 1320

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 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 caaggaataa gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc      360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaaag      540
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccagggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a              651

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<210> 1322

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1322

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

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A-1937-WO-PCT_ST25

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 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 cttccccggt	540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagtgt agcccaaatc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc tccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080

A-1937-WO-PCT_ST25

ccatccccggg 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
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cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat 1560
accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt 1620
accgcctacc tgagtgagg cagcctgaag gcctcggaca ccgccatgta ttactgtgcg 1680
agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtgcc 1740
tccaccaagg gcccatcggc 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
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tcttgt 2046

<210> 1324
<211> 682
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic polypeptide
<400> 1324

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc 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> 1326
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1326

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

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

A-1937-WO-PCT_ST25

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 catcggggtt 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 ttcccgccat ctgatgagca gttgaaatct 420

ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480

A-1937-WO-PCT_ST25

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agcaaggaca	gcacctacag	cctcaagagc	accctgacgc	tgagcaaagc	agactacgag	600
aaacacaaaag	tctacgcctg	cgaagtcacc	catcagggcc	tgagctcgcc	cgtcacaaaag	660
agcttcaaca	ggggagagtg	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	720
ctcctggggg	gaccgtcagt	cttcctcttc	cccccaaac	ccaaggacac	cctcatgata	780
tcccggaccc	ctgaggtcac	atgcgtgggt	gtggacgtga	gccacgaaga	ccctgaggtc	840
aagttcaact	ggtacgtgga	cggcgtggag	gtgcataatg	ccaagacaaa	gccgtgtgag	900
gagcagtacg	gcagcacgta	ccgttgtgtc	agcgtcctca	ccgtcctgca	ccaggactgg	960
ctgaatggca	aggagtacaa	gtgcaagggt	tccaacaaaag	ccctcccagc	ccccatcgag	1020
aaaaccatct	caaagccaa	agggcagccc	cgagaaccac	aggtgtacac	cctgccccca	1080
tcccgggagg	agatgaccaa	gaaccagggt	agcctgacct	gcctgggtcaa	aggcttctat	1140
cccagcgaca	tcgccgtgga	gtgggagagc	aatgggcagc	cggagaacaa	ctacaagacc	1200
acgcctcccg	tgctggactc	cgacggctcc	ttcttctctt	atagcaagct	caccgtggac	1260
aagagcaggt	ggcagcaggg	gaacgtcttc	tcatgtctcc	tgatgcatga	ggctctgcac	1320
aaccactaca	cgcagaagag	cctctccctg	tctccgggtg	gtggcggatc	gggaggtggc	1380
ggatcccagg	tgagttaca	gcagtcgggc	gcaggactgt	tgaagccttc	ggagaccctg	1440
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cagccaccag	ggaaggggct	agagtggatt	ggggaaatca	atcatgctgg	aaacaccaac	1560
tacaacccgt	ccctcaagag	tcgagtcacc	atatcattag	acacgtccaa	gaaccagttc	1620
tccctgacgc	tgacctctgt	gaccgccg	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	ccttcccggc	tgctctacag	1920
tcctcaggac	tctactccct	cgagagcgtg	gtgaccgtgc	cctccagcag	cttgggcacc	1980
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gagcccaa	atctgt					2055

<210> 1328

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1328

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 cccctggca 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
aagggtggaca 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

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat 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> 1332

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1332

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

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

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

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

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

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

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

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A-1937-WO-PCT_ST25

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

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
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agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
agtacggtgg ctgcaccatc tgtcttcac tccccccat 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 ggggagagt tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 780
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900
gagcagtacg gcagcacgta ccgttggtgc agcgtcctca ccgtcctgca ccaggactgg 960
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1020

A-1937-WO-PCT_ST25

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 acgcctcccg tgctggactc cgacgggtcc ttcttctctt atagcaagct caccgtggac 1260
 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320
 aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
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 tccctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg 1500
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 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

A-1937-WO-PCT_ST25

Leu Gln Met Asn Ser₈₅ Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys
 Ala Lys Val Ser₁₀₀ Tyr Leu Ser Thr Ala₁₀₅ Ser Ser Leu Asp Tyr₁₁₀ Trp Gly
 Gln Gly Thr₁₁₅ Leu Val Thr Val Ser₁₂₀ Ser Thr Val Ala Ala₁₂₅ Pro Ser Val
 Phe Ile₁₃₀ Phe Pro Pro Ser Asp₁₃₅ Glu Gln Leu Lys Ser₁₄₀ Gly Thr Ala Ser
 Val₁₄₅ Val Cys Leu Leu Asn₁₅₀ Asn Phe Tyr Pro Arg₁₅₅ Glu Ala Lys Val Gln₁₆₀
 Trp Lys Val Asp Asn₁₆₅ Ala Leu Gln Ser Gly₁₇₀ Asn Ser Gln Glu Ser₁₇₅ Val
 Thr Glu Gln Asp₁₈₀ Ser Lys Asp Ser Thr₁₈₅ Tyr Ser Leu Lys Ser₁₉₀ Thr Leu
 Thr Leu Ser₁₉₅ Lys Ala Asp Tyr Glu₂₀₀ Lys His Lys Val Tyr₂₀₅ Ala Cys Glu
 Val Thr₂₁₀ His Gln Gly Leu Ser₂₁₅ Ser Pro Val Thr Lys₂₂₀ Ser Phe Asn Arg
 Gly₂₂₅ Glu Cys Asp Lys Thr₂₃₀ His Thr Cys Pro Pro₂₃₅ Cys Pro Ala Pro Glu₂₄₀
 Leu Leu Gly Gly Pro₂₄₅ Ser Val Phe Leu Phe₂₅₀ Pro Pro Lys Pro Lys₂₅₅ Asp
 Thr Leu Met Ile₂₆₀ Ser Arg Thr Pro Glu₂₆₅ Val Thr Cys Val Val₂₇₀ Val Asp
 Val Ser His₂₇₅ Glu Asp Pro Glu Val₂₈₀ Lys Phe Asn Trp Tyr₂₈₅ Val Asp Gly
 Val Glu₂₉₀ Val His Asn Ala Lys₂₉₅ Thr Lys Pro Cys Glu₃₀₀ Glu Gln Tyr Gly
 Ser Thr Tyr Arg Cys Val₃₁₀ Ser Val Leu Thr Val₃₁₅ Leu His Gln Asp Trp₃₂₀
 Leu Asn Gly Lys Glu₃₂₅ Tyr Lys Cys Lys Val₃₃₀ Ser Asn Lys Ala Leu₃₃₅ Pro
 Ala Pro Ile Glu₃₄₀ Lys Thr Ile Ser Lys₃₄₅ Ala Lys Gly Gln Pro₃₅₀ Arg Glu

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

Gln Leu Gln 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

A-1937-WO-PCT_ST25

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
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ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctgaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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
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atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcactt tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

A-1937-WO-PCT_ST25

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480
 caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc 540
 ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

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

<220>
 <223> Synthetic polypeptide

<400> 1338

Asp Ile Gln Met 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

A-1937-WO-PCT_ST25

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
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 cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
 agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct 420
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480
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 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900
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 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaaag ccctcccagc ccccatcgag 1020
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 aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
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 tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 1500
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A-1937-WO-PCT_ST25

tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc	1620
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tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg	1740
accacggtca ccgtctcctc agcctccacc aagggcccat cggctcttccc cctggcaccc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc	1980
agcagcttgg gcaccagac 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

A-1937-WO-PCT_ST25

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

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

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

Val Thr 210 His Gln Gly Leu Ser 215 Ser Pro Val Thr Lys 220 Ser Phe Asn Arg

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

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

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

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

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

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

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

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

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

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

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

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

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

A-1937-WO-PCT_ST25

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 Ser 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 ggaatccgg aattacctcg catggtatca gcaaaaaccc 120
 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg 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 gcccaaactc 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

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1344
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1344

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

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

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

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

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

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 ccggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcgggtgggt gcgccagatg	120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tgggggtcttg actactgggg ccagggaaacc 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 ggaagtcca 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
taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg tctccaacaa agccctcca 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 ctaccctggg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggtcttgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatcca ggtgcagtta	1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc	1440
catggtgggt ctttcagtgg ttactactgg aactggattc gccagccacc aggggaagggg	1500
ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaaccg gtccctcaag	1560
agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct	1620
gtgaccgccg cggacacggc tgtgtattac tgtgagagag gatattgtag aagtaccacc	1680
tgctactttg actactgggg ccagggaaacc ctagtaccg tctcctcagc ctccaccaag	1740
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	1800
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc	1860
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	1920
ctcgagagcg tgggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac	1980

gtgaatcaca agcccagcaa caccaaggtg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Pro Gly Lys Gly₅₀₀ Leu Glu Trp Ile Gly₅₀₅ Glu Ile Asn His Ala₅₁₀ Gly Asn

Thr Asn Tyr₅₁₅ Asn Pro Ser Leu Lys₅₂₀ Ser Arg Val Thr Ile₅₂₅ Ser Leu Asp

Thr Ser₅₃₀ Lys Asn Gln Phe Ser₅₃₅ Leu Thr Leu Thr Ser₅₄₀ Val Thr Ala Ala

Asp₅₄₅ Thr Ala Val Tyr Tyr₅₅₀ Cys Ala Arg Gly Tyr₅₅₅ Cys Arg Ser Thr Thr₅₆₀

Cys Tyr Phe Asp Tyr₅₆₅ Trp Gly Gln Gly Thr₅₇₀ Leu Val Thr Val Ser₅₇₅ Ser

Ala Ser Thr Lys₅₈₀ Gly Pro Ser Val Phe₅₈₅ Pro Leu Ala Pro Ser₅₉₀ Ser Lys

Ser Thr Ser₅₉₅ Gly Gly Thr Ala Ala₆₀₀ Leu Gly Cys Leu Val₆₀₅ Lys Asp Tyr

Phe Pro₆₁₀ Glu Pro Val Thr Val₆₁₅ Ser Trp Asn Ser Gly₆₂₀ Ala Leu Thr Ser

Gly Val His Thr Phe Pro₆₃₀ Ala Val Leu Gln Ser₆₃₅ Ser Gly Leu Tyr Ser₆₄₀

Leu Glu Ser Val Val₆₄₅ Thr Val Pro Ser Ser₆₅₀ Ser Leu Gly Thr Gln Thr₆₅₅

Tyr Ile Cys Asn₆₆₀ Val Asn His Lys Pro₆₆₅ Ser Asn Thr Lys Val₆₇₀ Asp Lys

Lys Val Glu₆₇₅ Pro Lys Ser Cys

<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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

A-1937-WO-PCT_ST25

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 caagaaagtt gagcccaaat 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

A-1937-WO-PCT_ST25

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

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

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 1349

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1349

gacatccaga 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 gttcggccaa	300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcga	360
tctgatgagc agttgaaatc tgggtaccgcc tctgtttgtg gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
tggggtcttg actactgggg ccaggaacc 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

A-1937-WO-PCT_ST25

tacgcgcca	agagctacct	gagcctgacg	cccagacagt	ggaagtcca	cagaagctac	600
agctgccagg	tcacgcatga	agggagcacc	gtggagaaga	cagtggcccc	tacagaatgt	660
tcagacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	aactcctggg	gggaccgtca	720
gtcttcctct	ttccccaaa	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	agccctcca	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	ccttcttctt	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	tgggtggcga	tcgggaggtg	gcggatcca	ggtgcagctg	1380
caggagtcgg	gcccaggact	ggtgaagcct	tcggagacct	tgtccctcac	ctgcactgtc	1440
tctggtggct	ccatcagtag	ttacttctgg	agctggattc	ggcagcccc	aggtaagga	1500
ctggagtggg	ttggctatat	ctattacagt	gggcagacca	aatacaacct	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	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcctgggtca	aggactactt	ccccgaaccg	gtgacgggtg	cgtggaactc	aggcgccctg	1860
accagcggcg	tgacacactt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtggtga	ccgtgccctc	cagcagcttg	ggcaccacga	cctacatctg	caacgtgaat	1980
cacaagccca	gcaacaccaa	ggtggacaag	aaagttgagc	ccaaatcttg	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		

A-1937-WO-PCT_ST25

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

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

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

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

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

Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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tttccaggaa cagccccaa actcctcatc caaggtaaca gcaatcggcc ctccagggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
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ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
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gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat 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

A-1937-WO-PCT_ST25

<400> 1355
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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 gaggcaggaca 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

A-1937-WO-PCT_ST25

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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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtca gcccaaggcc 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
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctcaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

A-1937-WO-PCT_ST25

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
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 gggaaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
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 aaaggccttg agtggatagg aaggacatac tacagggtcca agtgggtataa tgattatgca 1560
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 aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg 1680
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 tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 1800
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 1860
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1920
 tcaggactct actccctcga gagcgtggtg accgtgccct ccagcagctt gggcacccag 1980
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 2040
 cccaaatctt gt 2052

<210> 1358
 <211> 684
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1358

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

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

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

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

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

A-1937-WO-PCT_ST25

Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val
 Thr Val Ser₁₁₅ Ser Gln Pro Lys Ala₁₂₀ Asn Pro Thr Val Thr₁₂₅ Leu Phe Pro
 Pro Ser₁₃₀ Ser Glu Glu Leu Gln₁₃₅ Ala Asn Lys Ala Thr₁₄₀ Leu Val Cys Leu
 Ile Ser Asp Phe Tyr Pro₁₅₀ Gly Ala Val Thr Val₁₅₅ Ala Trp Lys Ala Asp₁₆₀
 Gly Ser Pro Val Lys₁₆₅ Ala Gly Val Glu Thr₁₇₀ Thr Lys Pro Ser Lys₁₇₅ Gln
 Ser Asn Asn Lys₁₈₀ Tyr Ala Ala Lys Ser₁₈₅ Tyr Leu Ser Leu Thr₁₉₀ Pro Glu
 Gln Trp Lys₁₉₅ Ser His Arg Ser Tyr₂₀₀ Ser Cys Gln Val Thr₂₀₅ His Glu Gly
 Ser Thr Val Glu Lys Thr Val₂₁₅ Ala Pro Thr Glu Cys₂₂₀ Ser Asp Lys Thr
 His Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀
 Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser Val Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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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tttccaggaa cagccccaa 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 cgaaagcgtg	540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag	600
cccagcaaca ccaaggtgga caagaaagt 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

A-1937-WO-PCT_ST25

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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ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg	180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc	240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa	300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca	360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg	540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<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

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<400> 1363
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ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac      180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg      240
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agaagtacca cctgctactt tgactactgg ggccaggga cctagtcac cgtctcctca      360
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga      420
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aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc      540
aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa      600
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc      660
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ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc      780
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aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa     1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc      1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc      1140
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cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag      1260
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cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa      1500
gcgcctggaa aagggctcga gtggggttcc gccattacgt ggaatagcgg acacatcgat      1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg      1620
taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc      1680

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A-1937-WO-PCT_ST25

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tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1860
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tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc	1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	2040
gagcccaaatt 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

A-1937-WO-PCT_ST25

Glu Gln Asp Ser₁₈₀ Lys Asp Ser Thr Tyr₁₈₅ Ser Leu Lys Ser Thr₁₉₀ Leu Thr
 Leu Ser Lys₁₉₅ Ala Asp Tyr Glu Lys₂₀₀ His Lys Val Tyr Ala₂₀₅ Cys Glu Val
 Thr His₂₁₀ Gln Gly Leu Ser Ser₂₁₅ Pro Val Thr Lys Ser₂₂₀ Phe Asn Arg Gly
 Glu₂₂₅ Cys Asp Lys Thr His₂₃₀ Thr Cys Pro Pro Cys₂₃₅ Pro Ala Pro Glu Leu₂₄₀
 Leu Gly Gly Pro Ser₂₄₅ Val Phe Leu Phe Pro₂₅₀ Pro Lys Pro Lys Asp₂₅₅ Thr
 Leu Met Ile Ser₂₆₀ Arg Thr Pro Glu Val₂₆₅ Thr Cys Val Val Val₂₇₀ Asp Val
 Ser His₂₇₅ Glu Asp Pro Glu Val Lys₂₈₀ Phe Asn Trp Tyr Val₂₈₅ Asp Gly Val
 Glu Val₂₉₀ His Asn Ala Lys Thr₂₉₅ Lys Pro Cys Glu Glu₃₀₀ Gln Tyr Gly Ser
 Thr₃₀₅ Tyr Arg Cys Val Ser₃₁₀ Val Leu Thr Val Leu₃₁₅ His Gln Asp Trp Leu₃₂₀
 Asn Gly Lys Glu Tyr₃₂₅ Lys Cys Lys Val Ser₃₃₀ Asn Lys Ala Leu Pro₃₃₅ Ala
 Pro Ile Glu Lys₃₄₀ Thr Ile Ser Lys Ala₃₄₅ Lys Gly Gln Pro Arg₃₅₀ Glu Pro
 Gln Val Tyr₃₅₅ Thr Leu Pro Pro Ser₃₆₀ Arg Glu Glu Met Thr₃₆₅ Lys Asn Gln
 Val Ser₃₇₀ Leu Thr Cys Leu Val₃₇₅ Lys Gly Phe Tyr Pro₃₈₀ Ser Asp Ile Ala
 Val₃₈₅ Glu Trp Glu Ser Asn₃₉₀ Gly Gln Pro Glu Asn₃₉₅ Asn Tyr Lys Thr Thr₄₀₀
 Pro Pro Val Leu Asp₄₀₅ Ser Asp Gly Ser Phe₄₁₀ Phe Leu Tyr Ser Lys₄₁₅ Leu
 Thr Val Asp Lys₄₂₀ Ser Arg Trp Gln Gln₄₂₅ Gly Asn Val Phe Ser₄₃₀ Cys Ser
 Val Met His₄₃₅ Glu Ala Leu His Asn₄₄₀ His Tyr Thr Gln Lys₄₄₅ Ser Leu Ser

A-1937-WO-PCT_ST25

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

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ctctcctgca gggccagtca gagtgtaga agcagttact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc 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 tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

```

<210> 1366

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1366

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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 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

```


A-1937-WO-PCT_ST25

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
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctccaggggtc 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 cgcggccaaag 540
agctatctga gcctgacgcc tgagcagtg 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

A-1937-WO-PCT_ST25

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

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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120

ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180

A-1937-WO-PCT_ST25

ccgtccctca	agagtcgagt	caccatatca	ttagacacgt	ccaagaacca	gttctccctg	240
acgctgacct	ctgtgaccgc	cgcggaacgc	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
cacaaagtct	acgcctgcga	agtcacccat	cagggcctga	gctcgcccgt	cacaaagagc	660
ttcaacaggg	gagagtgtga	caaaactcac	acatgcccac	cgtgcccagc	acctgaactc	720
ctggggggac	cgtcagtctt	cctcttcccc	ccaaaaccca	aggacaccct	catgatctcc	780
cggacccttg	aggtcacatg	cgtgggtggtg	gacgtgagcc	acgaagaccc	tgaggtcaag	840
ttcaactggg	acgtggacgg	cgtggaggtg	cataatgcca	agacaaagcc	gtgtgaggag	900
cagtacggca	gcacgtaccg	ttgtgtcagc	gtcctcaccg	tcctgcacca	ggactggctg	960
aatggcaagg	agtacaagtg	caaggtctcc	aacaaagccc	tcccagcccc	catcgagaaa	1020
accatctcca	aagccaaagg	gcagccccga	gaaccacagg	tgtacaccct	gccccatcc	1080
cgggaggaga	tgaccaagaa	ccaggtcagc	ctgacctgcc	tgggtcaaagg	cttctatccc	1140
agcgacatcg	ccgtggagtg	ggagagcaat	gggcagccgg	agaacaacta	caagaccacg	1200
cctcccgtgc	tggactccga	cggctccttc	ttcctctata	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	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	gggccaggga	accctggtca	ccgtctctag	tgctccacc	1740
aagggcccat	cggctctccc	cctggcacc	tcctccaaga	gcacctctgg	gggcacagcg	1800
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaactca	1860
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	1920
tccctcgaga	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	1980
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaattctgt	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
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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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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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

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> 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
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgctttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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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 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

A-1937-WO-PCT_ST25

cctgaggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tgggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag 900
 ggcagcacgt accgtttgtg 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 cggggtttac tttcgatgat tatgcgatgc attgggtccg gcaagcgcct 1500
 ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca 1560
 gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt 1620
 cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcttac 1680
 ttgtctacag cttcgtcgtc cgactattgg ggtcaaggaa cgttgggtcac 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Glu₄₆₀ Val Gln Leu Val
 Glu₄₆₅ Ser Gly Gly Gly Leu₄₇₀ Val Gln Pro Gly Arg₄₇₅ Ser Leu Arg Leu Ser₄₈₀
 Cys Ala Ala Ser Gly₄₈₅ Phe Thr Phe Asp Asp₄₉₀ Tyr Ala Met His Trp₄₉₅ Val
 Arg Gln Ala Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Val Ser Ala Ile₅₁₀ Thr Trp
 Asn Ser Gly₅₁₅ His Ile Asp Tyr Ala₅₂₀ Asp Ser Val Glu Gly₅₂₅ Arg Phe Thr
 Ile Ser₅₃₀ Arg Asp Asn Ala Lys₅₃₅ Asn Ser Leu Tyr Leu₅₄₀ Gln Met Asn Ser
 Leu Arg Ala Glu Asp Thr₅₅₀ Ala Val Tyr Tyr Cys₅₅₅ Ala Lys Val Ser Tyr₅₆₀
 Leu Ser Thr Ala Ser₅₆₅ Ser Leu Asp Tyr Trp₅₇₀ Gly Gln Gly Thr Leu₅₇₅ Val
 Thr Val Ser Ser₅₈₀ Ala Ser Thr Lys Gly₅₈₅ Pro Ser Val Phe Pro₅₉₀ Leu Ala

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcg cggtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

A-1937-WO-PCT_ST25

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

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

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

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

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

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

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

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

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 cgcggccaaag 540
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1380

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1380

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

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

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

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

A-1937-WO-PCT_ST25

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
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 agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgctgtgt 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
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac 1320

A-1937-WO-PCT_ST25

acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag 1380
 gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccc gggagtctct gaagatctcc 1440
 tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg ccagatgccc 1500
 gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc 1560
 ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg 1620
 cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgcgag aagtaactgg 1680
 ggtcttgact actggggcca ggaaccctg gtcaccgtct ctagtgccct 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> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaactt 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

A-1937-WO-PCT_ST25

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
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1386
<211> 214

A-1937-WO-PCT_ST25

<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

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cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat	180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac	240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca	300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag	480
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gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	660
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
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gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac	1680
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acgttggtca ccgtctctag tgcctccacc aagggcccat cggctctccc cctggcacc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc	1860
cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920

A-1937-WO-PCT_ST25

ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtggtgac cgtgccctcc 1980
 agcagcttgg gcaccagac 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
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Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
 20 25 30

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

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

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

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

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

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

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 145 150 155 160

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 165 170 175

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 180 185 190

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Gly Arg Ser Leu Arg₄₈₅ Leu Ser Cys Ala Ala₄₉₀ Ser Gly Phe Thr Phe₄₉₅ Asp

Asp Tyr Ala Met₅₀₀ His Trp Val Arg Gln₅₀₅ Ala Pro Gly Lys Gly₅₁₀ Leu Glu

Trp Val Ser₅₁₅ Ala Ile Thr Trp Asn₅₂₀ Ser Gly His Ile Asp₅₂₅ Tyr Ala Asp

Ser Val₅₃₀ Glu Gly Arg Phe Thr₅₃₅ Ile Ser Arg Asp Asn₅₄₀ Ala Lys Asn Ser

Leu Tyr Leu Gln Met₅₅₀ Ser Leu Arg Ala Glu₅₅₅ Asp Thr Ala Val Tyr₅₆₀

Tyr Cys Ala Lys Val₅₆₅ Ser Tyr Leu Ser Thr₅₇₀ Ala Ser Ser Leu Asp₅₇₅ Tyr

Trp Gly Gln Gly₅₈₀ Thr Leu Val Thr Val₅₈₅ Ser Ser Ala Ser Thr₅₉₀ Lys Gly

Pro Ser Val₅₉₅ Phe Pro Leu Ala Pro₆₀₀ Ser Ser Lys Ser Thr₆₀₅ Ser Gly Gly

Thr Ala₆₁₀ Ala Leu Gly Cys Leu₆₁₅ Val Lys Asp Tyr Phe₆₂₀ Pro Glu Pro Val

Thr Val₆₂₅ Ser Trp Asn Ser₆₃₀ Gly Ala Leu Thr Ser₆₃₅ Gly Val His Thr Phe₆₄₀

Pro Ala Val₆₄₅ Leu Gln Ser Ser Gly Leu Tyr₆₅₀ Ser Leu Glu Ser Val₆₅₅ Val

Thr Val₆₆₀ Pro Ser Ser Ser Leu Gly Thr₆₆₅ Gln Thr Tyr Ile Cys₆₇₀ Asn Val

Asn His Lys₆₇₅ Pro Ser Asn Thr Lys₆₈₀ Val Asp Lys Lys Val₆₈₅ Glu Pro Lys

Ser Cys₆₉₀

<210> 1389
<211> 651
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic polynucleotide

<400> 1389
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc
Page 922

A-1937-WO-PCT_ST25

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagc 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 ctccccaag agcacctctg ggggcacagc ggccctgggc 420
 tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
 agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

<210> 1390
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1390

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

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

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

A-1937-WO-PCT_ST25

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

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

Tyr Ser Leu 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

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tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg	300
gtgttcggcg gagggacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc	360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc	480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaaag	540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc	600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a	651

<210> 1392

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1392

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

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

A-1937-WO-PCT_ST25

Tyr Asp Val₃₅ His Trp Tyr Gln₄₀ Gln Phe Pro Gly Thr Ala₄₅ Pro Lys Leu

Leu Ile₅₀ Gln Gly Asn Ser₅₅ Asn Arg Pro Ser Gly Val₆₀ Pro Asp Arg Phe

Ser Gly Ser Lys Ser₇₀ Gly Thr Ser Ala Ser₇₅ Leu Ala Ile Thr Gly₈₀ Leu

Gln Ala Glu Asp₈₅ Glu Ala Asp Tyr Tyr₉₀ Cys Gln Ser Tyr Asp₉₅ Ser Ser

Leu Ser Gly₁₀₀ Ser Val Phe Gly Gly₁₀₅ Thr Lys Leu Thr Val₁₁₀ Leu Gly

Gln Pro Lys₁₁₅ Ala Ala Pro Ser₁₂₀ Val Thr Leu Phe Pro₁₂₅ Pro Ser Ser Glu

Glu Leu₁₃₀ Gln Ala Asn Lys₁₃₅ Ala Thr Leu Val Cys₁₄₀ Leu Ile Ser Asp Phe

Tyr Pro Gly Ala Val₁₅₀ Thr Val Ala Trp Lys₁₅₅ Ala Asp Ser Ser Pro Val₁₆₀

Lys Ala Gly Val₁₆₅ Glu Thr Thr Thr Pro₁₇₀ Ser Lys Gln Ser Asn₁₇₅ Asn Lys

Tyr Ala Ala Lys₁₈₀ Ser Tyr Leu Ser₁₈₅ Leu Thr Pro Glu Gln Trp₁₉₀ Lys Ser

His Arg Ser₁₉₅ Tyr Ser Cys Gln₂₀₀ Val Thr His Glu Gly₂₀₅ Ser Thr Val Glu

Lys Thr₂₁₀ Val Ala Pro Thr₂₁₅ Glu Cys Ser

<210> 1393

<211> 2055

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1393

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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120

cagccccag ggaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180

aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240

cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300

A-1937-WO-PCT_ST25

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gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgtttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc	540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa	600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	660
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttctctt tcccccaaa acccaaggac	780
accctcatga tctcccgga cctgaggtc acatgcgtgg tgggtggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgtttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca	1020
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080
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aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC	1200
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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
gagcccaaat cttgt	2055

<210> 1394
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1394

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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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 ttactgggc atctaccgg 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
tgcctgggtca aggactactt ccccgaaccg gtgacgggtgt cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600

cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t

651

<210> 1396
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1396

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

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

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
 35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 100 105 110

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125

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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 ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
 aggttttagcg ggtccggggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgcttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtacggtg gctgcacat 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> 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

A-1937-WO-PCT_ST25

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 gaacgttggt caccgtctct 360
agtgcctcca ccaagggccc atcgggtctt 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
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840

A-1937-WO-PCT_ST25

tggtacgtgg	acggcgtgga	ggtgcataat	gccaaagaaa	agccgtgtga	ggagcagtag	900
ggcagcacgt	accgtttgtgt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaaggt	ctccaacaaa	gccctcccag	cccccatcga	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	ctcatgtctc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	ggtggcggat	cgggaggtgg	cggatcccag	1380
gtgcagttac	agcagtcggg	cgcaggactg	ttgaagcctt	cggagaccct	gtccctcacc	1440
tgcgctgtcc	atggtgggtc	cttcagtggg	tactactgga	actggattcg	ccagccacca	1500
gggaaggggc	tagagtggat	tggggaaatc	aatcatgctg	gaaacaccaa	ctacaacccg	1560
tccctcaaga	gtcgagtcac	catatcatta	gacacgtcca	agaaccagtt	ctccctgacg	1620
ctgacctctg	tgaccgccgc	ggacacggct	gtgtattact	gtgcgagagg	atattgtaga	1680
agtaccacct	gctactttga	ctactggggc	cagggaaccc	tagtcaccgt	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	aagcaccctg	acgctgagca	aagcagacta	cgagaaacac	1980
aaagtctacg	cctgcgaagt	cacccatcag	ggcctgagct	cggccgtcac	aaagagcttc	2040
aacaggggag	agtg					2055

<210> 1400
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 1400

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1			5					10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
		20					25					30			

Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40					45				

Ser	Ala	Ile	Thr	Trp	Asn	Ser	Gly	His	Ile	Asp	Tyr	Ala	Asp	Ser	Val
	50					55				60					

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
610 615 620

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
625 630 635 640

Asp Ser Thr Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp
645 650 655

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
660 665 670

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
675 680 685

<210> 1401
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1401
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt cccctggca 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> 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

A-1937-WO-PCT_ST25

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 accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggatatca gcaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240

A-1937-WO-PCT_ST25

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgctttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taactttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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 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
tacttgctta cagcttcgtc gctcgactat tggggtcagg gaacgttggg caccgtctct 360
agtgcctcca ccaagggccc atcgggtctt cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctgggt aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 780
cctgaggtca catgctgggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
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ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggag 1080
gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tcccagcagc 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcagtctcc gtgatgcatg aggtcttgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380

A-1937-WO-PCT_ST25

gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 1440
 tgcactgtct ctggtggctc catcagtagt tactttctgga gctggattcg gcagccccc 1500
 ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc 1560
 tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620
 ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680
 tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc aactgtggct 1740
 gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1800
 gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 1860
 aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 1920
 acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 1980
 tacgcctgcg aagtcacca 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccttgga 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
 tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gcccaaactt 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

A-1937-WO-PCT_ST25

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
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat 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> 1410
<211> 214

A-1937-WO-PCT_ST25

<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

gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt	60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt cgggcaagcg	120
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat	180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac	240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc	300
tacttgtcta cagcttcgtc gctcgactat tggggtcag gaacgttgggt caccgtctct	360
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct	420
gggggcacag 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 ctcccggacc	780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgtttgtgt 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 cggatcccag	1380
gtacagttgc aggagtacag tccaggactg gtgaagccct cggagaccct ctactcacc	1440
tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag	1500
cccccaggga 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 tgcaccatct gtcttcatct tcccgccatc tgatgagcag	1800
ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc	1860
aaagtacagt ggaaggtgga taacgccctc caatcgggta actcccagga gagtgtcaca	1920

A-1937-WO-PCT_ST25

gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980
gactacgaga aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040
gtcacaaaga gcttcaacag gggagagtgt 2070

<210> 1412
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1412

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

60

A-1937-WO-PCT_ST25

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 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
 tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
 agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg 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

A-1937-WO-PCT_ST25

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215

<210> 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 caaggaataa gcaatcggcc ctccaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag 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

A-1937-WO-PCT_ST25

Tyr Asp Val₃₅ His Trp Tyr Gln₄₀ Gln Phe Pro Gly Thr Ala₄₅ Pro Lys Leu
 Leu Ile₅₀ Gln Gly Asn Ser₅₅ Asn Arg Pro Ser Gly Val₆₀ Pro Asp Arg Phe
 Ser Gly Ser Lys Ser₇₀ Gly Thr Ser Ala Ser₇₅ Leu Ala Ile Thr Gly Leu₈₀
 Gln Ala Glu Asp₈₅ Glu Ala Asp Tyr Tyr₉₀ Cys Gln Ser Tyr Asp Ser₉₅ Ser
 Leu Ser Gly Ser₁₀₀ Val Phe Gly Gly₁₀₅ Thr Lys Leu Thr Val₁₁₀ Leu Gly
 Gln Pro Lys₁₁₅ Ala Ala Pro Ser Val₁₂₀ Thr Leu Phe Pro₁₂₅ Pro Ser Ser Glu
 Glu Leu₁₃₀ Gln Ala Asn Lys Ala₁₃₅ Thr Leu Val Cys Leu₁₄₀ Ile Ser Asp Phe
 Tyr Pro Gly Ala Val₁₅₀ Thr Val Ala Trp Lys Ala₁₅₅ Asp Ser Ser Pro Val₁₆₀
 Lys Ala Gly Val₁₆₅ Glu Thr Thr Thr Pro Ser₁₇₀ Lys Gln Ser Asn Asn₁₇₅ Lys
 Tyr Ala Ala Glu₁₈₀ Ser Tyr Leu Ser Leu₁₈₅ Thr Pro Glu Gln Trp Lys Ser
 His Arg Ser₁₉₅ Tyr Ser Cys Gln Val₂₀₀ Thr His Glu Gly Ser₂₀₅ Thr Val Glu
 Lys Thr₂₁₀ Val Ala Pro Thr Glu₂₁₅ Cys Ser

<210> 1417

<211> 2040

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1417

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60

tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300

A-1937-WO-PCT_ST25

tggggtcttg	actactgggg	ccaggaacc	ctggtcaccg	tctctagtgc	ctccaccaag	360
ggcccatcgg	tcttccccct	ggcaccctcc	tccaagagca	cctctggggg	cacagcggcc	420
ctgggctgcc	tgggtcaagga	ctacttcccc	gaaccgggtga	cgggtgtcgtg	gaactcaggg	480
gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	540
ctcaaaagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagacctt	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tggggggacc	gtcagtcttc	720
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtggtggtg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
gtggaggtgc	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	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	cgggtggtgg	cggatcggga	ggtggcggat	cccaggtgca	gttacagcag	1380
tcgggcgag	gactgttgaa	gccttcggag	accctgtccc	tcacctgcgc	tgtccatggt	1440
gggtccttca	gtggttacta	ctggaactgg	attcgccagc	caccagggaa	ggggctagag	1500
tggattgggg	aatcaatca	tgctggaaac	accaactaca	accgctccct	caagagtcga	1560
gtcaccatat	cattagacac	gtccaagaac	cagttctccc	tgacgtgac	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	ggaaggtgga	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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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 cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtcg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1420
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1420

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
 165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 195 200 205

Lys Ser Cys
 210

<210> 1421
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1421
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 tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
 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 tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<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

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110

A-1937-WO-PCT_ST25

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1423

<211> 2034

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1423

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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tgggggtcttg actactgggg ccagggaacc ctgggtcaccg tctctagtgc ctccaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag 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 ataattgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt	900

A-1937-WO-PCT_ST25

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	cgggtggtgg	cggatcggga	ggtggcggat	cccaggtgca	gctgcaggag	1380
tcgggcccag	gactggtgaa	gccttcggag	accctgtccc	tcacctgcac	tgtctctggt	1440
ggctccatca	gtagttactt	ctggagctgg	attcggcagc	cccaggtaa	gggactggag	1500
tggattggct	atatctatta	cagtgggcag	accaaataca	acccctccct	caagagtcga	1560
gtcaccatat	caatagacac	gtccaagaac	cagttctccc	tgaagctgag	ctctgtgacc	1620
gctgcggaca	cggccgtgta	ttactgtgcg	agagaaactg	ggagctacta	cggctttgac	1680
tactggggcc	agggaaacct	ggtcaccgtc	tcctcaactg	tggctgcacc	atctgtcttc	1740
atcttcccgc	catctgatga	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	gcccgtcaca	aagagcttca	acaggggaga	gtgt	2034

<210> 1424
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1424

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
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Ser	Leu	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Glu	Tyr	Ser	Phe	Thr	Ser	Tyr
			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

A-1937-WO-PCT_ST25

Leu Gln Trp Ser Ser₈₅ Leu Lys Ala Ser Asp₉₀ Thr Ala Met Tyr Tyr₉₅ Cys
 Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val
 Thr Val Ser₁₁₅ Ser Ala Ser Thr Lys₁₂₀ Gly Pro Ser Val Phe₁₂₅ Pro Leu Ala
 Pro Ser₁₃₀ Ser Lys Ser Thr Ser₁₃₅ Gly Gly Thr Ala Ala₁₄₀ Leu Gly Cys Leu
 Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀
 Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser
 Gly Leu Tyr Ser₁₈₀ Leu Lys Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Cys Glu Glu Gln Tyr₂₉₅ Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val
 Leu Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro

A-1937-WO-PCT_ST25

Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val

Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly

Gln Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀

Gly Ser Phe Phe Leu₄₀₅ Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp

Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His

Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly Gly

Ser Gly₄₅₀ Gly Gly Gly Ser Gln₄₅₅ Val Gln Leu Gln Glu₄₆₀ Ser Gly Pro Gly

Leu Val Lys Pro Ser Glu₄₇₀ Thr Leu Ser Leu Thr₄₇₅ Cys Thr Val Ser Gly₄₈₀

Gly Ser Ile Ser Ser₄₈₅ Tyr Phe Trp Ser Trp₄₉₀ Ile Arg Gln Pro Pro₄₉₅ Gly

Lys Gly Leu Glu₅₀₀ Trp Ile Gly Tyr Ile₅₀₅ Tyr Tyr Ser Gly Gln₅₁₀ Thr Lys

Tyr Asn Pro₅₁₅ Ser Leu Lys Ser Arg₅₂₀ Val Thr Ile Ser Ile₅₂₅ Asp Thr Ser

Lys Asn₅₃₀ Gln Phe Ser Leu Lys₅₃₅ Leu Ser Ser Val Thr₅₄₀ Ala Ala Asp Thr

Ala Val Tyr Tyr Cys Ala₅₅₀ Arg Glu Thr Gly Ser₅₅₅ Tyr Tyr Gly Phe Asp₅₆₀

Tyr Trp Gly Gln Gly₅₆₅ Thr Leu Val Thr Val₅₇₀ Ser Ser Thr Val Ala₅₇₅ Ala

Pro Ser Val Phe₅₈₀ Ile Phe Pro Pro Ser₅₈₅ Asp Glu Gln Leu Lys₅₉₀ Ser Gly

Thr Ala Ser₅₉₅ Val Val Cys Leu Leu₆₀₀ Asn Asn Phe Tyr Pro₆₀₅ Arg Glu Ala

Lys Val₆₁₀ Gln Trp Lys Val Asp₆₁₅ Asn Ala Leu Gln Ser₆₂₀ Gly Asn Ser Gln

A-1937-WO-PCT_ST25

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
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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa 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 tgggcacca 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

A-1937-WO-PCT_ST25

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

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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctgaggggctc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1429
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1429
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cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggtcttg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
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gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
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gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
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tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggtctcca acaaagccct ccagcccc atcgagaaaa ccattctcaa 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 cgggtggtgg cggatcggga ggtggcggat ccaggtaca gttgcaggag 1380
tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc 1500

A-1937-WO-PCT_ST25

cttgagtgga taggaaggac atactacagg tccaagtggg ataatgatta tgcagtttct 1560
ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg 1620
agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc 1680
tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcttcaact 1740
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980
aaagtctacg cctgcgaagt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly
450 455 460

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly
465 470 475 480

Asp Ser Val Ser Thr Asn Ser Val Ala Trp Asn Trp Ile Arg Gln Pro
485 490 495

Pro Gly Lys Gly Leu Glu Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys
500 505 510

Trp Tyr Asn Asp Tyr Ala Val Ser Leu Lys Ser Arg Val Thr Ile Ser
515 520 525

Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr
530 535 540

Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser
545 550 555 560

Tyr Tyr Arg Tyr Gly Met Asp Val Trp Gly 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
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 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tggtagcagc 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 gtgacgggtg cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
 agcgtgggtga ccgtgccctc cagcagcttg ggcaccaga 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

A-1937-WO-PCT_ST25

Lys Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215

<210> 1433
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1433
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggtagcgcc tctgtttgtg gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1434
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1434

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 1435

<211> 2055

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

A-1937-WO-PCT_ST25

<400> 1435

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acctgcgctg	tccatggtgg	gtccttcagt	ggttactact	ggaactggat	ccgccagcca	120
ccaggggaagg	ggctagagtg	gattggggaa	atcaatcatg	ctggaaacac	caactacaac	180
ccgtccctca	agagtcgagt	caccatatca	ttagacacgt	ccaagaacca	gttctccctg	240
acgctgacct	ctgtgaccgc	cgcgacacg	gctgtgtatt	actgtgagag	aggatattgt	300
agaagtacca	cctgctactt	tgactactgg	ggccagggaa	ccctagtcac	cgtctcctca	360
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
aaatcttgtg	acaaaactca	cacatgccca	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcctgatctc	ccggaccctt	780
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	840
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgtgtgagga	gcagtacggc	900
agcacgtacc	gttgtgtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	960
gagtacaagt	gcaaggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1020
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccgggaggag	1080
atgaccaaga	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	ggcggatcgg	gaggtggcgg	atccgaggtg	1380
caactggtgg	aatcaggtgg	aggtttggtg	cagccgggga	gatcgtcag	gcttagctgt	1440
gcggcatcgg	ggtttacttt	cgatgattat	gcgatgcatt	gggtccggca	agcgcttggg	1500
aaagggctcg	agtgggtttc	cgccattacg	tggaatagcg	gacacatcga	ttatgcagac	1560
agtgtggagg	gcagattcac	aatctcacga	gacaatgcta	agaacagcct	gtaccttcag	1620
atgaactcac	ttcgcgcgga	agataccgcc	gtatactact	gcgccaaagt	ctcctacttg	1680
tctacagctt	cgtcgctcga	ctattggggg	caaggaacgt	tggtcaccgt	ctctagtact	1740
gtggctgcac	catctgtctt	catcttcccc	ccatctgatg	agcagttgaa	atctggaact	1800
gcctctgttg	tgtgcctgct	gaataacttc	tatcccagag	aggccaaagt	acagtgggag	1860
gtggataacg	ccctccaatc	gggtaactcc	caggagagtg	tcacagagca	ggacagcaag	1920
gacagcacct	acagcctcga	aagcaccctg	acgctgagca	aagcagacta	cgagaaacac	1980
aaagtctacg	cctgcgaagt	cacccatcag	ggcctgagct	cgcccgtcac	aaagagcttc	2040

aacaggggag agtgt

<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

A-1937-WO-PCT_ST25

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
 290 295 300
 Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 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

A-1937-WO-PCT_ST25

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 accatcgctc gtttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgctcg 180

aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

A-1937-WO-PCT_ST25

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 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> 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

A-1937-WO-PCT_ST25

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1439
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1439
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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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 cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

A-1937-WO-PCT_ST25

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ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc      600
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aaatcttgtg acaaaaactca cacatgccc aacgtgcccag cacctgaact cctgggggga      720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
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agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1080
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc     1140
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ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg     1320
cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcg atccgaggtg     1380
cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt     1440
aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgca gatgcccggg     1500
aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg     1560
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tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggt     1680
cttgactact ggggccaggg aaccctggtc accgtctcta gtcagcccaa ggccaacccc     1740
actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagtg     1800
tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc     1860
cccgtcaagg cgggagtgga gaccacaaa ccctccaaac agagcaacaa caagtacgcg     1920
gccgagagct acctgagcct gacgcccagc cagtggaagt cccacagaag ctacagctgc     1980
caggtcacgc atgaaggagg caccgtggag aagacagtgg cccctacaga atgttca      2037

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<210> 1442
 <211> 679
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1442

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30

A-1937-WO-PCT_ST25

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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

A-1937-WO-PCT_ST25

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln
 450 455 460
 Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys
 465 470 475 480
 Lys 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

A-1937-WO-PCT_ST25

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
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagccccaa actcctcatc caaggtaaca gcaatcggcc ctccaggggtc 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 cagcgccctt gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactcctt caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt 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

A-1937-WO-PCT_ST25

<400> 1445
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 gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
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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 catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780
acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
taccgtttgtg 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

A-1937-WO-PCT_ST25

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttctt ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg tggtagcgga tcgggaggtg gcggatccga ggtacaactg 1380
gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca 1440
tcgggggttta ctttcgatga ttatgcatg cattgggtcc ggcaagcgcc tggaaaaggg 1500
ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg 1560
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac 1620
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680
gcttcgtcgc tcgactattg gggtaagga acgttggtca ccgtctctag tactgtggct 1740
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 1860
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 1920
acctacagcc tcgaaagcac cctgacgtg agcaaagcag actacgagaa acacaaagtc 1980
tacgcctgcg aagtcacca 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

A-1937-WO-PCT_ST25

Arg Glu Thr Gly₁₀₀ Ser Tyr Tyr Gly Phe₁₀₅ Asp Tyr Trp Gly Gln₁₁₀ Gly Thr
 Leu Val Thr₁₁₅ Val Ser Ser Ala Ser₁₂₀ Thr Lys Gly Pro Ser₁₂₅ Val Phe Pro
 Leu Ala₁₃₀ Pro Ser Ser Lys Ser₁₃₅ Thr Ser Gly Gly Thr₁₄₀ Ala Ala Leu Gly
 Cys₁₄₅ Leu Val Lys Asp Tyr₁₅₀ Phe Pro Glu Pro Val₁₅₅ Thr Val Ser Trp Asn₁₆₀
 Ser Gly Ala Leu Thr₁₆₅ Ser Gly Val His Thr₁₇₀ Phe Pro Ala Val Leu₁₇₅ Gln
 Ser Ser Gly Leu₁₈₀ Tyr Ser Leu Lys Ser₁₈₅ Val Val Thr Val Pro₁₉₀ Ser Ser
 Ser Leu Gly₁₉₅ Thr Gln Thr Tyr Ile₂₀₀ Cys Asn Val Asn His₂₀₅ Lys Pro Ser
 Asn Thr₂₁₀ Lys Val Asp Lys Lys₂₁₅ Val Glu Pro Lys Ser₂₂₀ Cys Asp Lys Thr
 His₂₂₅ Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀
 Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser Val₃₀₅ Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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 tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg 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

A-1937-WO-PCT_ST25

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 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 gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

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<400> 1453
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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 cggtgacggg gtcgtggaac      480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc      540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc      600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga 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
taccgtttgt 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 gaggtctctg acaaccacta cacgcagaag     1320
agcctctccc tgtctccggg tgggtggcga 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 gggctcttgac     1680

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A-1937-WO-PCT_ST25

tactggggcc aggggaaccct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc 1740
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atcagtgact tctacccggg agctgtgaca gtggcctgga aggcagatgg cagccccgtc 1860
aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccgag 1920
agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccaggtc 1980
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 2031

<210> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met
485 490 495

Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly Asp Ser
500 505 510

Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala
515 520 525

Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala
530 535 540

Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly Leu Asp
545 550 555 560

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

<400> 1455
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1456
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1456

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc 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> 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

A-1937-WO-PCT_ST25

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

caggtagct 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

A-1937-WO-PCT_ST25

cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca	300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc	420
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggct	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 tccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggc caaaggcttc	1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1200
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg	1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt	1380
ggcggatccg aggtacaact ggtggaatca ggtggaggtt tgggtgcagcc ggggagatcg	1440
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cggcaagcgc ctggaaaagg gctcagagtgg gtttccgcca ttacgtggaa tagcggacac	1560
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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 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> 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

A-1937-WO-PCT_ST25

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 290 295 300
 Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 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

A-1937-WO-PCT_ST25

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 accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctccaggactc tactccctca aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct tgt	633

<210> 1462
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1462

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
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		

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgcctc 480
caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc 540
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1464
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1464

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

Val Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

A-1937-WO-PCT_ST25

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
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga cttggatcagg 120
cagccccag ggaaggcct 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 ccatcggctt tccccctggc accctcctcc 420
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

A-1937-WO-PCT_ST25

aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg 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
tggttgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc 1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080
ccatccccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt 1380
ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct 1440
ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg 1500
cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat 1560
accagatata gcccgctcct ccaaggccag gtcaccatct cagccgacaa gtccatcagt 1620
accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg 1680
agaagtaact ggggtcttga ctactggggc cagggaaccc tggtcaccgt ctctagtcag 1740
cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac 1800
aaggccacac tagtgtgtct gatcagtgac ttctaccgg gagctgtgac agtggcctgg 1860
aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc 1920
aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtccac 1980
agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct 2040
acagaatggt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcgggtc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactcctt caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt 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

gaggtacaac tggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt

60

A-1937-WO-PCT_ST25

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cctggaaaag	ggctcgagtg	ggttttccgcc	attacgtgga	atagcggaca	catcgattat	180
gcagacagtg	tggaagggcag	attcacaatc	tcacgagaca	atgctaagaa	cagcctgtac	240
cttcagatga	actcacttcg	cgcggaagat	accgccgtat	actactgcgc	caaagtctcc	300
tacttgtcta	cagcttcgtc	gctcgactat	tggggtcaag	gaacgttgggt	caccgtctct	360
agtacggtgg	ctgcaccatc	tgtcttcatc	ttcccgccat	ctgatgagca	gttgaaatct	420
ggaactgcct	ctgttgtgtg	cctgctgaat	aacttctatc	ccagagaggc	caaagtacag	480
tggaaggtgg	ataacgccct	ccaatcgggt	aactcccagg	agagtgtcac	agagcaggac	540
agcaaggaca	gcacctacag	cctcaagagc	accctgacgc	tgagcaaagc	agactacgag	600
aaacacaaaag	tctacgcctg	cgaagtcacc	catcagggcc	tgagctcgcc	cgtcacaaaag	660
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ctcctggggg	gaccgtcagt	cttcctcttc	ccccaaaac	ccaaggacac	cctcatgatac	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	ttcttctctt	atagcaagct	caccgtggac	1260
aagagcaggt	ggcagcaggg	gaacgtcttc	tcattgctccg	tgatgcatga	ggctctgcac	1320
aaccactaca	cgcagaagag	cctctccctg	tctccgggtg	gtggcggatc	gggaggtggc	1380
ggatcccagg	tgagttaca	gcagtcgggc	gcaggactgt	tgaagccttc	ggagaccctg	1440
tccctcacct	gcgctgtcca	tggtgggtcc	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	tactggggcc	agggaaacct	agtcaccgtc	1740
tcctcaactg	tggtctgcac	atctgtcttc	atcttcccgc	catctgatga	gcagttgaaa	1800
tctggaactg	cctctgttgt	gtgcctgctg	aataacttct	atcccagaga	ggccaaagta	1860
cagtggaaag	tggaataacgc	cctccaatcg	ggtaactccc	aggagagtgt	cacagagcag	1920
gacagcaagg	acagcaccta	cagcctcgaa	agcaccctga	cgctgagcaa	agcagactac	1980
gagaaacaca	aagtctacgc	ctgcgaagtc	acccatcagg	gcctgagctc	gcccgtcaca	2040
aagagcttca	acagggggaga	gtgt				2064

<210> 1470
 <211> 688
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1470

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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

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A-1937-WO-PCT_ST25

Gly 225 Glu Cys Asp Lys Thr 230 His Thr Cys Pro 235 Pro Cys Pro Ala Pro Glu 240
 Leu Leu Gly Gly Pro 245 Ser Val Phe Leu Phe 250 Pro Pro Lys Pro Lys 255 Asp
 Thr Leu Met Ile 260 Ser Arg Thr Pro Glu 265 Val Thr Cys Val 270 Val Val Asp
 Val Ser His 275 Glu Asp Pro Glu Val 280 Lys Phe Asn Trp Tyr 285 Val Asp Gly
 Val Glu 290 Val His Asn Ala Lys 295 Thr Lys Pro Cys Glu 300 Glu Gln Tyr Gly
 Ser 305 Thr Tyr Arg Cys Val 310 Ser Val Leu Thr Val 315 Leu His Gln Asp Trp 320
 Leu Asn Gly Lys Glu 325 Tyr Lys Cys Lys Val 330 Ser Asn Lys Ala Leu 335 Pro
 Ala Pro Ile Glu 340 Lys Thr Ile Ser Lys 345 Ala Lys Gly Gln Pro 350 Arg Glu
 Pro Gln Val 355 Tyr Thr Leu Pro Pro 360 Ser Arg Glu Glu Met 365 Thr Lys Asn
 Gln Val 370 Ser Leu Thr Cys Leu 375 Val Lys Gly Phe Tyr 380 Pro Ser Asp Ile
 Ala Val Glu Trp Glu 390 Ser Asn Gly Gln Pro Glu 395 Asn Asn Tyr Lys Thr 400
 Thr Pro Pro Val 405 Leu Asp Ser Asp Gly Ser 410 Phe Phe Leu Tyr Ser 415 Lys
 Leu Thr Val 420 Asp Lys Ser Arg Trp Gln 425 Gln Gly Asn Val Phe 430 Ser Cys
 Ser Val Met 435 His Glu Ala Leu 440 Asn His Tyr Thr Gln 445 Lys Ser Leu
 Ser Leu 450 Ser Pro Gly Gly 455 Gly Ser Gly Gly 460 Gly Gly Ser Gln Val
 Gln 465 Leu Gln Gln Ser Gly 470 Ala Gly Leu Leu Lys 475 Pro Ser Glu Thr Leu 480
 Ser Leu Thr Cys 485 Ala Val His Gly Gly Ser 490 Phe Ser Gly Tyr Tyr 495 Trp

A-1937-WO-PCT_ST25

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 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 cccctggga 360

A-1937-WO-PCT_ST25

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttccccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt 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

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 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 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

A-1937-WO-PCT_ST25

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1473
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1473
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
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
ttcccggtg tcctacagtc ctgaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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
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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
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ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540
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A-1937-WO-PCT_ST25

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ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgata	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
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aaggacagca cctacagcct cgaaagcacc ctgacgtga gcaaagcaga ctacgagaaa	1980
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcggccgt cacaaagagc	2040
ttcaacaggg gagagtgt	2058

<210> 1476
 <211> 686
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1476

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactcctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca 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

A-1937-WO-PCT_ST25

<400> 1479
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attacctgtc gcgcgtccca ggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1481
<211> 2079
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1481
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agctgtgcgg catcgggggtt 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
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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
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tcccggaccc ctgaggtcac atgctgtgtg gtggacgtga gccacgaaga ccctgaggtc 840
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tcccgggagg agatgaccaa gaaccaggct agcctgacct gcctggtcaa aggcttctat 1140

A-1937-WO-PCT_ST25

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cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200
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agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg 1980
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 2040
agctcgcccc tcacaaagag cttcaacagg ggagagtgt 2079

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<210> 1482
 <211> 693
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1482

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

A-1937-WO-PCT_ST25

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga 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

A-1937-WO-PCT_ST25

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 accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
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A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctccaggactc tactccctcg aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct 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		

A-1937-W0-PCT_ST25

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
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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccaggggaacc ctgggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac 600
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
taccgtttgtg 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
gagtgaggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttct ctatagcaag ctaccctggg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg tgggtggcgga tcgggaggtg gcggatccca ggtgcagtta 1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgctgtgtc 1440
catggtgggt cttcagtgg ttactactgg aactggattc gccagccacc aggggaagggg 1500
ctagagtgga ttgggggaaat caatcatgct ggaaacacca actacaaccc gtccctcaag 1560

A-1937-WO-PCT_ST25

agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct 1620
 gtgaccgccc cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc 1680
 tgctactttg actactgggg ccagggaacc ctagtcaccg tctcctcaac tgtggctgca 1740
 ccatctgtct tcattctccc 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 tcgcccgta 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

A-1937-WO-PCT_ST25

Gly Ser Pro Val Lys₁₆₅ Ala Gly Val Glu Thr₁₇₀ Thr Lys Pro Ser Lys₁₇₅ Gln
 Ser Asn Asn Lys₁₈₀ Tyr Ala Ala Lys Ser₁₈₅ Tyr Leu Ser Leu Thr₁₉₀ Pro Glu
 Gln Trp Lys₁₉₅ Ser His Arg Ser Tyr₂₀₀ Ser Cys Gln Val Thr₂₀₅ His Glu Gly
 Ser Thr₂₁₀ Val Glu Lys Thr Val₂₁₅ Ala Pro Thr Glu Cys₂₂₀ Ser Asp Lys Thr
 His₂₂₅ Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀
 Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser₃₀₅ Val Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys
 Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser
 Asn₃₈₅ Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀
 Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser
 Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala

A-1937-WO-PCT_ST25

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445
 Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln 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

A-1937-WO-PCT_ST25

<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 catcgggtctt ccccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcgggtc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat cttgt 645

<210> 1492
<211> 215
<212> PRT
<213> 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 ccggggagtc tctgaagatc

60

A-1937-WO-PCT_ST25

tcctgtaaga	cttctgaata	cagctttacc	agctactgga	tcggctgggt	gcgccagatg	120
cccgggaaag	gcctggagtg	gatggggatc	atctatcttg	gtgactcaga	taccagatac	180
agcccgtcct	tccaaggcca	ggtcaccatc	tcagccgaca	agtccatcag	taccgcctac	240
ctgcagtgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	gagaagtaac	300
tggggctctt	actactgggg	ccagggaaac	ctggtcaccg	tctctagtca	gccaaggcc	360
aacccccact	tcactctgtt	cccgccctcc	tctgaggagc	tccaagccaa	caaggccaca	420
ctagtgtgtc	tgatcagtga	cttctacccg	ggagctgtga	cagtggcctg	gaaggcagat	480
ggcagccccg	tcaaggcggg	agtggagacc	accaaaccct	ccaaacagag	caacaacaag	540
tacgcggcca	agagctacct	gagcctgacg	cccagacagt	ggaagtccca	cagaagctac	600
agctgccagg	tcacgcatga	agggagcacc	gtggagaaga	cagtggcccc	tacagaatgt	660
tcagacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	aactcctggg	gggaccgtca	720
gtcttcctct	tcccccaaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	960
aagtgcaagg	tctccaacaa	agccctccca	gccccatcg	agaaaaccat	ctccaagacc	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
caggagtccg	gcccaggact	ggtgaagcct	tcggagaccc	tgtccctcac	ctgcactgtc	1440
tctggtggct	ccatcagtag	ttacttctgg	agctggattc	ggcagcccc	aggtaagggg	1500
ctggagtgga	ttggctatat	ctattacagt	gggcagacca	aatacaaccc	ctccctcaag	1560
agtcgagtca	ccatatcaat	agacacgtcc	agaaccagt	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	ggaagggtga	taacgccctc	1860
caatcgggta	actcccagga	gagtgtcaca	gagcaggaca	gcaaggacag	cacctacagc	1920
ctcgaagca	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

A-1937-WO-PCT_ST25

Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser₃₀₅ Val Leu Thr Val₃₁₀ Leu His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val₃₂₅ Ser Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys
 Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser
 Asn Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀
 Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser
 Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala
 Leu His Asn₄₃₅ His Tyr Thr Gln Lys₄₄₀ Ser Leu Ser Leu Ser₄₄₅ Pro Gly Gly
 Gly Gly₄₅₀ Ser Gly Gly Gly Gly₄₅₅ Ser Gln Val Gln Leu₄₆₀ Gln Glu Ser Gly
 Pro Gly Leu Val Lys Pro₄₇₀ Ser Glu Thr Leu Ser₄₇₅ Leu Thr Cys Thr Val₄₈₀
 Ser Gly Gly Ser Ile₄₈₅ Ser Ser Tyr Phe Trp₄₉₀ Ser Trp Ile Arg Gln₄₉₅ Pro
 Pro Gly Lys Gly₅₀₀ Leu Glu Trp Ile Gly₅₀₅ Tyr Ile Tyr Tyr Ser₅₁₀ Gly Gln

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300

gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctccaggactc tactccctca aaagcgtggt 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		

A-1937-W0-PCT_ST25

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 caaggttaaca gcaatcggcc ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggctc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat 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

A-1937-WO-PCT_ST25

Gln Ala Glu Asp Glu₈₅ Ala Asp Tyr Tyr Cys₉₀ Gln Ser Tyr Asp Ser₉₅ Ser
 Leu Ser Gly Ser₁₀₀ Val Phe Gly Gly₁₀₅ Thr Lys Leu Thr Val₁₁₀ Leu Gly
 Ala Ser Thr₁₁₅ Lys Gly Pro Ser Val₁₂₀ Phe Pro Leu Ala Pro₁₂₅ Ser Ser Lys
 Ser Thr₁₃₀ Ser Gly Gly Thr Ala₁₃₅ Ala Leu Gly Cys₁₄₀ Leu Val Lys Asp Tyr
 Phe Pro Glu Pro Val₁₄₅ Thr₁₅₀ Val Ser Trp Asn Ser₁₅₅ Gly Ala Leu Thr Ser₁₆₀
 Gly Val His Thr Phe₁₆₅ Pro Ala Val Leu Gln₁₇₀ Ser Ser Gly Leu Tyr₁₇₅ Ser
 Leu Glu Ser Val₁₈₀ Val Thr Val Pro Ser₁₈₅ Ser Ser Leu Gly Thr₁₉₀ Gln Thr
 Tyr Ile Cys₁₉₅ Asn Val Asn His Lys₂₀₀ Pro Ser Asn Thr Lys₂₀₅ Val Asp Lys
 Lys Val₂₁₀ Glu Pro Lys Ser Cys₂₁₅

<210> 1499
 <211> 2061
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1499
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 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
 agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
 tggggctctg actactgggg ccaggaacc ctgggtaccg tctctagtca gcccaaggcc 360
 aacccactg tcaactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
 ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
 ggagccccc tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
 tacgcgcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac 600
 agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660

A-1937-WO-PCT_ST25

tcagacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	aactcctggg	gggaccgtca	720
gtcttcctct	tcccccaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgctgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	960
aagtgcagg	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	ccttcttct	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	tggtggcgga	tcgggaggtg	gcggatccca	ggtacagttg	1380
caggagtcag	gtccaggact	ggtgaagccc	tcggagaccc	tctcactcac	ctgtaccatc	1440
tccggggaca	gtgtctctac	caacagtgtt	gcttggaact	ggattaggca	gccccagggg	1500
aaaggccttg	agtggatagg	aaggacatac	tacaggtcca	agtgggtataa	tgattatgca	1560
gtttctctga	aaagtcgagt	aaccatcagc	ccagacacat	ccaagaacca	gttctccctg	1620
aagctgagct	ctgtgactgc	cgcgacacg	gctgtgtatt	actgtgcaag	agaggatggg	1680
gatagctact	accgctacgg	tatggacgtc	tggggccaa	ggaccacggt	caccgtctcc	1740
tcaactgtgg	ctgcaccatc	tgtcttcatc	ttcccgccat	ctgatgagca	gttgaaatct	1800
ggaactgcct	ctgttggtg	cctgctgaat	aacttctatc	ccagagaggc	caaagtacag	1860
tggaaggtgg	ataacgccct	ccaatcgggt	aactcccagg	agagtgtcac	agagcaggac	1920
agcaaggaca	gcacctacag	cctcgaaagc	accctgacgc	tgagcaaagc	agactacgag	1980
aaacacaaag	tctacgcctg	cgaagtcacc	catcagggcc	tgagctcgcc	cgtcacaaag	2040
agcttcaaca	ggggagagtg	t				2061

<210> 1500
 <211> 687
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1500

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	

Ser	Leu	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Glu	Tyr	Ser	Phe	Thr	Ser	Tyr
			20					25					30		

A-1937-WO-PCT_ST25

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg 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

60

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120
ccaggaagg ggctagagt gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccaggga cctagtcac 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 ctgacgtga gcaaagcaga ctacgagaaa 600
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgccac cgtgcccagc acctgaactc 720
ctggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtaaccct gccccatcc 1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccagc 1200

A-1937-WO-PCT_ST25

cctcccgatg tggactccga cggctccttc ttcctctata gcaagctcac cgtggacaag 1260
 agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1320
 cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga 1380
 tccgaggtac aactggtgga atcaggtgga ggtttggtgc agccggggag atcgtcagg 1440
 cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa 1500
 gcgcctggaa aagggctcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat 1560
 tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg 1620
 taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc 1680
 tcctacttgt ctacagcttc gtcgctcgac tattgggggtc aaggaacggt 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> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
675 680 685

<210> 1507
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1507
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagtga gcccaaattc 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

A-1937-WO-PCT_ST25

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 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 cccctggca 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

<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
 caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120
 ccaggaagg ggctagagt 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 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
 ctggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 780
 cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
 ttcaactggt acgtggacgg cgtggagggt cataatgcc agacaaagcc gtgtgaggag 900
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
 aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
 cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
 agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
 cctcccgtgc tggactccga cggctccttc ttctctata 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 ggtgcgccag 1500
 atgcccggga aaggcctgga gtggatgggg atcatctatc ttggtgactc agataccaga 1560
 tacagcccgt cttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc 1620
 tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt 1680
 aactgggggtc ttgactactg gggccaggga accctggtca ccgtctctag tcagcccaag 1740

A-1937-WO-PCT_ST25

gccaacccca ctgtcactct gttcccgcgc tcctctgagg agctccaagc caacaaggcc 1800
 aactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca 1860
 gatggcagcc ccgtcaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac 1920
 aagtacgcgg ccgagagcta cctgagcctg acgcccagagc agtggaagtc ccacagaagc 1980
 tacagctgcc aggtcacgca tgaaggagc 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

A-1937-WO-PCT_ST25

Glu Gln Asp Ser₁₈₀ Lys Asp Ser Thr Tyr₁₈₅ Ser Leu Lys Ser Thr₁₉₀ Leu Thr
 Leu Ser Lys₁₉₅ Ala Asp Tyr Glu Lys₂₀₀ His Lys Val Tyr Ala₂₀₅ Cys Glu Val
 Thr His₂₁₀ Gln Gly Leu Ser Ser₂₁₅ Pro Val Thr Lys Ser₂₂₀ Phe Asn Arg Gly
 Glu₂₂₅ Cys Asp Lys Thr His₂₃₀ Thr Cys Pro Pro Cys₂₃₅ Pro Ala Pro Glu Leu₂₄₀
 Leu Gly Gly Pro Ser₂₄₅ Val Phe Leu Phe Pro₂₅₀ Pro Lys Pro Lys Asp₂₅₅ Thr
 Leu Met Ile Ser₂₆₀ Arg Thr Pro Glu Val₂₆₅ Thr Cys Val Val₂₇₀ Val Asp Val
 Ser His Glu₂₇₅ Asp Pro Glu Val Lys₂₈₀ Phe Asn Trp Tyr Val₂₈₅ Asp Gly Val
 Glu Val₂₉₀ His Asn Ala Lys Thr₂₉₅ Lys Pro Cys Glu Glu₃₀₀ Gln Tyr Gly Ser
 Thr Tyr Arg Cys Val Ser₃₁₀ Val Leu Thr Val Leu₃₁₅ His Gln Asp Trp Leu₃₂₀
 Asn Gly Lys Glu Tyr₃₂₅ Lys Cys Lys Val Ser₃₃₀ Asn Lys Ala Leu Pro₃₃₅ Ala
 Pro Ile Glu Lys₃₄₀ Thr Ile Ser Lys Ala₃₄₅ Lys Gly Gln Pro Arg₃₅₀ Glu Pro
 Gln Val Tyr₃₅₅ Thr Leu Pro Pro Ser₃₆₀ Arg Glu Glu Met Thr₃₆₅ Lys Asn Gln
 Val Ser₃₇₀ Leu Thr Cys Leu Val₃₇₅ Lys Gly Phe Tyr Pro₃₈₀ Ser Asp Ile Ala
 Val₃₈₅ Glu Trp Glu Ser Asn₃₉₀ Gly Gln Pro Glu Asn₃₉₅ Asn Tyr Lys Thr Thr₄₀₀
 Pro Pro Val Leu Asp₄₀₅ Ser Asp Gly Ser Phe₄₁₀ Phe Leu Tyr Ser Lys₄₁₅ Leu
 Thr Val Asp Lys₄₂₀ Ser Arg Trp Gln Gln₄₂₅ Gly Asn Val Phe Ser₄₃₀ Cys Ser
 Val Met His₄₃₅ Glu Ala Leu His Asn₄₄₀ His Tyr Thr Gln Lys₄₄₅ Ser Leu Ser

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<400> 1513
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 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

A-1937-WO-PCT_ST25

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 ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt cccctggca 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> 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

A-1937-WO-PCT_ST25

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

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

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ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaataacaac 180

ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240

A-1937-WO-PCT_ST25

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg	300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacgggtg	360
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc	420
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg	480
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac	540
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa	600
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac	660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgctgggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcattgtcc gtgatgcatg aggtcttgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc	1440
tgtgcggcat cggggtttac tttcgatgat tatgcatgac attgggtccg gcaagcgcct	1500
ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca	1560
gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt	1620
cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcttac	1680
ttgtctacag cttcgtcgct cgactattgg ggtcaaggaa cgttggtcac 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 ctgacgtga gcaaagcaga ctacgagaaa	1980
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc	2040
ttcaacaggg gagagtgt	2058

<210> 1518
 <211> 686
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1518

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 115 120 125

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 130 135 140

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

A-1937-WO-PCT_ST25

Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr Val₄₁₅
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Glu₄₆₀ Val Gln Leu Val
 Glu Ser Gly Gly Gly Leu₄₇₀ Val Gln Pro Gly Arg₄₇₅ Ser Leu Arg Leu Ser₄₈₀
 Cys Ala Ala Ser Gly₄₈₅ Phe Thr Phe Asp Asp₄₉₀ Tyr Ala Met His Trp Val₄₉₅
 Arg Gln Ala Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Val Ser Ala Ile₅₁₀ Thr Trp
 Asn Ser Gly₅₁₅ His Ile Asp Tyr Ala₅₂₀ Asp Ser Val Glu Gly₅₂₅ Arg Phe Thr

A-1937-WO-PCT_ST25

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 accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt cccctggca 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540

A-1937-WO-PCT_ST25

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca 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 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 gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

cctgaggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tgggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag 900
 ggcagcacgt accgtttgtgt 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 aggtcttgca 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 tatcttggtg actcagatac cagatacagc 1560
 ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtag cgcctacctg 1620
 cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgtag aagtaactgg 1680
 ggtcttgact actggggcca ggaaccctg gtcaccgtct ctagtcagcc caaggccaac 1740
 cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta 1800
 gtgtgtctga tcagtactt ctaccggga gctgtgacag tggcctggaa ggcagatggc 1860
 agccccgtca aggcgggagt ggagaccacc aaaccctcca aacagagcaa caacaagtac 1920
 gcggccgaga gctacctgag cctgacgcc gagcagtgga agtcccacag aagctacagc 1980
 tgccaggtca 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

A-1937-WO-PCT_ST25

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 caaggaata 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 tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

A-1937-WO-PCT_ST25

gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt cccctcggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtcg 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

A-1937-WO-PCT_ST25

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
caggtagagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
cagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc 720
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac 780
accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa 840
gaccctgagg tcaagttaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctccca 1020
gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1140
aaaggcttct atcccagca catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttct ctatagcaag 1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga 1380

A-1937-WO-PCT_ST25

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 gcttcgctgc tcgactattg gggtaagga 1740
 acgttggta ccgtctctag tactgtggct gcaccatctg tcttcattct 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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly
450 455 460

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
465 470 475 480

Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
485 490 495

Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
500 505 510

Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp
515 520 525

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
545 550 555 560

Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr
565 570 575

Trp Gly 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

A-1937-WO-PCT_ST25

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 accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca ggaatccgg aattacctg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagtcct 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
ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggt 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggg 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
 tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctgt 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
 agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt 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 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 gtcttctct tcccccaaa acccaaggac 780
 accctcatga tctcccgac ccctgaggtc acatgcgtgg tgggtggacgt 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 catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1140
 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200
 aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttct ctatagcaag 1260
 ctaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1320
 gaggtcttgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga 1380
 tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc 1440
 ggggagtctc tgaagatctc ctgtaagact tctgaatata 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 tactggggcc agggaaccct ggtcaccgtc 1740
 tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctctc tgaggagctc 1800

A-1937-WO-PCT_ST25

caagccaaca aggccacact agtgtgtctg atcagtgact tctacccggg agctgtgaca 1860
gtggcctgga aggcatgag cagccccgtc aaggcgggag tggagaccac caaacctcc 1920
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg 1980
aagttccaca gaagctacag ctgccaggtc 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 cagcggcctt 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> 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

A-1937-WO-PCT_ST25

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 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggg 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
tgcctgggtca aggactactt ccccgaaccg gtgacgggtgt cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt 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

A-1937-WO-PCT_ST25

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 accatcgctg 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

A-1937-WO-PCT_ST25

gggacaaaag tcgagatcaa gcgtacggtg gctgcacccat ctgtcttcat cttccccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcc 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
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agctgtgcgg catcggggtt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120
cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcdc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
agtcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggtgtg cctacagtcc 540

A-1937-WO-PCT_ST25

tcaggactct	actccctcaa	aagcgtggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	cccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtacgtgg	acggcgtgga	ggtgcataat	gccaaagaaa	agccgtgtga	ggagcagtac	900
ggcagcacgt	accgtttgtgt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaaggt	ctccaacaaa	gccctcccag	cccccatcga	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
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	cagggaaacc	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	tgaatcacia	gcccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

<210> 1546

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1546

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Arg
1				5					10					15	

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
450 455 460

Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
465 470 475 480

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

A-1937-WO-PCT_ST25

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
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 gctgcacat 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> 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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgccca      360
tctgatgagc agttgaaatc tgggtaccgcc tctgtttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaaggtg 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

```

A-1937-WO-PCT_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcggtgtt 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
agtgcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa 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
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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
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccggag 1080

A-1937-WO-PCT_ST25

gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggaagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcagtctcc gtgatgcatg aggctctgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtcctcacc 1440
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ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc 1560
tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620
ctgagctctg tgaccgtgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680
tactacggct ttgactactg gggccaggga accctgggtca ccgtctcctc agcctccacc 1740
aagggcccat cggctctccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1860
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac 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

A-1937-WO-PCT_ST25

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys
675 680

<210> 1553
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1553
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attacctgtc gcgcgctcca 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 gcgtacggtg gctgcacat ctgtcttcat cttcccgcc 360
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cccagagagg ccaaagtaca gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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
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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 gaacgggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgcctc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

A-1937-WO-PCT_ST25

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
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 cctggaaaag ggctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
 agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt 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 cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
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 ggagcagcgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctccag ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggag 1080
 gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggaagaca actacaagac cagcctccc 1200
 gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260
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 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

A-1937-WO-PCT_ST25

gaggatgggg atagctacta ccgctacggt atggacgtct ggggcccaagg gaccacggtc 1740
accgtctcct cagcctccac 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
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040
aaagttgagc ccaaattctg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
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tttccaggaa cagcccccaa actcctcatc caaggaataa gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc      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 ctgccagggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a                651

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<210> 1560

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1560

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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 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

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A-1937-WO-PCT_ST25

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
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac 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 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

A-1937-WO-PCT_ST25

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

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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180

A-1937-WO-PCT_ST25

agcccgctcct	tccaaggcca	ggtcaccatc	tcagccgaca	agtccatcag	taccgcctac	240
ctgcagtggga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	gagaagtaac	300
tggggctcttg	actactgggg	ccaggggaacc	ctgggtcaccg	tctctagtgc	ctccaccaag	360
ggcccatcgg	tcttccccct	ggcaccctcc	tccaagagca	cctctggggg	cacagcggcc	420
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gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	540
ctcaaaagcg	tgggtgaccgt	gccctccagc	agcttgggca	cccagacctc	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaagggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tgggggggacc	gtcagtcttc	720
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtgggtggtg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
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tgtgtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	960
aaggctctcca	acaaagccct	cccagcccc	atcgagaaaa	ccatctccaa	agccaaaggg	1020
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accagcggcg	tgcacacctt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtggtga	ccgtgccctc	cagcagcttg	ggcaccacga	cctacatctg	caacgtgaat	1980
cacaagccca	gcaacaccaa	ggtggacaag	aaagttgagc	ccaaatcttg	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
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Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Asn Gln Phe Ser Leu Thr Leu Thr Ser Val Thr Ala Ala Asp Thr
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr
545 550 555 560

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 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 cagccccaa 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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 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
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagacctc catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

A-1937-WO-PCT_ST25

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataatgcca 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 ggagccgga gaacaactac aagaccacgc ctcccgctgt ggactccgac 1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtgca gctgcaggag 1380
tcggggcccag gactggtgaa gccttcggag accctgtccc tcacctgcac tgtctctggt 1440
ggctccatca gtagttactt ctggagctgg attcggaagc cccaggtaa gggactggag 1500
tggattggct atatctatta cagtgggagc accaaatata acccctccct caagagtcga 1560
gtcaccatat caatagacac gtccaagaac cagttctccc tgaagctgag ctctgtgacc 1620
gctgcggaca cggccgtgta ttactgtgag agagaaactg ggagctacta cggctttgac 1680
tactggggcc agggaaacct ggtcaccgtc tcctcagcct ccaccaaggg cccatcggtc 1740
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 1800
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 1860
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct cgagagcgtg 1920
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 1980
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gcagggttatg 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 cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

A-1937-WO-PCT_ST25

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 ggaaggtgga taacgccttc 480
caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc 540
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1574

<211> 220

<212> PRT

<213> Artificial Sequence

<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

A-1937-WO-PCT_ST25

Ser Thr Tyr Ser₁₈₀ Leu Lys Ser Thr Leu₁₈₅ Thr Leu Ser Lys Ala₁₉₀ Asp Tyr

Glu Lys His₁₉₅ Lys Val Tyr Ala Cys₂₀₀ Glu Val Thr His Gln₂₀₅ Gly Leu Ser

Ser Pro Val Thr Lys Ser Phe₂₁₅ Asn Arg Gly Glu Cys₂₂₀

<210> 1575
<211> 2046
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1575
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccagggaacc ctgggtcaccg 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 cccagacctc catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggagggtc 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 ttctatccca gcgacatcgc 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

A-1937-WO-PCT_ST25

tcagggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggaagccccc agggaaaggc 1500
cttgagtgga taggaaggac atactacagg tccaagtggg ataatgatta tgcagtttct 1560
ctgaaaagtc gagtaacat cagcccagac acatccaaga accagttctc cctgaagctg 1620
agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc 1680
tactaccgct acggtatgga cgtctggggc caagggacca cggtcaccgt ctcctcagcc 1740
tccaccaagg gcccatcggg cttccccctg gcaccctcct ccaagagcac ctctgggggc 1800
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 1860
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 1920
ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 1980
atctgcaacg tgaatcaca gccagcaac accaaggtgg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
 gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggtagcgcc tctgtttgtg gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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
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attacctgtc gcgcgtccca ggaatccgg aattacctcg catggtatca ggagaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggt 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

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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgcaagcca	120
ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac	180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg	240
acgctgacct ctgtgaccgc cgcgagacg 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
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga	720
ccgtcagttc tcctcttccc cccaaaaccc aaggacaccc tcattgatctc ccggaccctc	780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc	900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag	1080
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg	1320
cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggta	1380
caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgtcag gcttagctgt	1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggtccgga agcgcctgga	1500
aaagggctcg agtggggttc cgccattacg tggaatagcg gacacatcga ttatgcagac	1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag	1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgcaaagt ctctacttg	1680
tctacagctt cgtcgctcga ctattggggg caaggaacgt tggtcaccgt ctctagtgcc	1740
tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	1800
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	1860
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	1920

A-1937-WO-PCT_ST25

ctctactccc tcgagagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 1980
atctgcaacg tgaatcacia gccagcaac 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
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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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1585
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1585
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tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
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actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcacctg 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

A-1937-WO-PCT_ST25

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

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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

A-1937-WO-PCT_ST25

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aatcttctgt acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga      720
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gagtacaagt gcaaggctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag     1080
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cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg     1380
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aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg     1560
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tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggg     1680
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tgcttggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg     1860
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag     1920
agcgtgggtg ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat     1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t      2031

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<210> 1588

<211> 677

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1588

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

A-1937-WO-PCT_ST25

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Asn Trp Ile Arg 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

A-1937-WO-PCT_ST25

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
 290 295 300
 Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln
 450 455 460
 Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys
 465 470 475 480
 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

A-1937-WO-PCT_ST25

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
565 570 575

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
580 585 590

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
595 600 605

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
610 615 620

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu
625 630 635 640

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
645 650 655

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
660 665 670

Glu Pro Lys Ser Cys
675

<210> 1589
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1589
gacatccaga tgaccagtc 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 gtggaaggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1590
<211> 214

A-1937-WO-PCT_ST25

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1590

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

A-1937-WO-PCT_ST25

<220>

<223> Synthetic polynucleotide

<400> 1591

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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 gctgcacat 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

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<210> 1592

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1592

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
          100          105          110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
          115          120          125

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A-1937-WO-PCT_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
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acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc 120
ccaggtgaagg gactggagtg gattggctat atctattaca gtgggcagac caaataacaac 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
gcggccctgg gctgcctggt caaggactac ttcccgaac cgggtgacggt gtcgtggaac 480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga 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
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc 1020

A-1937-WO-PCT_ST25

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
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ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg 1560
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac 1620
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca 1680
gcttcgtcgc tcgactattg gggtaagga acgttggtca ccgtctctag tgcctccacc 1740
aagggcccat cggcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 1800
gccctgggct gcctggtaaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1860
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcaccagac 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

A-1937-WO-PCT_ST25

Arg Glu Thr Gly₁₀₀ Ser Tyr Tyr Gly Phe₁₀₅ Asp Tyr Trp Gly Gln Gly Thr
 Leu Val Thr₁₁₅ Val Ser Ser Ala Ser₁₂₀ Thr Lys Gly Pro Ser₁₂₅ Val Phe Pro
 Leu Ala Pro Ser Ser Lys Ser₁₃₅ Thr Ser Gly Gly Thr₁₄₀ Ala Ala Leu Gly
 Cys₁₄₅ Leu Val Lys Asp Tyr₁₅₀ Phe Pro Glu Pro Val₁₅₅ Thr Val Ser Trp Asn₁₆₀
 Ser Gly Ala Leu Thr₁₆₅ Ser Gly Val His Thr₁₇₀ Phe Pro Ala Val Leu₁₇₅ Gln
 Ser Ser Gly Leu₁₈₀ Tyr Ser Leu Lys Ser₁₈₅ Val Val Thr Val Pro₁₉₀ Ser Ser
 Ser Leu Gly₁₉₅ Thr Gln Thr Tyr Ile₂₀₀ Cys Asn Val Asn His₂₀₅ Lys Pro Ser
 Asn Thr₂₁₀ Lys Val Asp Lys Lys₂₁₅ Val Glu Pro Lys Ser₂₂₀ Cys Asp Lys Thr
 His₂₂₅ Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀
 Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser Val₃₀₅ Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
645 650 655

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
660 665 670

Lys Lys Val Glu Pro Lys Ser Cys
675 680

<210> 1595
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1595
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gggaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat 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> 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

A-1937-WO-PCT_ST25

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

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tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag	120
tttccaggaa cagccccaa actcctcatc caaggaataa gcaatcggcc ctcaggggctc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg	300
gtgttcggcg gagggacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc	360
actctgttcc cgccctctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgctc	480

A-1937-WO-PCT_ST25

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540
agctatctga gcctgacgcc tgagcagtgg 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

A-1937-WO-PCT_ST25

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
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ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180
ccctccctca agatcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagcctcc 360
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gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
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tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga cctgaggtc 780
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taccgtttg tgcagctcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc 1020
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gtgcagtctg gagcagaggt gaaaaagccc ggggagtctc tgaagatctc ctgtaagact 1440
tctgaataca gctttaccag ctactggatc ggctgggtgc gcaagatgcc cgggaaagggc 1500
ctggagtgga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc 1560
caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc 1620

A-1937-WO-PCT_ST25

agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac 1680
 tactggggcc aggggaaccct ggtcaccgtc tctagtgcct ccaccaaggg cccatcggtc 1740
 ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 1800
 gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 1860
 ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgagagcgtg 1920
 gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 1980
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 2025

<210> 1600
 <211> 675
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1600

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Phe Trp Ser Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly
450 455 460

Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Thr
465 470 475 480

Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg 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

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gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttggtgtgc      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> 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

```


A-1937-WO-PCT_ST25

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
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
caggtagcagc tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120

aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180

A-1937-WO-PCT_ST25

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	tgtcgtggaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac	cttcccggct	540
gtcctacagt	cctcaggact	ctactccctc	aaaagcgtgg	tgaccgtgcc	ctccagcagc	600
ttgggcaccc	agacctacat	ctgcaacgtg	aatcacaagc	ccagcaacac	caaggtggac	660
aagaaagtgt	agcccaaadc	ttgtgacaaa	actcacacat	gcccaccgtg	cccagcacct	720
gaactcctgg	ggggaccgtc	agtcttcctc	ttcccccaa	aaccaagga	caccctcatg	780
atctcccggg	cccctgaggt	cacatgcgtg	gtggtggacg	tgagccacga	agaccctgag	840
gtcaagttca	actggtacgt	ggacggcgtg	gaggtgcata	atgccaagac	aaagccgtgt	900
gaggagcagt	acggcagcac	gtaccgttgt	gtcagcgtcc	tcaccgtcct	gcaccaggac	960
tggctgaatg	gcaaggagta	caagtgcgaag	gtctccaaca	aagccctccc	agccccatc	1020
gagaaaacca	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	caccctgccc	1080
ccatcccggg	aggagatgac	caagaaccag	gtcagcctga	cctgcctggg	caaaggcttc	1140
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gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1320
cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtggtggcgg	atcgggaggt	1380
ggcggatccg	aggtacaact	ggtggaatca	ggtggaggtt	tggtgcagcc	ggggagatcg	1440
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cggaaagcgc	ctggaaaagg	gctcgagtgg	gtttccgcca	ttacgtggaa	tagcggacac	1560
atcgattatg	cagacagtgt	ggagggcaga	ttcacaatct	cacgagacaa	tgctaagaac	1620
agcctgtacc	ttcagatgaa	ctcacttcgc	gcggaagata	ccgccgtata	ctactgcgcc	1680
aaagtctcct	acttgtctac	agcttcgtcg	ctcgaactatt	ggggtcaagg	aacgttgggtc	1740
accgtctcta	gtgcctccac	caagggccca	tcggtcttcc	ccctggcacc	ctcctccaag	1800
agcacctctg	ggggcacagc	ggccctgggc	tgcttggtca	aggactactt	ccccgaaccg	1860
gtgacggtgt	cgtggaactc	aggcgccctg	accagcggcg	tgcacacctt	ccgggctgtc	1920
ctacagtcct	caggactcta	ctccctcgag	agcgtggtga	ccgtgccctc	cagcagcttg	1980
ggcaccacga	cctacatctg	caacgtgaat	cacaagccca	gcaacaccaa	ggtggacaag	2040
aaagttgagc	ccaaatcttg	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

A-1937-WO-PCT_ST25

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
290 295 300

Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
305 310 315

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggg 180

gaatccgggg 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 ggaaggtgga taacgcctc 480

A-1937-WO-PCT_ST25

caatcgggta actcccagga gagtgtcaca gacgaggaca 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

A-1937-WO-PCT_ST25

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 caaggaata gcaatcggcc ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggctc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggctc 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

A-1937-WO-PCT_ST25

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

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa 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 ctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc 420

aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

gtcctacagt ctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660

aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct 720

A-1937-WO-PCT_ST25

gaactcctgg	ggggaccgtc	agtcttcctc	ttcccccaa	aaccaagga	caccctcatg	780
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gtcaagttca	actggtacgt	ggacggcgtg	gaggtgcata	atgccaagac	aaagccgtgt	900
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accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctatagcaa	gctcaccgtg	1260
gacaagagca	ggtggcagca	ggggaacgtc	ttctcatgct	ccgtgatgca	tgaggctctg	1320
cacaaccact	acacgcagaa	gagcctctcc	ctgtctccgg	gtggtggcgg	atcgggaggt	1380
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agaagtaact	ggggtcttga	ctactggggc	cagggaaacc	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	tgaatcacia	gcccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

<210> 1612
 <211> 682
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1612

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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	Lys	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Trp Leu Asn Gly Lys₃₂₅ Glu Tyr Lys Cys Lys₃₃₀ Val Ser Asn Lys Ala₃₃₅ Leu

Pro Ala Pro Ile₃₄₀ Glu Lys Thr Ile Ser₃₄₅ Lys Ala Lys Gly Gln₃₅₀ Pro Arg

Glu Pro Gln₃₅₅ Val Tyr Thr Leu Pro₃₆₀ Pro Ser Arg Glu Glu₃₆₅ Met Thr Lys

Asn Gln₃₇₀ Val Ser Leu Thr Cys₃₇₅ Leu Val Lys Gly Phe₃₈₀ Tyr Pro Ser Asp

Ile₃₈₅ Ala Val Glu Trp Glu₃₉₀ Ser Asn Gly Gln₃₉₅ Pro Glu Asn Asn Tyr Lys₄₀₀

Thr Thr Pro Pro Val₄₀₅ Leu Asp Ser Asp Gly₄₁₀ Ser Phe Phe Leu Tyr₄₁₅ Ser

Lys Leu Thr Val₄₂₀ Asp Lys Ser Arg Trp₄₂₅ Gln Gln Gly Asn Val₄₃₀ Phe Ser

Cys Ser Val₄₃₅ Met His Glu Ala₄₄₀ Leu His Asn His Tyr Thr₄₄₅ Gln Lys Ser

Leu Ser₄₅₀ Leu Ser Pro Gly Gly₄₅₅ Gly Gly Ser Gly Gly₄₆₀ Gly Gly Ser Glu

Val₄₆₅ Gln Leu Val Gln₄₇₀ Ser Gly Ala Glu Val Lys₄₇₅ Lys Pro Gly Glu Ser₄₈₀

Leu Lys Ile Ser Cys₄₈₅ Lys Thr Ser Glu Tyr₄₉₀ Ser Phe Thr Ser Tyr₄₉₅ Trp

Ile Gly Trp Val₅₀₀ Arg Lys Met Pro Gly₅₀₅ Lys Gly Leu Glu Trp₅₁₀ Met Gly

Ile Ile Tyr₅₁₅ Leu Gly Asp Ser Asp₅₂₀ Thr Arg Tyr Ser Pro₅₂₅ Ser Phe Gln

Gly Gln₅₃₀ Val Thr Ile Ser Ala₅₃₅ Asp Lys Ser Ile Ser₅₄₀ Thr Ala Tyr Leu

Gln₅₄₅ Trp Ser Ser Leu Lys₅₅₀ Ala Ser Asp Thr Ala₅₅₅ Met Tyr Tyr Cys Ala₅₆₀

Arg Ser Asn Trp Gly₅₆₅ Leu Asp Tyr Trp Gly₅₇₀ Gln Gly Thr Leu Val₅₇₅ Thr

Val Ser Ser Ala₅₈₀ Ser Thr Lys Gly Pro₅₈₅ Ser Val Phe Pro Leu₅₉₀ Ala Pro

A-1937-WO-PCT_ST25

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
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcacat 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> 1614
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1614

A-1937-WO-PCT_ST25

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
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agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaaagcg 120
Page 1174

A-1937-WO-PCT_ST25

cctggaaaag	ggctcgagtg	ggtttccgcc	attacgtgga	atagcggaca	catcgattat	180
gcagacagtg	tggagggcag	attcacaatc	tcacgagaca	atgctaagaa	cagcctgtac	240
cttcagatga	actcacttcg	cgcggaagat	accgccgtat	actactgcgc	caaagtctcc	300
tacttgtcta	cagcttcgtc	gctcgactat	tggggccaag	gaacgttggt	caccgtctct	360
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ctcctggggg	gaccgtcagt	cttcctcttc	ccccaaaac	ccaaggacac	cctcatgata	780
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gtgtcgtgga	actcaggcgc	cctgaccagc	ggcgtgcaca	ccttcccggc	tgctctacag	1920
tcctcaggac	tctactccct	cgagagcgtg	gtgaccgtgc	cctccagcag	cttgggcacc	1980
cagacctaca	tctgcaacgt	gaatcacaag	cccagcaaca	ccaaggtgga	caagaaagtt	2040
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<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
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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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

A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
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tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct tgt	633

<210> 1618
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1618

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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	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		

A-1937-WO-PCT_ST25

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
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atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc 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> 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
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Glu Arg Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

A-1937-WO-PCT_ST25

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
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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
tacttgctta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 420
ggaactgcct ctgttggttg 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

A-1937-WO-PCT_ST25

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agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa      720
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tcccggaccc ctgagggtcac atgctgtgtg gtggacgtga gccacgaaga ccctgagggtc      840
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag      900
gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg      960
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ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc     1980
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc     2040
aaatcttgt                                     2049

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt cccctggca 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> 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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc

60

A-1937-WO-PCT_ST25

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
 gaatccgggg 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 tgttggtgtgc 420
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
 ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 1626

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1626

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

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

A-1937-WO-PCT_ST25

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 tactttcgat gattatgcga tgcattgggt ccggaagcg	120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat	180
gcagacagt tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac	240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc	300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct	360
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	420
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	480
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac	540
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag	600
aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag	660
agcttcaaca ggggagagt tgacaaaact cacacatgcc caccgtgccc agcacctgaa	720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac	780
tcccggaacc ctgaggtcac atgctgtgtg 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

A-1937-WO-PCT_ST25

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aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 1440
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attaggaagc ccccagggaa aggccttgag tggataggaa ggacatacta caggtccaag 1560
tggtataatg attatgcagt ttctctgaaa agtcgagtaa ccatcagccc agacacatcc 1620
aagaaccagt tctccctgaa gctgagctct gtgactgccg cggacacggc tgtgtattac 1680
tgtgcaagag aggatgggga tagctactac cgctacggta tggacgtctg gggccaaggg 1740
accacgggtc ccgtctctc agcctccacc aagggcccat cggctcttccc cctggcacc 1800
tcctccaaga gcacctctg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 1860
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 1920
ccggctgtcc tacagtctc 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

A-1937-WO-PCT_ST25

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val
115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu
180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
210 215 220

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
290 295 300

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
660 665 670

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
675 680 685

Ser Cys
690

<210> 1629
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1629
gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca ggaatccgg aattacctcg catggtatca ggaaaaaccc 120
ggaaaagcac cgaagtcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt cccctggca 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> 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

A-1937-WO-PCT_ST25

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

gaaatttgtg	tgacgcagtc	tccaggcacc	ctgtctttgt	ctccagggga	aagagccacc	60
ctctcctgca	gggccagtc	gagtgttaga	agcagttact	tagcctggta	ccaggagaaa	120
cctggccagg	ctcccaggct	cctcatctat	ggtgcatcca	gcagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtctgggaca	gacttcactc	tcaccatcag	cagactggag	240
cctgaagatt	ttgcagtgt	ttactgtcag	cagtatggta	gctcacctac	cttcggccaa	300
gggacacgac	tggagattaa	acgaacggtg	gctgcacat	ctgtcttcat	cttcccgcca	360
tctgatgagc	agttgaaatc	tggtaccgcc	tctgttgtgt	gcctgctgaa	taacttctat	420
cccagagagg	ccaaagtaca	gtggaagggtg	gataacgcc	tccaatcggg	taactcccag	480

A-1937-WO-PCT_ST25

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

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<400> 1633
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc      60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg      120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac      180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac      240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac      300
tggggctcttg actactgggg ccaggaacc 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 gaggctgacg ccgagcagc ggaagtcca cagaagctac      600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt      660
tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca      720
gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga ccctgaggctc      780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg      900
taccgttttg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      960
aagtgaagg tctccaacaa agccctcca gccccatcg agaaaaccat ctccaaagcc     1020
aaagggcagc ccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc     1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg     1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac     1200
tccgacggct ctttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag     1260
gggaacgtct tctcatgctc cgtgatgcat gaggtctgc acaaccacta cacgcagaag     1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatcca ggtgcagtta     1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc     1440
catggtgggt cttcagtgg ttactactgg aactggattc gcaagccacc aggggaagggg     1500
ctagagtgga ttggggaaat caatcatgct ggaaacacca actacaacc gtccctcaag     1560
agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct     1620

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A-1937-WO-PCT_ST25

gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc 1680
tgctactttg actactgggg ccaggggaacc ctagtcaccg tctcctcagc ctccaccaag 1740
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1800
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc 1860
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 1920
ctcgagagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1980
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgt 2037

<210> 1634
<211> 679
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1634

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag      120
tttccaggaa cagcccccaa actcctcatc caaggaataa gcaatcggcc ctcagggggtc      180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc      240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg      300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcgggtc      360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg      420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      480
ggcgtgcaca cttccccggc tgtcctacag tcctcaggac tctactcctc cgaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt                      645

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<210> 1636

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1636

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1          5          10          15
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20        25        30
Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
35        40        45
Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50        55        60
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65        70        75        80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85        90        95
Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100       105       110
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
115       120       125

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A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln 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
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180

A-1937-WO-PCT_ST25

agcccgctcct	tccaaggcca	ggtcaccatc	tcagccgaca	agtccatcag	taccgcctac	240
ctgcagtggga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	gagaagtaac	300
tggggctcttg	actactgggg	ccaggggaacc	ctgggtcaccg	tctctagtca	gcccgaaggcc	360
aacccccactg	tcactctgtt	cccgcctcc	tctgaggagc	tccaagccaa	caaggccaca	420
ctagtgtgtc	tgatcagtga	cttctacccg	ggagctgtga	cagtggcctg	gaaggcagat	480
ggcagccccg	tcaaggcggg	agtggagacc	accaaaccct	ccaaacagag	caacaacaag	540
tacgcggcca	agagctacct	gagcctgacg	cccgagcagt	ggaagtcca	cagaagctac	600
agctgccagg	tcacgcatga	agggagcacc	gtggagaaga	cagtggcccc	tacagaatgt	660
tcagacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	aactcctggg	gggaccgtca	720
gtcttcctct	tcccccaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	960
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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
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caggagtccg	gcccaggact	ggtgaagcct	tcggagaccc	tgtccctcac	ctgcactgtc	1440
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ctggagtggga	ttggctatat	ctattacagt	gggcagacca	aatacaacc	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	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcctgggtca	aggactactt	ccccgaaccg	gtgacggtgt	cgtggaactc	aggcgccctg	1860
accagcggcg	tgcacacctt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtggtga	ccgtgccctc	cagcagcttg	ggcaccaga	cctacatctg	caacgtgaat	1980
cacaagccca	gcaacaccaa	ggtggacaag	aaagttgagc	ccaaatcttg	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

A-1937-WO-PCT_ST25

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

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

A-1937-WO-PCT_ST25

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 cagccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggctc 360

ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactcct cgaaagcgtg 540

A-1937-WO-PCT_ST25

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt 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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaagggtg gagatcaaac gaacgggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttggtgtgc 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

A-1937-WO-PCT_ST25

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 ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tctactgtgt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
tacgcggcca agagctacct gagcctgacg ccgagcagc ggaagtccca cagaagctac 600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660
tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780

A-1937-WO-PCT_ST25

acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
 taccgtttgtg 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 ctttcttctt ctatagcaag ctaccctgtg acaagagcag gtggcagcag 1260
 gggaacgtct tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacgcagaag 1320
 agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtacagttg 1380
 caggagtacg gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc 1440
 tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggaa gccccaggg 1500
 aaaggccttg agtggatagg aaggacatac tacagggtcca agtgggtataa tgattatgca 1560
 gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg 1620
 aagctgagct ctgtgactgc cgcgacacg gctgtgtatt actgtgcaag agaggatggg 1680
 gatagctact accgctacgg tatggacgtc tggggccaag ggaccacggg caccgtctcc 1740
 tcagcctcca ccaagggccc atcgggtctt cccctggcac cctcctccaa gagcacctct 1800
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 1860
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1920
 tcaggactct actccctcga gagcgtggtg accgtgccct ccagcagctt gggcacccag 1980
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 2040
 cccaaatctt gt 2052

<210> 1646
 <211> 684
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1646

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr
 20 25 30

Trp Ile Gly Trp Val Arg Lys Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

A-1937-WO-PCT_ST25

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
145 150 155 160

Gly Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

A-1937-WO-PCT_ST25

Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys
 Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser
 Asn Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀
 Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser
 Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala
 Leu His Asn₄₃₅ His Tyr Thr Gln Lys₄₄₀ Ser Leu Ser Leu Ser₄₄₅ Pro Gly Gly
 Gly Gly₄₅₀ Ser Gly Gly Gly₄₅₅ Ser Gln Val Gln Leu₄₆₀ Gln Glu Ser Gly
 Pro Gly Leu Val Lys Pro₄₇₀ Ser Glu Thr Leu Ser₄₇₅ Leu Thr Cys Thr Ile₄₈₀
 Ser Gly Asp Ser Val₄₈₅ Ser Thr Asn Ser Val₄₉₀ Ala Trp Asn Trp Ile₄₉₅ Arg
 Lys Pro Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Ile Gly Arg Thr Tyr₅₁₀ Tyr Arg
 Ser Lys Trp₅₁₅ Tyr Asn Asp Tyr Ala₅₂₀ Val Ser Leu Lys Ser₅₂₅ Arg Val Thr
 Ile Ser₅₃₀ Pro Asp Thr Ser Lys₅₃₅ Asn Gln Phe Ser Leu₅₄₀ Lys Leu Ser Ser
 Val Thr Ala Ala Asp Thr₅₅₀ Ala Val Tyr Tyr Cys₅₅₅ Ala Arg Glu Asp Gly₅₆₀
 Asp Ser Tyr Tyr Arg₅₆₅ Tyr Gly Met Asp Val₅₇₀ Trp Gly Gln Gly Thr₅₇₅ Thr
 Val Thr Val Ser₅₈₀ Ser Ala Ser Thr Lys₅₈₅ Gly Pro Ser Val Phe₅₉₀ Pro Leu

A-1937-WO-PCT_ST25

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 cagccccaa 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 cttccccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat cttgt 645

<210> 1648
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1648

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

A-1937-WO-PCT_ST25

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 accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

A-1937-WO-PCT_ST25

aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcga 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<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

A-1937-WO-PCT_ST25

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
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgcaagcca 120
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agatcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcgacacg 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
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
cggacccttg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
cgggaggaga tgaccaagaa ccaggctcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1320

A-1937-WO-PCT_ST25

cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga 1380
tccgaggtac aactggtgga atcaggtgga ggtttggtgc agccggggag atcgctcagg 1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccgga 1500
gcgcttgaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat 1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg 1620
taccttcaga tgaactcact tcgcgcgga gataccgccg tatactactg cgccaaagtc 1680
tcctacttgt ctacagcttc gtcgctcgac tattggggtc aaggaacgtt ggtcaccgtc 1740
tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 1800
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 1860
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgcctacag 1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2040
gagcccaa at 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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 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> 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

A-1937-WO-PCT_ST25

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 ctccagggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggcacact ggtgtgtctc 420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcgccaag 540
agctatctga gcctgacgcc tgagcagtg aagtcacaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1656

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1656

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
 20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
 35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
 85 90 95

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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1657
 caggtgcagt tacagcagtc gggcgagga 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 cgcgacacg gctgtgtatt actgtgagag aggatattgt 300
 agaagtacca cctgctactt tgactactgg ggccaggga ccctagtcac cgtctcctca 360
 acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480
 aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540
 aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660
 ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
 ctggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 780
 cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
 ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gtgtgaggag 900
 cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
 aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
 cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
 cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260
 agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320
 cactacagc 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 tgcctccacc 1740
 aagggcccat cggcttctcc cctggcacc tcctccaaga gcacctctgg gggcacagcg 1800
 gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1860

A-1937-WO-PCT_ST25

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
 tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 1658
 <211> 680
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1658

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30

Tyr Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttccccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca 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

A-1937-WO-PCT_ST25

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 gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat 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> 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

A-1937-WO-PCT_ST25

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 gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420

A-1937-WO-PCT_ST25

tctgttgtgt 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 cccccaaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc	1440
tgtgcggcat cggggtttac tttcgatgat tatgcatgac attgggtccg gaaagcgctt	1500
ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca	1560
gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt	1620
cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcttac	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> 1664
 <211> 683
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 1664

A-1937-WO-PCT_ST25

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Phe Trp Ser Trp Ile Arg 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

A-1937-WO-PCT_ST25

Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Glu₄₆₀ Val Gln Leu Val
 Glu₄₆₅ Ser Gly Gly Gly Leu₄₇₀ Val Gln Pro Gly Arg₄₇₅ Ser Leu Arg Leu Ser₄₈₀
 Cys Ala Ala Ser Gly₄₈₅ Phe Thr Phe Asp Asp₄₉₀ Tyr Ala Met His Trp₄₉₅ Val
 Arg Lys Ala Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Val Ser Ala Ile₅₁₀ Thr Trp
 Asn Ser Gly₅₁₅ His Ile Asp Tyr Ala₅₂₀ Asp Ser Val Glu Gly₅₂₅ Arg Phe Thr
 Ile Ser₅₃₀ Arg Asp Asn Ala Lys₅₃₅ Asn Ser Leu Tyr Leu₅₄₀ Gln Met Asn Ser

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca	120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa	300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt cccctggca	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> 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 gcagggttatg 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 tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
 aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaaag 540
 agctatctga gcctgacgcc tgagcagtg 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

A-1937-WO-PCT_ST25

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Lys Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1669
<211> 2034
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1669
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggaagccc 120
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 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 tcttctctct cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

A-1937-WO-PCT_ST25

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 ctcattgctcc gtgatgcatg aggctctgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag 1380
gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccg 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 actgtgagag aagtaactgg 1680
ggtcttgact actggggcca ggaaccctg gtcaccgtct ctagtgctc caccaagggc 1740
ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgcgtggaa ctcaggcgcc 1860
ctgaccagcg gcgtgcacac cttcccggt gtcctacagt cctcaggact ctactccctc 1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1980
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc 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

A-1937-WO-PCT_ST25

Lys Leu Ser Ser Val₈₅ Thr Ala Ala Asp Thr₉₀ Ala Val Tyr Tyr Cys₉₅ Ala
 Arg Glu Thr Gly₁₀₀ Ser Tyr Tyr Gly Phe₁₀₅ Asp Tyr Trp Gly Gln₁₁₀ Gly Thr
 Leu Val Thr₁₁₅ Val Ser Ser Thr Val₁₂₀ Ala Ala Pro Ser Val₁₂₅ Phe Ile Phe
 Pro Pro₁₃₀ Ser Asp Glu Gln Leu₁₃₅ Lys Ser Gly Thr Ala₁₄₀ Ser Val Val Cys
 Leu₁₄₅ Leu Asn Asn Phe Tyr₁₅₀ Pro Arg Glu Ala Lys₁₅₅ Val Gln Trp Lys Val₁₆₀
 Asp Asn Ala Leu Gln₁₆₅ Ser Gly Asn Ser Gln₁₇₀ Glu Ser Val Thr Glu₁₇₅ Gln
 Asp Ser Lys Asp₁₈₀ Ser Thr Tyr Ser Leu₁₈₅ Lys Ser Thr Leu Thr₁₉₀ Leu Ser
 Lys Ala Asp₁₉₅ Tyr Glu Lys His Lys₂₀₀ Val Tyr Ala Cys Glu₂₀₅ Val Thr His
 Gln Gly₂₁₀ Leu Ser Ser Pro Val₂₁₅ Thr Lys Ser Phe Asn₂₂₀ Arg Gly Glu Cys
 Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀
 Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
 Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val

A-1937-WO-PCT_ST25

Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Glu₄₆₀ Val Gln Leu Val
 Gln₄₆₅ Ser Gly Ala Glu Val₄₇₀ Lys Lys Pro Gly Glu₄₇₅ Ser Leu Lys Ile Ser₄₈₀
 Cys Lys Thr Ser Glu₄₈₅ Tyr Ser Phe Thr Ser₄₉₀ Tyr Trp Ile Gly Trp₄₉₅ Val
 Arg Lys Met Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Met Gly Ile Ile₅₁₀ Tyr Leu
 Gly Asp Ser₅₁₅ Asp Thr Arg Tyr Ser₅₂₀ Pro Ser Phe Gln Gly₅₂₅ Gln Val Thr
 Ile Ser₅₃₀ Ala Asp Lys Ser Ile₅₃₅ Ser Thr Ala Tyr Leu₅₄₀ Gln Trp Ser Ser
 Leu₅₄₅ Lys Ala Ser Asp Thr₅₅₀ Ala Met Tyr Tyr Cys₅₅₅ Ala Arg Ser Asn Trp₅₆₀
 Gly Leu Asp Tyr Trp₅₆₅ Gly Gln Gly Thr Leu₅₇₀ Val Thr Val Ser Ser₅₇₅ Ala
 Ser Thr Lys Gly₅₈₀ Pro Ser Val Phe Pro₅₈₅ Leu Ala Pro Ser Ser₅₉₀ Lys Ser
 Thr Ser Gly₅₉₅ Gly Thr Ala Ala Leu₆₀₀ Gly Cys Leu Val Lys₆₀₅ Asp Tyr Phe
 Pro Glu₆₁₀ Pro Val Thr Val Ser₆₁₅ Trp Asn Ser Gly Ala₆₂₀ Leu Thr Ser Gly

A-1937-WO-PCT_ST25

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 tgaccagtc 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 cccctcggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggagaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

A-1937-WO-PCT_ST25

cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-W0-PCT_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 1675
 <211> 2070
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1675
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 acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
 aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
 agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
 gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
 cagttgaaat ctggaactgc ctctgttgtg tgcctgctga ataacttcta tcccagagag 480
 gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540
 acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600
 gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660
 cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctacacatg cccaccgtgc 720
 ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac 780
 accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt 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 acaggtgtac 1080
 accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1140
 aaaggcttct atcccagca catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200
 aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttct ctatagcaag 1260
 ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1320
 gaggtctctg acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga 1380
 tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggagggtt ggtgcagccg 1440
 gggagatcgc tcaggcttag ctgtgcggca tcggggttta ctttcgatga ttatgcgatg 1500
 cattgggtcc ggaaagcgcc tggaaaaggg ctcgagtggg tttccgcat tacgtggaat 1560

A-1937-WO-PCT_ST25

agcggacaca tcgattatgc agacagtgtg gagggcagat tcacaatctc acgagacaat 1620
gctaagaaca gcctgtacct tcagatgaac tcacttcgcg cggaagatac cgccgtatac 1680
tactgcgcca aagtctccta cttgtctaca gcttcgtcgc tcgactattg gggtaagga 1740
acgttgggtca ccgtctctag tgcctccacc aagggcccat cggctcttccc cctggcaccc 1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 1860
cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 1920
ccggctgtcc tacagtcctc aggactctac tccctcgaga gcgtgggtgac cgtgccctcc 1980
agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 2040
gtggacaaga aagttgagcc caaatcttgt 2070

<210> 1676
<211> 690
<212> PRT
<213> 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
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

A-1937-WO-PCT_ST25

Ala Lys Val Gln Trp₁₆₅ Lys Val Asp Asn Ala₁₇₀ Leu Gln Ser Gly Asn₁₇₅ Ser
Gln Glu Ser Val₁₈₀ Thr Glu Gln Asp Ser₁₈₅ Lys Asp Ser Thr Tyr₁₉₀ Ser Leu
Lys Ser Thr₁₉₅ Leu Thr Leu Ser Lys₂₀₀ Ala Asp Tyr Glu Lys₂₀₅ His Lys Val
Tyr Ala₂₁₀ Cys Glu Val Thr His₂₁₅ Gln Gly Leu Ser Ser₂₂₀ Pro Val Thr Lys
Ser₂₂₅ Phe Asn Arg Gly Glu₂₃₀ Cys Asp Lys Thr His₂₃₅ Thr Cys Pro Pro Cys₂₄₀
Pro Ala Pro Glu Leu₂₄₅ Leu Gly Gly Pro Ser₂₅₀ Val Phe Leu Phe Pro₂₅₅ Pro
Lys Pro Lys Asp₂₆₀ Thr Leu Met Ile Ser₂₆₅ Arg Thr Pro Glu Val₂₇₀ Thr Cys
Val Val Val₂₇₅ Asp Val Ser His Glu₂₈₀ Asp Pro Glu Val Lys₂₈₅ Phe Asn Trp
Tyr Val₂₉₀ Asp Gly Val Glu Val₂₉₅ His Asn Ala Lys Thr₃₀₀ Lys Pro Cys Glu
Glu₃₀₅ Gln Tyr Gly Ser Thr₃₁₀ Tyr Arg Cys Val Ser₃₁₅ Val Leu Thr Val Leu₃₂₀
His Gln Asp Trp Leu₃₂₅ Asn Gly Lys Glu Tyr₃₃₀ Lys Cys Lys Val Ser₃₃₅ Asn
Lys Ala Leu Pro₃₄₀ Ala Pro Ile Glu Lys₃₄₅ Thr Ile Ser Lys Ala₃₅₀ Lys Gly
Gln Pro Arg₃₅₅ Glu Pro Gln Val Tyr₃₆₀ Thr Leu Pro Pro Ser₃₆₅ Arg Glu Glu
Met Thr₃₇₀ Lys Asn Gln Val Ser₃₇₅ Leu Thr Cys Leu Val₃₈₀ Lys Gly Phe Tyr
Pro₃₈₅ Ser Asp Ile Ala Val₃₉₀ Glu Trp Glu Ser Asn₃₉₅ Gly Gln Pro Glu Asn₄₀₀
Asn Tyr Lys Thr Thr₄₀₅ Pro Pro Val Leu Asp₄₁₀ Ser Asp Gly Ser Phe₄₁₅ Phe
Leu Tyr Ser Lys₄₂₀ Leu Thr Val Asp Lys₄₂₅ Ser Arg Trp Gln Gln₄₃₀ Gly Asn

A-1937-WO-PCT_ST25

Val Phe Ser₄₃₅ Cys Ser Val Met₄₄₀ His₄₄₀ Glu Ala Leu His Asn₄₄₅ His Tyr Thr
 Gln Lys₄₅₀ Ser Leu Ser Leu Ser₄₅₅ Pro Gly Gly Gly₄₆₀ Ser Gly Gly Gly
 Gly₄₆₅ Ser Glu Val Gln Leu₄₇₀ Val Glu Ser Gly Gly₄₇₅ Gly Leu Val Gln Pro₄₈₀
 Gly Arg Ser Leu Arg₄₈₅ Leu Ser Cys Ala Ala₄₉₀ Ser Gly Phe Thr Phe₄₉₅ Asp
 Asp Tyr Ala Met₅₀₀ His Trp Val Arg Lys₅₀₅ Ala Pro Gly Lys Gly₅₁₀ Leu Glu
 Trp Val Ser₅₁₅ Ala Ile Thr Trp Asn₅₂₀ Ser Gly His Ile Asp₅₂₅ Tyr Ala Asp
 Ser Val₅₃₀ Glu Gly Arg Phe Thr₅₃₅ Ile Ser Arg Asp Asn₅₄₀ Ala Lys Asn Ser
 Leu Tyr Leu Gln Met₅₅₀ Asn Ser Leu Arg Ala Glu₅₅₅ Asp Thr Ala Val Tyr₅₆₀
 Tyr Cys Ala Lys Val₅₆₅ Ser Tyr Leu Ser Thr₅₇₀ Ala Ser Ser Leu Asp₅₇₅ Tyr
 Trp Gly Gln Gly₅₈₀ Thr Leu Val Thr Val₅₈₅ Ser Ser Ala Ser Thr₅₉₀ Lys Gly
 Pro Ser Val₅₉₅ Phe Pro Leu Ala Pro₆₀₀ Ser Ser Lys Ser Thr₆₀₅ Ser Gly Gly
 Thr Ala₆₁₀ Ala Leu Gly Cys Leu₆₁₅ Val Lys Asp Tyr Phe₆₂₀ Pro Glu Pro Val
 Thr Val Ser Trp Asn Ser₆₃₀ Gly Ala Leu Thr Ser₆₃₅ Gly Val His Thr Phe₆₄₀
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr₆₅₀ Ser Leu Glu Ser Val₆₅₅ Val
 Thr Val Pro Ser₆₆₀ Ser Ser Leu Gly Thr₆₆₅ Gln Thr Tyr Ile Cys₆₇₀ Asn Val
 Asn His Lys₆₇₅ Pro Ser Asn Thr Lys₆₈₀ Val Asp Lys Lys Val₆₈₅ Glu Pro Lys
 Ser Cys₆₉₀

<210> 1677
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1677
 gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccggt 180
 gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
 atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
 cctctcactt tcggcggagg gaccaagggtg gagatcaaac gagcctccac caagggccca 360
 tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggccctgggc 420
 tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
 agcgtgggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctaccgagg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccagggtc 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

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 cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgtttgtg tgcctgctga ataacttcta tcccagagag	480
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc	540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa	600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	660
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac	780
accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt 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 catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga	1380
tcgggagggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc	1440
ggggagtctc tgaagatctc ctgtaagact tctgaatata gctttaccag ctactggatc	1500
ggctgggtgc gcaagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttgg	1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag	1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctctgac tactggggcc agggaaccct ggtcaccgtc	1740
tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc	1800
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1860
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc	1980

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2040
gagcccaaatt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccggggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

A-1937-WO-PCT_ST25

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg 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

A-1937-WO-PCT_ST25

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 accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca ggaatccgg aattacctg catggtatca ggaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgcccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat 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> 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

A-1937-WO-PCT_ST25

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 catcggggtt tactttcgat gattatgcga tgcattgggt ccggaaagcg 120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtgcccca ccaagggccc atcggctctc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480

A-1937-WO-PCT_ST25

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac	900
ggcagcacgt accgtttgtgt 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 cggatcccag	1380
gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc	1440
tgcgctgtcc atggtgggtc cttcagtggg tactactgga actggattcg caagccacca	1500
gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaaccg	1560
tccctcaaga gtcgagtcac catatcatta gacacgtcca agaaccagtt ctccctgacg	1620
ctgacctctg tgaccgccgc ggacacggct gtgtattact gtgagagagg atattgtaga	1680
agtaccacct gctactttga ctactggggc cagggaaccc tagtcaccgt ctctcaact	1740
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact	1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag	1860
gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag	1920
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac	1980
aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc	2040
aacaggggag agtgt	2055

<210> 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	

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
 290 295 300
 Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
 450 455 460
 Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr
 465 470 475 480
 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

A-1937-WO-PCT_ST25

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 gagtgttaga agcagttact tagcctggta ccaggagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aagggtggaca agaaagttga gcccaaattct 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 cgctttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat 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> 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

```

A-1937-WO-PCT_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1693
<211> 2049
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1693
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggaagcg 120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagt tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgctta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
agtgcctcca ccaagggccc atcgggtctt 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 cctcatgat ctcccggacc 780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020

A-1937-WO-PCT_ST25

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
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gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 1440
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ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc 1560
tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620
ctgagctctg tgaccgctgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680
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gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 1860
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 1920
acctacagcc tcgaaagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 1980
tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 2040
ggagagtgt 2049

<210> 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

A-1937-WO-PCT_ST25

Leu Gln Met Asn Ser₈₅ Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys
 Ala Lys Val Ser₁₀₀ Tyr Leu Ser Thr Ala₁₀₅ Ser Ser Leu Asp Tyr₁₁₀ Trp Gly
 Gln Gly Thr₁₁₅ Leu Val Thr Val Ser₁₂₀ Ser Ala Ser Thr Lys₁₂₅ Gly Pro Ser
 Val Phe₁₃₀ Pro Leu Ala Pro Ser₁₃₅ Ser Lys Ser Thr Ser₁₄₀ Gly Gly Thr Ala
 Ala₁₄₅ Leu Gly Cys Leu Val₁₅₀ Lys Asp Tyr Phe Pro₁₅₅ Glu Pro Val Thr Val₁₆₀
 Ser Trp Asn Ser Gly₁₆₅ Ala Leu Thr Ser Gly₁₇₀ Val His Thr Phe Pro₁₇₅ Ala
 Val Leu Gln Ser₁₈₀ Ser Gly Leu Tyr Ser₁₈₅ Leu Lys Ser Val Val₁₉₀ Thr Val
 Pro Ser Ser₁₉₅ Ser Leu Gly Thr Gln₂₀₀ Thr Tyr Ile Cys Asn₂₀₅ Val Asn His
 Lys Pro₂₁₀ Ser Asn Thr Lys Val₂₁₅ Asp Lys Lys Val Glu₂₂₀ Pro Lys Ser Cys
 Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀
 Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
 Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val

A-1937-WO-PCT_ST25

Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Gln₄₆₀ Val Gln Leu Gln
 Glu₄₆₅ Ser Gly Pro Gly Leu₄₇₀ Val Lys Pro Ser Glu₄₇₅ Thr Leu Ser Leu Thr₄₈₀
 Cys Thr Val Ser Gly₄₈₅ Gly Ser Ile Ser Ser₄₉₀ Tyr Phe Trp Ser Trp₄₉₅ Ile
 Arg Lys Pro Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Ile Gly Tyr Ile₅₁₀ Tyr Tyr
 Ser Gly Gln₅₁₅ Thr Lys Tyr Asn Pro₅₂₀ Ser Leu Lys Ser Arg₅₂₅ Val Thr Ile
 Ser Ile₅₃₀ Asp Thr Ser Lys Asn₅₃₅ Gln Phe Ser Leu Lys₅₄₀ Leu Ser Ser Val
 Thr₅₄₅ Ala Ala Asp Thr Ala₅₅₀ Val Tyr Tyr Cys Ala₅₅₅ Arg Glu Thr Gly Ser₅₆₀
 Tyr Tyr Gly Phe Asp₅₆₅ Tyr Trp Gly Gln Gly₅₇₀ Thr Leu Val Thr Val₅₇₅ Ser
 Ser Thr Val Ala₅₈₀ Ala Pro Ser Val Phe₅₈₅ Ile Phe Pro Pro Ser₅₉₀ Asp Glu
 Gln Leu Lys₅₉₅ Ser Gly Thr Ala Ser₆₀₀ Val Val Cys Leu Leu₆₀₅ Asn Asn Phe
 Tyr Pro₆₁₀ Arg Glu Ala Lys Val₆₁₅ Gln Trp Lys Val Asp₆₂₀ Asn Ala Leu Gln

A-1937-WO-PCT_ST25

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 tgaccagtc 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 cccctcggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 accatcgctg 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 gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

A-1937-WO-PCT_ST25

cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1699
<211> 2070
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1699
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggaagcg 120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgctta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540
tcaggactct actccctcaa aagcgtggtg 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
cctgaggtca catgctggtt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggag 1080
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggaagaaa actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcattgctc gtgatgcatg aggtcttgca 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

A-1937-WO-PCT_ST25

gattatgcag tttctctgaa aagtcgagta accatcagcc cagacacatc caagaaccag 1620
 ttctccctga agctgagctc tgtgactgcc gcggacacgg ctgtgtatta ctgtgcaaga 1680
 gaggatgggg atagctacta ccgctacggt atggacgtct ggggccaagg gaccacggtc 1740
 accgtctcct caactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 1800
 ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860
 aaagtacagt ggaagggtga 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

A-1937-WO-PCT_ST25

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
290 295 300

Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagg 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 gtgacggtgt cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
 agcgtgggtga ccgtgccctc cagcagcttg ggcaccaga 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

A-1937-WO-PCT_ST25

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
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccagggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 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 ccggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg	120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tggggctcttg actactgggg ccagggaaacc ctggtcaccg tctctagtgc ctccaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac	660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc gtcagtcttc	720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	840
gtggagggtgc ataatgcaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt	900
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctcaa 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 gcagggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat ccaggtgca gttacagcag	1380
tcgggcgag gactgttgaa gccttcggag accctgtccc tcacctgcgc tgtccatggt	1440
gggtccttca gtggttacta ctggaactgg attcgcaagc caccagggaa ggggctagag	1500
tggattgggg aaatcaatca tgctggaaac accaactaca acccgctcct caagagtcga	1560
gtcaccatat cattagacac gtccaagaac cagttctccc tgacgtgac ctctgtgacc	1620
gccgcggaca cggctgtgta ttactgtgag agaggatatt gtagaagtac cacctgctac	1680
tttgactact ggggccaggg aaccctagtc accgtctcct caactgtggc tgcaccatct	1740
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc	1800
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgcctc	1860
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc	1920
ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	1980

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 2040

<210> 1706
 <211> 680
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1706

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

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

A-1937-WO-PCT_ST25

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 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

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300

A-1937-WO-PCT_ST25

gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt 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 gcccaaattct 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

A-1937-WO-PCT_ST25

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1709
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1709
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120
tttccaggaa cagccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggctc 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 tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 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

A-1937-WO-PCT_ST25

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
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccaggaacc ctgggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

A-1937-WO-PCT_ST25

ctcaaaagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tgggggggacc	gtcagtcttc	720
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtggtggtgg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
gtggaggtgc	ataatgccaa	gacaaagccg	tgtgaggagc	agtacggcag	cacgtaccgt	900
tgtgtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	960
aaggtctcca	acaaagccct	cccagccccc	atcgagaaaa	ccatctccaa	agccaaaggg	1020
cagccccgag	aaccacaggt	gtacaccctg	cccccatccc	gggaggagat	gaccaagaac	1080
caggtcagcc	tgacctgcct	ggtcaaaggc	ttctatccca	gcgacatcgc	cgtggagtgg	1140
gagagcaatg	ggcagccgga	gaacaactac	aagaccacgc	ctcccgtgct	ggactccgac	1200
ggctccttct	tcctctatag	caagctcacc	gtggacaaga	gcaggtggca	gcaggggaac	1260
gtcttctcat	gctccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1320
tcctgtctc	cgggtggtgg	cggatcggga	ggtggcggat	cccaggtgca	gctgcaggag	1380
tcgggcccag	gactggtgaa	gccttcggag	accctgtccc	tcacctgcac	tgtctctggt	1440
ggctccatca	gtagttactt	ctggagctgg	attcggaagc	cccaggttaa	gggactggag	1500
tggattggct	atatctatta	cagtgggcag	accaaataca	accctccct	caagagtcga	1560
gtcaccatat	caatagacac	gtccaagaac	cagttctccc	tgaagctgag	ctctgtgacc	1620
gctgcggaca	cggccgtgta	ttactgtgcg	agagaaactg	ggagctacta	cggctttgac	1680
tactggggcc	agggaaacct	ggtcaccgtc	tcctcaactg	tggctgcacc	atctgtcttc	1740
atcttcccc	catctgatga	gcagttgaaa	tctggaactg	cctctgttgt	gtgcctgctg	1800
aataacttct	atcccagaga	ggccaaagta	cagtgggaagg	tggataacgc	cctccaatcg	1860
ggtaactccc	aggagagtgt	cacagagcag	gacagcaagg	acagcaccta	cagcctcgaa	1920
agcaccctga	cgctgagcaa	agcagactac	gagaaacaca	aagtctacgc	ctgcgaagtc	1980
acccatcagg	gcctgagctc	gcccgtcaca	aagagcttca	acaggggaga	gtgt	2034

<210> 1712
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1712

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	

Ser	Leu	Lys	Ile	Ser	Cys	Lys	Thr	Ser	Glu	Tyr	Ser	Phe	Thr	Ser	Tyr
			20					25					30		

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac 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> 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

A-1937-WO-PCT_ST25

<400> 1715
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1716
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1716

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15
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

A-1937-WO-PCT_ST25

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Glu Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1717
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1717
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc 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
aaggcttcca acaaagccct ccagcccc atcgagaaaa ccatctcaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

A-1937-WO-PCT_ST25

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
 tcagggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
 gacagtgtct ctaccaacag tgttgcttgg aactggatta ggaagccccc agggaaaggc 1500
 cttgagtggg taggaaggac atactacagg tccaagtggg 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 catcttcccg ccatctgatg agcagttgaa atctggaact 1800
 gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860
 gtggataacg ccctccaatc gggtaactcc caggagagtg tcacagagca ggacagcaag 1920
 gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980
 aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc 2040
 aacaggggag agtgt 2055

<210> 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

A-1937-WO-PCT_ST25

Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val
 Thr Val Ser₁₁₅ Ser Ala Ser Thr Lys₁₂₀ Gly Pro Ser Val Phe₁₂₅ Pro Leu Ala
 Pro Ser₁₃₀ Ser Lys Ser Thr Ser₁₃₅ Gly Gly Thr Ala Ala₁₄₀ Leu Gly Cys Leu
 Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀
 Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser
 Gly Leu Tyr Ser₁₈₀ Leu Lys Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Cys Glu Glu Gln Tyr₂₉₅ Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val
 Leu Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro
 Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc 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 gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcgggtcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtgggtga ccgtgccctc cagcagcttg ggcaccaga 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

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300

gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg 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 tccatgggtg gtccttcagt ggttactact ggaactggat ccgcaagcca 120
ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcacctt 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
aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900
agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg 1320
cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggta 1380
caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgtcag gcttagctgt 1440
gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggtccggaa agcgccctgga 1500
aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560
agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctctacttg 1680

A-1937-WO-PCT_ST25

tctacagctt	cgtcgctcga	ctattggggt	caaggaacgt	tggtcaccgt	ctctagtact	1740
gtggctgcac	catctgtctt	catcttcccg	ccatctgatg	agcagttgaa	atctggaact	1800
gcctctgttg	tgtgcctgct	gaataacttc	tatcccagag	aggccaaagt	acagtggaag	1860
gtggataacg	ccctccaatc	gggtaactcc	caggagagtg	tcacagagca	ggacagcaag	1920
gacagcacct	acagcctcga	aagcaccctg	acgctgagca	aagcagacta	cgagaaacac	1980
aaagtctacg	cctgcgaagt	cacccatcag	ggcctgagct	cgcccgtcac	aaagagcttc	2040
aacaggggag	agtg					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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa      300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg 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

```

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg 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> 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

A-1937-WO-PCT_ST25

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

cagggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgcaagcca 120

ccagggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180

A-1937-WO-PCT_ST25

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	gacggtgtcg	480
tggaactcag	gcgccctgac	cagcggcgtg	cacaccttcc	cggctgtcct	acagtcctca	540
ggactctact	ccctcaaaag	cgtggtgacc	gtgccctcca	gcagcttggg	caccagacc	600
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	660
aaatcttgtg	acaaaactca	cacatgcccc	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcatgatctc	ccggaccctt	780
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	840
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgtgtgagga	gcagtacggc	900
agcacgtacc	gttgtgtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	960
gagtacaagt	gcaaggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1020
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccgggaggag	1080
atgaccaaga	accaggtcag	cctgacctgc	ctgggtcaaag	gcttctatcc	cagcgacatc	1140
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	1200
ctggactccg	acggctcctt	cttcctctat	agcaagctca	ccgtggacaa	gagcaggtgg	1260
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	1320
cagaagagcc	tctccctgtc	tccgggtggt	ggcggatcgg	gaggtggcgg	atccgaggtg	1380
cagctggtgc	agtctggagc	agaggtgaaa	aagcccgggg	agtctctgaa	gatctcctgt	1440
aagacttctg	aatacagctt	taccagctac	tggatcggct	gggtgcgcaa	gatgcccggg	1500
aaaggcctgg	agtggatggg	gatcatctat	cttgggtgact	cagataccag	atacagcccg	1560
tccttccaag	gccaggtcac	catctcagcc	gacaagtcca	tcagtaccgc	ctacctgcag	1620
tggagcagcc	tgaaggcctc	ggacaccgcc	atgtattact	gtgcgagaag	taactggggg	1680
cttgactact	ggggccaggg	aaccctggtc	accgtctcta	gtcagcccaa	ggccaacccc	1740
actgtcactc	tgttcccgcc	ctcctctgag	gagctccaag	ccaacaaggc	cacactagtg	1800
tgtctgatca	gtgacttcta	cccgggagct	gtgacagtgg	cctggaaggc	agatggcagc	1860
cccgtcaagg	cgggagtgga	gaccacaaa	ccctccaaac	agagcaacaa	caagtacgcg	1920
gccgagagct	acctgagcct	gacgcccag	cagtggaagt	cccacagaag	ctacagctgc	1980
caggtcacgc	atgaaggggag	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

A-1937-WO-PCT_ST25

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
290 295 300

Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg 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

A-1937-WO-PCT_ST25

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 cagccccaa 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 cagcgccctt gggctgcctg 420

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480

ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactcctt caaaagcgtg 540

A-1937-WO-PCT_ST25

gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga 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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1735
<211> 2049
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1735
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat ccggaagccc 120
ccaggtaagg gactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180
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
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggg gaccgtgccc tccagcagct tgggcacca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780

A-1937-WO-PCT_ST25

acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgtttgtg	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	ggtacaactg	1380
gtggaatcag	gtggaggttt	ggtgcagccg	gggagatcgc	tcaggcttag	ctgtgcggca	1440
tcggggttta	ctttcgatga	ttatgcatg	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	gggtcaagga	acgttggtca	ccgtctctag	tactgtggct	1740
gcaccatctg	tcttcatctt	cccgccatct	gatgagcagt	tgaaatctgg	aactgcctct	1800
gttgtgtgcc	tgctgaataa	cttctatccc	agagaggcca	aagtacagtg	gaaggtggat	1860
aacgccctcc	aatcgggtaa	ctcccaggag	agtgtcacag	agcaggacag	caaggacagc	1920
acctacagcc	tcgaaagcac	cctgacgtg	agcaaagcag	actacgagaa	acacaaagtc	1980
tacgcctgcg	aagtcaccca	tcagggcctg	agctcgcccc	tcacaaagag	cttcaacagg	2040
ggagagtgt						2049

<210> 1736
 <211> 683
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1736

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1			5						10					15	

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
			20					25					30		

Phe	Trp	Ser	Trp	Ile	Arg	Lys	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40					45			

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu
 Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys
 Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser
 Asn Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀
 Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser
 Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala
 Leu His Asn₄₃₅ His Tyr Thr Gln Lys₄₄₀ Ser Leu Ser Leu Ser₄₄₅ Pro Gly Gly
 Gly Gly₄₅₀ Ser Gly Gly Gly₄₅₅ Ser Glu Val Gln Leu₄₆₀ Val Glu Ser Gly
 Gly Gly₄₆₅ Leu Val Gln Pro₄₇₀ Gly Arg Ser Leu Arg₄₇₅ Leu Ser Cys Ala Ala₄₈₀
 Ser Gly Phe Thr Phe₄₈₅ Asp Asp Tyr Ala Met₄₉₀ His Trp Val Arg Lys₄₉₅ Ala
 Pro Gly Lys Gly₅₀₀ Leu Glu Trp Val Ser₅₀₅ Ala Ile Thr Trp Asn₅₁₀ Ser Gly
 His Ile Asp₅₁₅ Tyr Ala Asp Ser Val₅₂₀ Glu Gly Arg Phe Thr₅₂₅ Ile Ser Arg
 Asp Asn₅₃₀ Ala Lys Asn Ser Leu₅₃₅ Tyr Leu Gln Met Asn₅₄₀ Ser Leu Arg Ala
 Glu Asp Thr Ala Val Tyr₅₅₀ Tyr Cys Ala Lys Val₅₅₅ Ser Tyr Leu Ser Thr₅₆₀
 Ala Ser Ser Leu Asp₅₆₅ Tyr Trp Gly Gln Gly₅₇₀ Thr Leu Val Thr Val₅₇₅ Ser
 Ser Thr Val Ala₅₈₀ Ala Pro Ser Val Phe₅₈₅ Ile Phe Pro Pro Ser₅₉₀ Asp Glu

A-1937-W0-PCT_ST25

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 accatcgctc 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 ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

A-1937-WO-PCT_ST25

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg 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> 1740

<211> 214

<212> PRT

<213> Artificial Sequence

<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

A-1937-WO-PCT_ST25

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 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 catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga 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
taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctcca 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 cagcagaag 1320

A-1937-WO-PCT_ST25

agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtgcagctg 1380
 gtgcagtctg gagcagaggt gaaaaagccc ggggagtctc tgaagatctc ctgtaagact 1440
 tctgaataca gctttaccag ctactggatc ggctgggtgc gcaagatgcc cgggaaaggc 1500
 ctggagtgga tggggatcat ctatcttggt gactcagata ccagatacag cccgtccttc 1560
 caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc 1620
 agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctttgac 1680
 tactggggcc agggaaacct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc 1740
 actctgttcc cgccctcctc tgaggagctc caagccaaca aggccacact agtgtgtctg 1800
 atcagtgact tctaccggg agctgtgaca gtggcctgga aggcagatgg cagccccgtc 1860
 aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccgag 1920
 agctacctga gcctgacgcc cgagcagtgg aagtcccaca gaagctacag ctgccaggtc 1980
 acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 2031

<210> 1742
 <211> 677
 <212> PRT
 <213> Artificial Sequence

<220>
 <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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val 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
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggaataa 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 tctactcctt caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 1744
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1744

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Glu Phe Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

A-1937-WO-PCT_ST25

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
165 170 175

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 1745
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1745
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc 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

A-1937-WO-PCT_ST25

<220>

<223> Synthetic polynucleotide

<400> 1747

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc	60
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 ccatcggctt tccccctggc accctcctcc	420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt	540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttctc tttccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
ccatccccgg 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 ggtggaggtt tgggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcggggttt actttcgatg attatgcat gcattgggtc	1500
cggaaagcgc ctggaaaagg gctcagagtgg gtttccgcca ttacgtggaa tagcggacac	1560
atcgattatg cagacagtgt ggagggcaga ttcacaatct cacgagacaa tgctaagaac	1620
agcctgtacc ttcagatgaa ctcaattcgc gcggaagata ccgccgtata ctactgcgc	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

A-1937-WO-PCT_ST25

gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980
gactacgaga aacacaaagt 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

A-1937-WO-PCT_ST25

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 210 215 220
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 290 295 300
 Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 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

A-1937-WO-PCT_ST25

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 accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg

60

A-1937-WO-PCT_ST25

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 cccctggca 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> 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1751
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1751
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca tttactgggc atctaccgga 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gaacgggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
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

A-1937-WO-PCT_ST25

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

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttggaa ctggatcagg 120

aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180

aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240

cagttctccc tgaagctgag ctctgtgact gccgcggaca cggtgtgta ttactgtgca 300

A-1937-WO-PCT_ST25

agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc accctcctcc	420
aagagcacct ctggggggcac agcgggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct	540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttctc ttcccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
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
accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgcaagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680
agaagtaact ggggtcttga ctactggggc cagggaaacc ttggtaccgt ctctagtcag	1740
cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac	1800
aaggccacac tagtgtgtct gatcagtgac ttctaccgg gagctgtgac agtggcctgg	1860
aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc	1920
aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtccac	1980
agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct	2040
acagaatggt ca	2052

<210> 1754
 <211> 684
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1754

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
 20 25 30
 Ser Val Ala Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Glu Asp Gly Asp Ser Tyr Tyr Arg Tyr Gly Met
 100 105 110
 Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135 140
 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

A-1937-WO-PCT_ST25

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr
 290 295 300
 Gly Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 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

A-1937-WO-PCT_ST25

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 caaggttaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc 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 tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt

<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 tacttttcgat gattatgcga tgcattgggt ccggaagcg 120
 cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
 tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct 360
 agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct 420
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480
 tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540
 agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600
 aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaag 660
 agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
 ctcttggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 780
 tcccggaccc ctgaggtcac atgctggtg 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
 acgctccccg tgctggactc cgacggctcc ttcttctct 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 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 aggaaccct agtcaccgtc 1740

A-1937-WO-PCT_ST25

tcctcaactg tggctgcacc atctgtcttc atcttcccg	catctgatga gcagttgaaa	1800
tctggaactg cctctgttgt gtgcctgctg aataacttct	atcccagaga ggccaaagta	1860
cagtgggaagg tggataacgc cctccaatcg ggtaactccc	aggagagtgt cacagagcag	1920
gacagcaagg acagcaccta cagcctcgaa agcaccctga	cgctgagcaa agcagactac	1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg	gcctgagctc gcccgtcaca	2040
aagagcttca acaggggaga gtgt		2064

<210> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Leu Ser Pro Gly Gly Gly Ser 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

A-1937-WO-PCT_ST25

<400> 1759
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 ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 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 ttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctctcca 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> 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

A-1937-WO-PCT_ST25

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
gagggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgctg catcgggggt tactttcgat gattatgcga tgcattgggt ccggaagcg 120
cctggaaaag ggctcgagt ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

A-1937-WO-PCT_ST25

cttcagatga	actcacttcg	cgcggaagat	accgccgtat	actactgcg	caaagtctcc	300
tacttgtcta	cagcttcgtc	gctcgactat	tgggggtcaag	gaacgttggt	caccgtctct	360
agtacggtgg	ctgcaccatc	tgtcttcac	ttcccgccat	ctgatgagca	gttgaaatct	420
ggaactgcct	ctgttgtgtg	cctgctgaat	aacttctatc	ccagagaggc	caaagtacag	480
tggaaggtgg	ataacgccct	ccaatcgggt	aactcccagg	agagtgtcac	agagcaggac	540
agcaaggaca	gcacctacag	cctcaagagc	accctgacgc	tgagcaaagc	agactacgag	600
aaacacaaaag	tctacgcctg	cgaagtcacc	catcagggcc	tgagctcgcc	cgtcacaaaag	660
agcttcaaca	ggggagagt	tgacaaaact	cacacatgcc	caccgtgccc	agcacctgaa	720
ctcctggggg	gaccgtcagt	cttcctcttc	ccccaaaaac	ccaaggacac	cctcatgatc	780
tcccggaccc	ctgaggtcac	atgctgtgtg	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	ttcttctctt	atagcaagct	caccgtggac	1260
aagagcaggt	ggcagcaggg	gaacgtcttc	tcattgtccg	tgatgcatga	ggctctgcac	1320
aaccactaca	cgagaagag	cctctccctg	tctccgggtg	gtggcggatc	gggaggtggc	1380
ggatcccagg	tgcagctgca	ggagtcgggc	ccaggactgg	tgaagccttc	ggagaccctg	1440
tccctcacct	gcactgtctc	tggtggctcc	atcagtagtt	acttctggag	ctggattcgg	1500
aagccccccag	gtaagggact	ggagtggatt	ggctatatct	attacagtgg	gcagacccaa	1560
tacaaccctc	ccctcaagag	tcgagtcacc	atatcaatag	acacgtccaa	gaaccagttc	1620
tccctgaagc	tgagctctgt	gaccgtgcg	gacacggccg	tgtattactg	tgcgagagaa	1680
actgggagct	actacggctt	tgactactgg	ggccagggaa	ccctgggtcac	cgtctcctca	1740
actgtggctg	caccatctgt	cttcattctt	ccgccatctg	atgagcagtt	gaaatctgga	1800
actgcctctg	ttgtgtgcct	gctgaataac	ttctatccca	gagaggccaa	agtacagtgg	1860
aaggtggata	acgccctcca	atcgggtaac	tcccaggaga	gtgtcacaga	gcaggacagc	1920
aaggacagca	cctacagcct	cgaaagcacc	ctgacgtgta	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

A-1937-WO-PCT_ST25

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
290 295 300

Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300

gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt cccctggga 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420

ttccccgaac cggtgacggg gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540

A-1937-WO-PCT_ST25

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
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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac ttactctca caatttcag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
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 tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaactt tgt 633

<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

A-1937-WO-PCT_ST25

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 catcggggtt 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 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
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgatc 780

A-1937-WO-PCT_ST25

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	cgagaagag	cctctccctg	tctccgggtg	gtggcggatc	gggaggtggc	1380
ggatcccagg	tacagttgca	ggagtcaggt	ccaggactgg	tgaagccctc	ggagaccctc	1440
tcactcacct	gtaccatctc	cggggacagt	gtctctacca	acagtgttgc	ttggaactgg	1500
attaggaagc	cccaggggaa	aggccttgag	tggataggaa	ggacatacta	caggtccaag	1560
tggtataatg	attatgcagt	ttctctgaaa	agtcgagtaa	ccatcagccc	agacacatcc	1620
aagaaccagt	tctccctgaa	gctgagctct	gtgactgccg	cggacacggc	tgtgtattac	1680
tgtgcaagag	aggatgggga	tagctactac	cgctacggta	tggacgtctg	gggccaaggg	1740
accacggtca	ccgtctcctc	aactgtggct	gcaccatctg	tcttcatctt	cccgccatct	1800
gatgagcagt	tgaaatctgg	aactgcctct	gttgtgtgcc	tgctgaataa	cttctatccc	1860
agagaggcca	aagtacagtg	gaagggtgat	aacgccctcc	aatcgggtaa	ctcccaggag	1920
agtgtcacag	agcaggacag	caaggacagc	acctacagcc	tcgaaagcac	cctgacgctg	1980
agcaaagcag	actacgagaa	acacaaagtc	tacgcctgcg	aagtcaccca	tcagggcctg	2040
agctcgcccc	tcacaaagag	cttcaacagg	ggagagtgt			2079

<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			

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 325 330 335
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 340 345 350
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 355 360 365
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 405 410 415
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445
 Ser Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 450 455 460
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
 465 470 475 480
 Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn Ser Val
 485 490 495
 Ala Trp Asn Trp Ile Arg 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

A-1937-WO-PCT_ST25

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
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg 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

gatatccaaa tgacacaatc accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg

60

A-1937-WO-PCT_ST25

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 cccctggca 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> 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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
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tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccagggaacc ctggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctaccgg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac 600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660
tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020
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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgaggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

A-1937-WO-PCT_ST25

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gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcgga tcgggaggtg gcggatccca ggtgcagtta	1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc	1440
catggtgggt ctttcagtgg ttactactgg aactggattc gcaagccacc aggggaagggg	1500
ctagagtggg ttggggaaat caatcatgct ggaaacacca actacaaccc gtcctcaag	1560
agtcgagtca ccatatcatt agacacgtcc aagaaccagt tctccctgac gctgacctct	1620
gtgaccgccg cggacacggc tgtgtattac tgtgcgagag gatattgtag aagtaccacc	1680
tgctactttg actactgggg ccaggaacc 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> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600

cccagcaaca ccaaggtgga caagaaagtt gagcccaaatt cttgt

<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
 gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
 tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgcaagatg 120
 cccgggaaag gcctggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
 agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
 tggggctctg actactgggg ccaggggaacc ctgggtcaccg 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 tctcccggac ccctgaggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
 taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080
 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
 gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
 tccgacggct ctttcttct ctatagcaag ctaccctggg acaagagcag gtggcagcag 1260
 gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
 agcctctccc tgtctccggg tgggtggcga tcgggagggtg gcggatccca ggtgcagctg 1380
 caggagtgcg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc 1440
 tctggtggct ccatcagtag ttacttctgg agctggattc ggaagcccc aggtaaggga 1500
 ctggagtgga ttggctatat ctattacagt gggcagacca aatacaacct ctccctcaag 1560
 agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct 1620
 gtgaccgtg cggaacggc cgtgtattac tgtgagagag aaactgggag ctactacggc 1680
 tttgactact ggggcccagg aaccctggtc accgtctcct caactgtggc tgcaccatct 1740

A-1937-WO-PCT_ST25

gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc	1800
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc	1860
caatcgggta actcccagga gagtgtcaca gaggaggaca gcaaggacag cacctacagc	1920
ctcgaaagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	1980
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	2040

<210> 1782
 <211> 680
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polypeptide
 <400> 1782

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

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

A-1937-WO-PCT_ST25

Gln Trp Lys₁₉₅ Ser His Arg Ser Tyr₂₀₀ Ser Cys Gln Val Thr₂₀₅ His Glu Gly

Ser Thr₂₁₀ Val Glu Lys Thr Val₂₁₅ Ala Pro Thr Glu Cys₂₂₀ Ser Asp Lys Thr

His Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀

Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg

Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro

Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala

Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val

Ser Val₃₀₅ Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀

Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr

Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu

Pro Pro Ser₃₅₅ Arg Glu Glu Met Thr₃₆₀ Lys Asn Gln Val Ser₃₆₅ Leu Thr Cys

Leu Val₃₇₀ Lys Gly Phe Tyr Pro₃₇₅ Ser Asp Ile Ala Val₃₈₀ Glu Trp Glu Ser

Asn Gly Gln Pro Glu Asn₃₉₀ Asn Tyr Lys Thr Thr₃₉₅ Pro Pro Val Leu Asp₄₀₀

Ser Asp Gly Ser Phe₄₀₅ Phe Leu Tyr Ser Lys₄₁₀ Leu Thr Val Asp Lys₄₁₅ Ser

Arg Trp Gln Gln₄₂₀ Gly Asn Val Phe Ser₄₂₅ Cys Ser Val Met His₄₃₀ Glu Ala

Leu His Asn₄₃₅ His Tyr Thr Gln Lys₄₄₀ Ser Leu Ser Leu Ser₄₄₅ Pro Gly Gly

Gly Gly₄₅₀ Ser Gly Gly Gly Gly₄₅₅ Ser Gln Val Gln Leu₄₆₀ Gln Glu Ser Gly

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

60

A-1937-WO-PCT_ST25

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 cccctcggca 360
 ccctcctcca agagcacctc tggggggcaca 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> 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1785
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1785
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccaggag 120
tttccaggaa cagcccccaa actcctcatc caaggaataa gcaatcggcc ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggacaa 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> 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

A-1937-WO-PCT_ST25

Tyr Asp Val₃₅ His Trp Tyr Gln Glu₄₀ Phe Pro Gly Thr Ala₄₅ Pro Lys Leu

Leu Ile₅₀ Gln Gly Asn Ser Asn₅₅ Arg Pro Ser Gly Val₆₀ Pro Asp Arg Phe

Ser Gly Ser Lys Ser Gly₇₀ Thr Ser Ala Ser Leu₇₅ Ala Ile Thr Gly Leu₈₀

Gln Ala Glu Asp Glu₈₅ Ala Asp Tyr Tyr Cys₉₀ Gln Ser Tyr Asp Ser₉₅ Ser

Leu Ser Gly Ser₁₀₀ Val Phe Gly Gly Gly₁₀₅ Thr Lys Leu Thr Val₁₁₀ Leu Gly

Ala Ser Thr₁₁₅ Lys Gly Pro Ser Val₁₂₀ Phe Pro Leu Ala Pro₁₂₅ Ser Ser Lys

Ser Thr₁₃₀ Ser Gly Gly Thr Ala₁₃₅ Ala Leu Gly Cys Leu₁₄₀ Val Lys Asp Tyr

Phe Pro Glu Pro Val₁₅₀ Thr Val Ser Trp Asn Ser₁₅₅ Gly Ala Leu Thr Ser₁₆₀

Gly Val His Thr Phe₁₆₅ Pro Ala Val Leu Gln₁₇₀ Ser Ser Gly Leu Tyr₁₇₅ Ser

Leu Glu Ser Val₁₈₀ Val Thr Val Pro Ser₁₈₅ Ser Ser Leu Gly Thr₁₉₀ Gln Thr

Tyr Ile Cys₁₉₅ Asn Val Asn His Lys₂₀₀ Pro Ser Asn Thr Lys₂₀₅ Val Asp Lys

Lys Val₂₁₀ Glu Pro Lys Ser Cys₂₁₅

<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

A-1937-WO-PCT_ST25

tggggtcttg	actactgggg	ccaggaacc	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	ccccccaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgtttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	960
aagtgcgaag	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	tggtggcgga	tcgggaggtg	gcggatccca	ggtacagttg	1380
caggagtcat	gtccaggact	ggtgaagccc	tcggagaccc	tctcactcac	ctgtaccatc	1440
tccggggaca	gtgtctctac	caacagtgtt	gcttggaact	ggattaggaa	gccccagggy	1500
aaaggccttg	agtggatagg	aaggacatac	tacaggtcca	agtgggtataa	tgattatgca	1560
gtttctctga	aaagtcgagt	aaccatcagc	ccagacacat	ccaagaacca	gttctccctg	1620
aagctgagct	ctgtgactgc	cgcgacacg	gctgtgtatt	actgtgcaag	agaggatggg	1680
gatagctact	accgctacgg	tatggacgtc	tggggccaag	ggaccacggt	caccgtctcc	1740
tcaactgtgg	ctgcaccatc	tgtcttcatc	ttcccgccat	ctgatgagca	gttgaaatct	1800
ggaactgcct	ctgttggtgtg	cctgctgaat	aacttctatc	ccagagaggc	caaagtacag	1860
tggaaggtgg	ataacgccct	ccaatcgggt	aactcccagg	agagtgtcac	agagcaggac	1920
agcaaggaca	gcacctacag	cctcgaaagc	accctgacgc	tgagcaaagc	agactacgag	1980
aaacacaaag	tctacgcctg	cgaagtcacc	catcaggggc	tgagctcgcc	cgtcacaaag	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

A-1937-WO-PCT_ST25

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr Arg Cys Val
 290 295 300
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445
 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360

tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420

tgcttggtca aggactactt ccccgaaccg gtgacggtgt 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> 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 caaggttaaca gcaatcggcc ctcaggggctc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
 gtgttcggcg gagggacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
 ttccccctgg caccctcctc 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> 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

A-1937-WO-PCT_ST25

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
ccaggaagg 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
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
ctggggggac cgtcagtcct cctcttcccc ccaaaccaca aggacaccct catgatctcc 780
cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 840

A-1937-WO-PCT_ST25

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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 tgggtcaaagg cttctatccc    1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg      1200
cctcccgtag tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag      1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac    1320
cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga    1380
tccgaggtag aactgggtga atcaggtgga ggtttggtgc agccggggag atcgctcagg      1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggaaa    1500
gcgcttgtaa aagggctcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat      1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg      1620
taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc    1680
tcctacttgt ctacagcttc gtcgctcgac tattggggtc aaggaacggt ggtcacgctc    1740
tctagtactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa    1800
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta    1860
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag      1920
gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac    1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca    2040
aagagcttca acaggggaga gtgt                                     2064

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<210> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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
ttccccggtg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
 gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtcgc tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1798
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1798

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

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

A-1937-WO-PCT_ST25

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 tccatggtgg gtccttcagt ggttactact ggaactggat tcgcaagcca 120
ccaggggaagg ggctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccaggga cctagtcac 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
caciaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt caciaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtctt cctcttcccc ccaaaccaca aggacaccct catgatctcc 780
cggacccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgagggtcaag 840
ttcaactggt 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 caagaccagc 1200
cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1320
cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga 1380

A-1937-WO-PCT_ST25

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
aactgggggtc ttgactactg gggccaggga accctgggtca ccgtctctag tcagcccaag 1740
gccaacccca ctgtcactct gttcccgcct tcctctgagg agctccaagc caacaaggcc 1800
acactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca 1860
gatggcagcc ccgtcaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac 1920
aagtacgcg ccgagagcta cctgagcctg acgcccagac agtggaagtc ccacagaagc 1980
tacagctgcc aggtcacgca tgaaggagac 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Pro Pro Val Leu Asp₄₀₅ Ser Asp Gly Ser Phe₄₁₀ Phe Leu Tyr Ser Lys₄₁₅ Leu
 Thr Val Asp Lys₄₂₀ Ser Arg Trp Gln₄₂₅ Gln Gly Asn Val Phe Ser₄₃₀ Cys Ser
 Val Met His₄₃₅ Glu Ala Leu His Asn₄₄₀ His Tyr Thr Gln Lys₄₄₅ Ser Leu Ser
 Leu Ser₄₅₀ Pro Gly Gly Gly₄₅₅ Ser Gly Gly Gly₄₆₀ Ser Glu Val Gln
 Leu₄₆₅ Val Gln Ser Gly Ala₄₇₀ Glu Val Lys Lys Pro₄₇₅ Gly Glu Ser Leu Lys₄₈₀
 Ile Ser Cys Lys Thr₄₈₅ Ser Glu Tyr Ser Phe₄₉₀ Thr Ser Tyr Trp Ile₄₉₅ Gly
 Trp Val Arg Lys₅₀₀ Met Pro Gly Lys Gly₅₀₅ Leu Glu Trp Met Gly₅₁₀ Ile Ile
 Tyr Leu Gly₅₁₅ Asp Ser Asp Thr Arg₅₂₀ Tyr Ser Pro Ser Phe₅₂₅ Gln Gly Gln
 Val Thr₅₃₀ Ile Ser Ala Asp Lys₅₃₅ Ser Ile Ser Thr Ala₅₄₀ Tyr Leu Gln Trp
 Ser₅₄₅ Ser Leu Lys Ala Ser₅₅₀ Asp Thr Ala Met Tyr₅₅₅ Tyr Cys Ala Arg Ser₅₆₀
 Asn Trp Gly Leu Asp₅₆₅ Tyr Trp Gly Gln Gly₅₇₀ Thr Leu Val Thr Val₅₇₅ Ser
 Ser Gln Pro Lys₅₈₀ Ala Asn Pro Thr Val₅₈₅ Thr Leu Phe Pro Pro₅₉₀ Ser Ser
 Glu Glu Leu₅₉₅ Gln Ala Asn Lys Ala₆₀₀ Thr Leu Val Cys Leu₆₀₅ Ile Ser Asp
 Phe Tyr₆₁₀ Pro Gly Ala Val Thr₆₁₅ Val Ala Trp Lys Ala₆₂₀ Asp Gly Ser Pro
 Val₆₂₅ Lys Ala Gly Val Glu₆₃₀ Thr Thr Lys Pro Ser₆₃₅ Lys Gln Ser Asn Asn₆₄₀
 Lys Tyr Ala Ala Glu₆₄₅ Ser Tyr Leu Ser Leu₆₅₀ Thr Pro Glu Gln Trp₆₅₅ Lys
 Ser His Arg Ser₆₆₀ Tyr Ser Cys Gln Val₆₆₅ Thr His Glu Gly Ser₆₇₀ Thr Val

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 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 tctactcctt caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga 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

A-1937-WO-PCT_ST25

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 ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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 caaatataac	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 tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccggacc	780
cctgagggtca catgctggtt ggtggacgtg agccacgaag accctgagggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgtttgtg 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 cttcttctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggagggtg cggatccgag	1380
gtacaactgg tggaatcagg tggagggttg 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 agtctcttac	1680
ttgtctacag cttcgtcgtc cgactattgg ggtcaaggaa cgttggtcac cgtctctagt	1740
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga	1800
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg	1860
aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc	1920

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca ggaaaaaccc 120

ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180

A-1937-WO-PCT_ST25

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
 ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcacca 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

A-1937-WO-PCT_ST25

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1809
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1809
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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
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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 cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420

A-1937-WO-PCT_ST25

tctgttgtgt gcctgctgaa taacttctat 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 cccccaaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggcctctga caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccc gggagtctct gaagatctcc	1440
tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgcg caagatgccc	1500
gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc	1560
ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtag cgcctacctg	1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg	1680
ggtcttgact actggggcca gggaaccctg gtcaccgtct ctagtcagcc caaggccaac	1740
cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta	1800
gtgtgtctga tcagtactt ctaccggga gctgtgacag tggcctggaa ggcagatggc	1860
agccccgtca aggcgggagt ggagaccacc aaaccctcca aacagagcaa caacaagtac	1920
gcggccgaga gctacctgag cctgacgcc gagcagtgga agtcccacag aagctacagc	1980
tgccagggtca cgcataagg gagcaccgtg gagaagacag tggcccctac agaatgttca	2040

<210> 1812

<211> 680

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1812

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	

A-1937-WO-PCT_ST25

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Phe Trp Ser Trp Ile Arg 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

A-1937-WO-PCT_ST25

His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly Ser Thr Tyr
 290 295 300
 Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 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

A-1937-WO-PCT_ST25

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 gcagggttatg 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 cccatcgggtc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt 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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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca ggagagacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa      300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt cccctcggca      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

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<210> 1816

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1816

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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 Ala Ser Thr Lys
          100          105          110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
          115          120          125

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A-1937-WO-PCT_ST25

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
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
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gtcaccgtct cctcaacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
cagttgaaat ctggaactgc ctctgtttgtg tgcctgctga ataacttcta tcccagagag 480
gccaaagtac agtgaaggt 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 ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa 840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg 960
caccaggact ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca 1020

A-1937-WO-PCT_ST25

gcccccatcg agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080
 accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggctc 1140
 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200
 aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag 1260
 ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1320
 gaggtctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggcggcgga 1380
 tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg 1440
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 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 gggcgaagga 1740
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 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 aagtcacca tcagggcctg 2040
 agctcgcccc 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
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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 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

A-1937-WO-PCT_ST25

Gln Phe Ser Leu Lys₈₅ Leu Ser Ser Val Thr₉₀ Ala Ala Asp Thr Ala₉₅ Val
 Tyr Tyr Cys Ala₁₀₀ Arg Glu Asp Gly Asp₁₀₅ Ser Tyr Tyr Arg Tyr₁₁₀ Gly Met
 Asp Val Trp₁₁₅ Gly Gln Gly Thr Thr₁₂₀ Val Thr Val Ser Ser₁₂₅ Thr Val Ala
 Ala Pro₁₃₀ Ser Val Phe Ile Phe₁₃₅ Pro Pro Ser Asp Glu Gln Leu Lys Ser
 Gly Thr Ala Ser Val Val₁₅₀ Cys Leu Leu Asn Asn₁₅₅ Phe Tyr Pro Arg Glu₁₆₀
 Ala Lys Val Gln Trp₁₆₅ Lys Val Asp Asn Ala₁₇₀ Leu Gln Ser Gly Asn Ser₁₇₅
 Gln Glu Ser Val₁₈₀ Thr Glu Gln Asp Ser₁₈₅ Lys Asp Ser Thr Tyr₁₉₀ Ser Leu
 Lys Ser Thr₁₉₅ Leu Thr Leu Ser Lys₂₀₀ Ala Asp Tyr Glu Lys₂₀₅ His Lys Val
 Tyr Ala₂₁₀ Cys Glu Val Thr His₂₁₅ Gln Gly Leu Ser Ser₂₂₀ Pro Val Thr Lys
 Ser₂₂₅ Phe Asn Arg Gly Glu₂₃₀ Cys Asp Lys Thr His₂₃₅ Thr Cys Pro Pro Cys₂₄₀
 Pro Ala Pro Glu Leu₂₄₅ Leu Gly Gly Pro Ser₂₅₀ Val Phe Leu Phe Pro₂₅₅ Pro
 Lys Pro Lys Asp₂₆₀ Thr Leu Met Ile Ser₂₆₅ Arg Thr Pro Glu Val₂₇₀ Thr Cys
 Val Val Val₂₇₅ Asp Val Ser His Glu₂₈₀ Asp Pro Glu Val Lys₂₈₅ Phe Asn Trp
 Tyr Val₂₉₀ Asp Gly Val Glu Val₂₉₅ His Asn Ala Lys Thr₃₀₀ Lys Pro Cys Glu
 Glu Gln Tyr Gly Ser Thr₃₁₀ Tyr Arg Cys Val Ser₃₁₅ Val Leu Thr Val Leu₃₂₀
 His Gln Asp Trp Leu₃₂₅ Asn Gly Lys Glu Tyr₃₃₀ Lys Cys Lys Val Ser₃₃₅ Asn
 Lys Ala Leu Pro₃₄₀ Ala Pro Ile Glu Lys₃₄₅ Thr Ile Ser Lys Ala₃₅₀ Lys Gly

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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attacctgtc gcgcgctcca ggaatccgg aattacctc catggtatca ggaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgctc 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtcgc tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga 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

A-1937-WO-PCT_ST25

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

gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60

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tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180

gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300

A-1937-WO-PCT_ST25

cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
 tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
 tgcctgggtca aggactactt ccccgaaccg gtgacgggtg cgtggaactc aggcgccttg 480
 accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
 agcgtgggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<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

A-1937-WO-PCT_ST25

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

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc	60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg	120
aagccccag ggaaaggcct tgagtggata ggaaggacat actacaggtc caagtggat	180
aatgattatg cagtttctct gaaaagtcga gtaaccatca 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 agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc	540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa	600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	660
cccgtcacia agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac	780
accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctcca	1020
gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080
accctgcccc catcccgga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc	1140
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac	1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaaactct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga	1380
tcgggagggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc	1440

A-1937-WO-PCT_ST25

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ggggagtctc tgaagatctc ctgtaagact tctgaataca gctttaccag ctactggatc 1500
ggctgggtgc gcaagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcttggc 1560
gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag 1620
tccatcagta ccgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat 1680
tactgtgcga gaagtaactg gggctcttgac tactggggcc agggaaccct ggtcaccgtc 1740
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc 1800
caagccaaca aggccacact agtgtgtctg atcagtgact tctaccggg agctgtgaca 1860
gtggcctgga aggcatgga cagccccgtc aaggcgggag tggagaccac caaacctcc 1920
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg 1980
aagtcccaca gaagctacag ctgccaggtc acgcatgaag ggagcaccgt ggagaagaca 2040
gtggccccta cagaatgttc a 2061

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<210> 1824
<211> 687
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic polypeptide
<400> 1824

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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 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Leu Tyr Ser Lys₄₂₀ Leu Thr Val Asp Lys₄₂₅ Ser Arg Trp Gln Gln₄₃₀ Gly Asn
 Val Phe Ser₄₃₅ Cys Ser Val Met His₄₄₀ Glu Ala Leu His Asn₄₄₅ His Tyr Thr
 Gln Lys₄₅₀ Ser Leu Ser Leu Ser₄₅₅ Pro Gly Gly Gly₄₆₀ Ser Gly Gly Gly
 Gly₄₆₅ Ser Glu Val Gln Leu₄₇₀ Val Gln Ser Gly Ala₄₇₅ Glu Val Lys Lys Pro₄₈₀
 Gly Glu Ser Leu Lys₄₈₅ Ile Ser Cys Lys Thr₄₉₀ Ser Glu Tyr Ser Phe₄₉₅ Thr
 Ser Tyr Trp Ile₅₀₀ Gly Trp Val Arg Lys₅₀₅ Met Pro Gly Lys Gly₅₁₀ Leu Glu
 Trp Met Gly₅₁₅ Ile Ile Tyr Leu Gly₅₂₀ Asp Ser Asp Thr Arg₅₂₅ Tyr Ser Pro
 Ser Phe₅₃₀ Gln Gly Gln Val Thr₅₃₅ Ile Ser Ala Asp Lys₅₄₀ Ser Ile Ser Thr
 Ala Tyr Leu Gln Trp Ser₅₅₀ Ser Leu Lys Ala Ser₅₅₅ Asp Thr Ala Met Tyr₅₆₀
 Tyr Cys Ala Arg Ser₅₆₅ Asn Trp Gly Leu Asp₅₇₀ Tyr Trp Gly Gln Gly₅₇₅ Thr
 Leu Val Thr Val₅₈₀ Ser Ser Gln Pro Lys₅₈₅ Ala Asn Pro Thr Val₅₉₀ Thr Leu
 Phe Pro Pro₅₉₅ Ser Ser Glu Glu Leu₆₀₀ Gln Ala Asn Lys Ala₆₀₅ Thr Leu Val
 Cys Leu Ile Ser Asp Phe Tyr₆₁₅ Pro Gly Ala Val Thr₆₂₀ Val Ala Trp Lys
 Ala Asp Gly Ser Pro Val₆₃₀ Lys Ala Gly Val Glu₆₃₅ Thr Thr Lys Pro Ser₆₄₀
 Lys Gln Ser Asn Asn₆₄₅ Lys Tyr Ala Ala Glu₆₅₀ Ser Tyr Leu Ser Leu₆₅₅ Thr
 Pro Glu Gln Trp₆₆₀ Lys Ser His Arg Ser₆₆₅ Tyr Ser Cys Gln Val₆₇₀ Thr His
 Glu Gly Ser Thr Val Glu Lys Thr₆₈₀ Val Ala Pro Thr Glu₆₈₅ Cys Ser

<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 caaggttaaca gcaatcggcc ctcagggggtc 180
 cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc 240
 caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
 gtgttcggcg gagggacaa 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> 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagg agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccggg 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 aggcgcctgt 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt t 651

<210> 1828
<211> 217
<212> PRT
<213> Artificial Sequence

A-1937-WO-PCT_ST25

<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

```

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attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc      120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg      180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc      240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa      300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca      360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat      420
cccagagagg ccaaagtaca gtggaaggtg 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> 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

```


A-1937-WO-PCT_ST25

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1831
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1831
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tggtagcgcc tctgtttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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 tggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60

agctgtgcgg catcgggggt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120

cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

A-1937-WO-PCT_ST25

gcagacagtg	tggagggcag	attcacaatc	tcacgagaca	atgctaagaa	cagcctgtac	240
cttcagatga	actcacttcg	cgcggaagat	accgccgtat	actactgcgc	caaagtctcc	300
tacttgtcta	cagcttcgtc	gctcgactat	tgggggtcaag	gaacgttggt	caccgtctct	360
agtgcctcca	ccaagggccc	atcgggtctt	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
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	actcctgggg	720
ggaccgtcag	tcttcctctt	ccccccaaaa	ccaaggaca	ccctcatgat	ctcccggacc	780
cctgaggtca	catgcgtggt	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tggtagctgg	acggcgtgga	ggtgcataat	gccaaagaaa	agccgtgtga	ggagcagtac	900
ggcagcacgt	accgttgtgt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgaaggt	ctccaacaaa	gccctcccag	cccccatcga	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
gtgcagttac	agcagtcggg	cgcaggactg	ttgaagcctt	cggagaccct	gtccctcacc	1440
tgcgctgtcc	atggtgggtc	cttcagtggg	tactactgga	actggattcg	ccagccacca	1500
gggaaggggc	tagagtggat	tggggaaatc	aatcatgctg	gaaacaccaa	ctacaacccg	1560
tccctcaaga	gtcgagtcac	catatcatta	gacacgtcca	agaaccagtt	ctccctgacg	1620
ctgacctctg	tgaccgccgc	ggacacggct	gtgtattact	gtgcgagagg	atattgtaga	1680
agtaccacct	gctactttga	ctactggggc	aagggaaccc	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	tgaatcacia	gcccagcaac	accaaggtgg	acaagaaagt	tgagcccaaa	2040
tcttgt						2046

<210> 1834

<211> 682

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1834

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1      5      10
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

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A-1937-WO-PCT_ST25

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
 Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Gln₄₆₀ Val Gln Leu Gln
 Gln Ser Gly Ala Gly Leu₄₇₀ Leu Lys Pro Ser Glu₄₇₅ Thr Leu Ser Leu Thr₄₈₀
 Cys Ala Val His Gly₄₈₅ Gly Ser Phe Ser Gly₄₉₀ Tyr Tyr Trp Asn Trp₄₉₅ Ile
 Arg Gln Pro Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Ile Gly Glu Ile₅₁₀ Asn His

A-1937-WO-PCT_ST25

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 gctgcacat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggtg gataacgcc tccaatcggg taactcccag 480

A-1937-WO-PCT_ST25

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 tgaccagtc 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 acgaacggtg gctgcacat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tgggtaccgc 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> 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

A-1937-WO-PCT_ST25

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

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agctgtgctg catcggtgtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120

cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

cttcagatga actcacttcg cgcggaagat accgccgtat actactgctc caaagtctcc 300

tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360

agtcctcca ccaagggccc atcgggtctt cccctggcac cctcctcaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720

A-1937-WO-PCT_ST25

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ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac      900
ggcagcacgt accgtttgtg cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggt ctccaacaaa gccctccag 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 ctcattgctc gtgatgcatg aggtctctga caaccactac     1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag     1380
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc     1440
tgactgtct ctggtggctc catcagtagt tacttctgga gctggattcg gcagccccca     1500
ggtaagggac tggagtggat tggctatatc tattacagtg ggcagaccaa atacaacccc     1560
tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag     1620
ctgagctctg tgaccgtgc ggacacggcc gtgtattact gtgcgagaga aactgggagc     1680
tactacggct ttgactactg gggcaaggga accctgggtca ccgtctcctc agcctccacc     1740
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg     1800
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca     1860
ggcgccctga ccagcggcgt gcacaccttc ccggtgttcc tacagtcctc aggactctac     1920
tccctcgaga gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc     1980
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt     2040

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Gln₄₆₀ Val Gln Leu Gln
 Glu₄₆₅ Ser Gly Pro Gly Leu₄₇₀ Val Lys Pro Ser Glu₄₇₅ Thr Leu Ser Leu Thr₄₈₀
 Cys Thr Val Ser Gly₄₈₅ Gly Ser Ile Ser Ser₄₉₀ Tyr Phe Trp Ser Trp₄₉₅ Ile
 Arg Gln Pro Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Ile Gly Tyr Ile₅₁₀ Tyr Tyr
 Ser Gly Gln₅₁₅ Thr Lys Tyr Asn Pro₅₂₀ Ser Leu Lys Ser Arg₅₂₅ Val Thr Ile
 Ser Ile₅₃₀ Asp Thr Ser Lys Asn₅₃₅ Gln Phe Ser Leu Lys₅₄₀ Leu Ser Ser Val
 Thr₅₄₅ Ala Ala Asp Thr Ala₅₅₀ Val Tyr Tyr Cys Ala₅₅₅ Arg Glu Thr Gly Ser₅₆₀
 Tyr Tyr Gly Phe Asp₅₆₅ Tyr Trp Gly Lys Gly₅₇₀ Thr Leu Val Thr Val₅₇₅ Ser
 Ser Ala Ser Thr₅₈₀ Lys Gly Pro Ser Val₅₈₅ Phe Pro Leu Ala Pro₅₉₀ Ser Ser

A-1937-W0-PCT_ST25

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 accatcgctg 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 gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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 ctgtctgcgt ctgtgggcga tagggtcacc 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

tggtaccagc agaaaccagg aaaggagcct aaactgctca ttactgggc atctaccgg 180

A-1937-WO-PCT_ST25

gaatccgggg 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 tgttggtgtgc	420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc	480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc	540
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	660

<210> 1844
 <211> 220
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polypeptide
 <400> 1844

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly	1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser	20 25 30
Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys	35 40 45
Glu Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50 55 60
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65 70 75 80
Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln	85 90 95
Tyr Tyr Lys Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	100 105 110
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

A-1937-WO-PCT_ST25

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 1845
<211> 2061
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1845
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggg caccgtctct 360
agtgcctcca ccaagggccc atcgggtctt cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtgggt accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggag 1080
gagatgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac 1320

A-1937-WO-PCT_ST25

acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380
 gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc 1440
 tgtaccatct ccggggacag tgtctctacc aacagtgttg cttggaactg gattaggcag 1500
 cccccaggga 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 cagcctccac caagggccca tcggtcttcc ccctggcacc ctctctcaag 1800
 agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 1860
 gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1920
 ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980
 ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040
 aaagttgagc ccaaattctg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 caaggaata gcaatcggcc ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggctc 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 ctgccaggctc 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

A-1937-WO-PCT_ST25

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 gagtgttaga agcagttact tagcctggta ccagcagaaa	120
cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa	300
gggacacgac tggagattaa 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> 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

A-1937-WO-PCT_ST25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1851
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cgggggagtc 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
tggggtcttg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac 600
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc 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
aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa 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 gcagggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tcctgtctc cgggtggtgg cggatcggga ggtggcggat cccagggtgca gttacagcag 1380
tcgggcgag gactgttgaa gccttcggag accctgtccc tcacctgccc tgtccatggt 1440
gggtccttca gtggttacta ctggaactgg attcgccagc caccagggaa ggggctagag 1500
tggtattggg aaatcaatca tgctggaac accaactaca acccgctcct caagagtcga 1560
gtcaccatat cattagacac gtccaagaac cagttctccc tgacgctgac ctctgtgacc 1620
gccgcggaca cggctgtgta ttactgtgag agaggatatt gtagaagtac cacctgctac 1680
tttgactact ggggcaaggg aaccctagtc accgtctcct cagcctccac caagggccca 1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 1800
tgcctggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgccttg 1860

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 cagccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

A-1937-WO-PCT_ST25

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 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

A-1937-WO-PCT_ST25

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 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagagc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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> 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

A-1937-WO-PCT_ST25

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
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cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggtcttg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

A-1937-WO-PCT_ST25

ctgggctgcc	tggtcaagga	ctacttcccc	gaaccggtga	cggtgtcgtg	gaactcaggc	480
gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	540
ctcaaaagcg	tggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tgggggggacc	gtcagtcttc	720
ctcttcccc	caaaacccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtggtggtg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
gtggaggtgc	ataatgcaa	gacaaagccg	tgtgaggagc	agtacggcag	cacgtaccgt	900
tgtgtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	960
aaggctctca	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
ggctccttct	tcctctatag	caagctcacc	gtggacaaga	gcaggtggca	gcaggggaac	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	attcggcagc	cccaggttaa	gggactggag	1500
tggattggct	atatctatta	cagtgggcag	accaaataca	accctccct	caagagtcga	1560
gtcaccatat	caatagacac	gtccaagaac	cagttctccc	tgaagctgag	ctctgtgacc	1620
gctgcggaca	cggccgtgta	ttactgtgcg	agagaaactg	ggagctacta	cggctttgac	1680
tactggggca	agggaaaccct	ggtcaccgtc	tcctcagcct	ccaccaaggg	cccatcggtc	1740
ttccccctgg	caccctcctc	caagagcacc	tctgggggca	cagcggccct	gggctgcctg	1800
gtcaaggact	acttccccga	accggtgacg	gtgtcgtgga	actcaggcgc	cctgaccagc	1860
ggcgtgcaca	ccttcccggc	tgtcctacag	tcctcaggac	tctactccct	cgagagcgtg	1920
gtgaccgtgc	cctccagcag	cttgggcacc	cagacctaca	tctgcaacgt	gaatcacaag	1980
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<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	

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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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 aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcacctg 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

```

gacatccaga tgaccagtc tccaagctcc ctgtctgcgt 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 gaccaaggtg gagatcaaac gaacggtggc tgcaccatct      360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc      420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc      480
caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc      540
ctcaagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
gaagtcacc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt      660

```

<210> 1862

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1862

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

```

```

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

```

A-1937-WO-PCT_ST25

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

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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 ccagggaaacc 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 tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag 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 ataagtccaa gacaaagccg tgtgaggagc agtacggcag cacgtaccgt	900
tgtgtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccattctcaa agccaaaggg	1020

A-1937-WO-PCT_ST25

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
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tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagcccc agggaaaggc 1500
cttgagtgga taggaaggac atactacagg tccaagtggg ataagtatta tgcagtttct 1560
ctgaaaagtc gagtaaccat cagcccagac acatccaaga accagttctc cctgaagctg 1620
agctctgtga ctgccgcca cacggctgtg tattactgtg caagagagga tggggatagc 1680
tactaccgct acggtatgga cgtctggggc aaagggacca cggtcaccgt ctcctcagcc 1740
tccaccaagg gcccatcggc 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 gccagcaac accaaggtgg 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

A-1937-WO-PCT_ST25

Leu Gln Trp Ser Ser₈₅ Leu Lys Ala Ser Asp₉₀ Thr Ala Met Tyr Tyr₉₅ Cys

Ala Arg Ser Asn₁₀₀ Trp Gly Leu Asp Tyr₁₀₅ Trp Gly Gln Gly Thr₁₁₀ Leu Val

Thr Val Ser₁₁₅ Ser Ala Ser Thr Lys₁₂₀ Gly Pro Ser Val Phe₁₂₅ Pro Leu Ala

Pro Ser₁₃₀ Ser Lys Ser Thr Ser₁₃₅ Gly Gly Thr Ala Ala₁₄₀ Leu Gly Cys Leu

Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀

Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser

Gly Leu Tyr Ser₁₈₀ Leu Lys Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu

Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr

Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr

Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀

Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro

Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val

Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr

Lys Pro₂₉₀ Cys Glu Glu Gln Tyr₂₉₅ Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val

Leu Thr Val₃₀₅ Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀

Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser

Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro

A-1937-WO-PCT_ST25

Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe Leu₄₀₅ Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp
 Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His
 Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly
 Ser Gly₄₅₀ Gly Gly Gly Ser Gln₄₅₅ Val Gln Leu Gln Glu₄₆₀ Ser Gly Pro Gly
 Leu Val Lys Pro Ser Glu₄₇₀ Thr Leu Ser Leu Thr₄₇₅ Cys Thr Ile Ser Gly₄₈₀
 Asp Ser Val Ser Thr₄₈₅ Asn Ser Val Ala Trp₄₉₀ Asn Trp Ile Arg Gln₄₉₅ Pro
 Pro Gly Lys Gly₅₀₀ Leu Glu Trp Ile Gly₅₀₅ Arg Thr Tyr Tyr Arg₅₁₀ Ser Lys
 Trp Tyr Asn₅₁₅ Asp Tyr Ala Val Ser₅₂₀ Leu Lys Ser Arg Val₅₂₅ Thr Ile Ser
 Pro Asp₅₃₀ Thr Ser Lys Asn Gln₅₃₅ Phe Ser Leu Lys Leu₅₄₀ Ser Ser Val Thr
 Ala₅₄₅ Ala Asp Thr Ala Val₅₅₀ Tyr Tyr Cys Ala Arg₅₅₅ Glu Asp Gly Asp Ser₅₆₀
 Tyr Tyr Arg Tyr Gly₅₆₅ Met Asp Val Trp Gly₅₇₀ Lys Gly Thr Thr Val₅₇₅ Thr
 Val Ser Ser Ala₅₈₀ Ser Thr Lys Gly Pro₅₈₅ Ser Val Phe Pro Leu₅₉₀ Ala Pro
 Ser Ser Lys₅₉₅ Ser Thr Ser Gly Gly₆₀₀ Thr Ala Ala Leu Gly₆₀₅ Cys Leu Val
 Lys Asp₆₁₀ Tyr Phe Pro Glu Pro₆₁₅ Val Thr Val Ser Trp₆₂₀ Asn Ser Gly Ala

A-1937-WO-PCT_ST25

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
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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 ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggcgag 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<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

A-1937-WO-PCT_ST25

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 accatcgctg 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 gcgtacggtg gctgcaccat ctgtcttcat cttcccgcga 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

A-1937-WO-PCT_ST25

cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 1869
 <211> 2046
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1869
 caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120
 ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
 ccgtcccctca 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 gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttctg acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
 gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1080
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg 1320
 cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggta 1380
 caactggtgg aatcaggtgg aggtttggtg cagccgggga gatcgctcag gcttagctgt 1440
 gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggtccggca agcgcttga 1500
 aaagggctcg agtgggtttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560

A-1937-WO-PCT_ST25

agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620
atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctctactttg 1680
tctacagctt cgtcgctcga ctattgggggt 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 gcttgggcac ccagacctac 1980
atctgcaacg tgaatcacia gccagcaac 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<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
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggcgag 300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccggca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccagcag 120
tttccaggaa cagagcccaa 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 aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 1874
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<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

caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc

60

A-1937-WO-PCT_ST25

acctgcgctg	tccatggtgg	gtccttcagt	ggttactact	ggaactggat	ccgccagcca	120
ccaggaaga	agctagagt	gattggggaa	atcaatcatg	ctggaaacac	caactacaac	180
ccgtccctca	agagtcgagt	caccatatca	ttagacacgt	ccaagaacca	gttctccctg	240
acgtgacct	ctgtgaccgc	cgcgacacg	gctgtgtatt	actgtgagag	aggatattgt	300
agaagtacca	cctgctactt	tgactactgg	ggccagggaa	ccctagtcac	cgtctcctca	360
gcctccacca	agggcccatc	ggtcttcccc	ctggcaccct	cctccaagag	cacctctggg	420
ggcacagcgg	ccctgggctg	cctgggtcaag	gactacttcc	ccgaaccggt	gacggtgtcg	480
tggaaactcag	gcgccctgac	cagcggcggt	cacaccttcc	cggctgtcct	acagtcctca	540
ggactctact	ccctcaaaag	cgtgggtgacc	gtgccctcca	gcagcttggg	caccagacc	600
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	660
aaatcttgtg	acaaaactca	cacatgccc	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	ccaaaaccc	aaggacaccc	tcattgatctc	ccggaccctt	780
gaggtcacat	gcgtgggtgt	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	tccgggtggt	ggcggatcgg	gaggtggcgg	atccgaggtg	1380
cagctggtgc	agtctggagc	agaggtgaaa	aagcccgggg	agtctctgaa	gatctcctgt	1440
aagacttctg	aatacagctt	taccagctac	tggatcggct	gggtgcgcca	gatgcccggg	1500
aaaggcctgg	agtggatggg	gatcatctat	cttgggtgact	cagataccag	atacagcccg	1560
tccttccaag	gccaggtcac	catctcagcc	gacaagtcca	tcagtaccgc	ctacctgcag	1620
tggagcagcc	tgaaggcctc	ggacaccgcc	atgtattact	gtgagagaag	taactggggg	1680
cttgactact	ggggcaagg	aaccctggtc	accgtctcta	gtgcctccac	caagggccca	1740
tcggtcttcc	ccctggcacc	ctcctccaag	agcacctctg	ggggcacagc	ggccctgggc	1800
tgcttggtca	aggactactt	ccccgaaccg	gtgacggtgt	cgtggaactc	aggcgccctg	1860
accagcggcg	tgcacacctt	cccggctgtc	ctacagtcct	caggactcta	ctccctcgag	1920
agcgtggtga	ccgtgccctc	cagcagcttg	ggcaccacga	cctacatctg	caacgtgaat	1980
cacaagccca	gcaacaccaa	ggtggacaag	aaagttgagc	ccaaatcttg	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

A-1937-WO-PCT_ST25

Pro Ser Val Phe Leu₂₄₅ Phe Pro Pro Lys Pro₂₅₀ Lys Asp Thr Leu Met₂₅₅ Ile
Ser Arg Thr Pro₂₆₀ Glu Val Thr Cys Val₂₆₅ Val Val Asp Val Ser₂₇₀ His Glu
Asp Pro Glu₂₇₅ Val Lys Phe Asn Trp₂₈₀ Tyr Val Asp Gly Val₂₈₅ Glu Val His
Asn Ala₂₉₀ Lys Thr Lys Pro Cys₂₉₅ Glu Glu Gln Tyr Gly₃₀₀ Ser Thr Tyr Arg
Cys₃₀₅ Val Ser Val Leu Thr₃₁₀ Val Leu His Gln Asp₃₁₅ Trp Leu Asn Gly Lys₃₂₀
Glu Tyr Lys Cys Lys₃₂₅ Val Ser Asn Lys Ala₃₃₀ Leu Pro Ala Pro Ile₃₃₅ Glu
Lys Thr Ile Ser₃₄₀ Lys Ala Lys Gly Gln₃₄₅ Pro Arg Glu Pro Gln₃₅₀ Val Tyr
Thr Leu Pro₃₅₅ Pro Ser Arg Glu Glu₃₆₀ Met Thr Lys Asn Gln₃₆₅ Val Ser Leu
Thr Cys₃₇₀ Leu Val Lys Gly Phe₃₇₅ Tyr Pro Ser Asp Ile₃₈₀ Ala Val Glu Trp
Glu₃₈₅ Ser Asn Gly Gln Pro₃₉₀ Glu Asn Asn Tyr Lys₃₉₅ Thr Thr Pro Pro Val₄₀₀
Leu Asp Ser Asp Glu₄₀₅ Ser Phe Phe Leu Tyr₄₁₀ Ser Lys Leu Thr Val₄₁₅ Asp
Lys Ser Arg Trp₄₂₀ Gln Gln Gly Asn Val₄₂₅ Phe Ser Cys Ser Val₄₃₀ Met His
Glu Ala Leu₄₃₅ His Asn His Tyr Thr₄₄₀ Gln Lys Ser Leu Ser₄₄₅ Leu Ser Pro
Gly Gly₄₅₀ Gly Gly Ser Gly Gly₄₅₅ Gly Gly Ser Glu Val₄₆₀ Gln Leu Val Gln
Ser₄₆₅ Gly Ala Glu Val Lys₄₇₀ Lys Pro Gly Glu Ser₄₇₅ Leu Lys Ile Ser Cys₄₈₀
Lys Thr Ser Glu Tyr₄₈₅ Ser Phe Thr Ser Tyr₄₉₀ Trp Ile Gly Trp Val₄₉₅ Arg
Gln Met Pro Gly₅₀₀ Lys Gly Leu Glu Trp₅₀₅ Met Gly Ile Ile Tyr₅₁₀ Leu Gly

A-1937-WO-PCT_ST25

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
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420

A-1937-WO-PCT_ST25

cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1879
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1879
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ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<210> 1880
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1880

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

A-1937-WO-PCT_ST25

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
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ccaggaaga aactggagtg gattggctat atctattaca gtgggcagac caaataacaac 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
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tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 660

A-1937-WO-PCT_ST25

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gagtgggaga	gcaatgggca	gccggagaac	aactacaaga	ccacgcctcc	cgtgctggac	1200
tccgacggct	ccttcttcct	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
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ctcgagtggg	tttccgccat	tacgtggaat	agcggacaca	tcgattatgc	agacagtgtg	1560
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gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaactca	1860
ggcgcccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	1920
tccctcgaga	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcaccagac	ctacatctgc	1980
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<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
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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Tyr
			20					25					30		

Phe	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Lys	Leu	Glu	Trp	Ile
		35					40					45			

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Cys Lys Val Ser 325 Asn Lys Ala Leu Pro 330 Ala Pro Ile Glu Lys 335 Thr
 Ile Ser Lys Ala 340 Lys Gly Gln Pro Arg 345 Glu Pro Gln Val Tyr 350 Thr Leu
 Pro Pro Ser 355 Arg Glu Glu Met Thr 360 Lys Asn Gln Val Ser 365 Leu Thr Cys
 Leu Val 370 Lys Gly Phe Tyr Pro 375 Ser Asp Ile Ala Val 380 Glu Trp Glu Ser
 Asn 385 Gly Gln Pro Glu Asn 390 Asn Tyr Lys Thr Thr 395 Pro Pro Val Leu Asp 400
 Ser Asp Gly Ser Phe 405 Phe Leu Tyr Ser Lys 410 Leu Thr Val Asp Lys 415 Ser
 Arg Trp Gln Gln 420 Gly Asn Val Phe Ser 425 Cys Ser Val Met His 430 Glu Ala
 Leu His 435 Asn His Tyr Thr Gln 440 Lys Ser Leu Ser Leu 445 Ser Pro Gly Gly
 Gly 450 Gly Ser Gly Gly Gly 455 Ser Glu Val Gln Leu 460 Val Glu Ser Gly
 Gly 465 Gly Leu Val Gln Pro 470 Gly Arg Ser Leu Arg 475 Leu Ser Cys Ala 480 Ala
 Ser Gly Phe Thr Phe 485 Asp Asp Tyr Ala Met 490 His Trp Val Arg Gln 495 Ala
 Pro Gly Lys Gly 500 Leu Glu Trp Val Ser 505 Ala Ile Thr Trp Asn 510 Ser Gly
 His Ile 515 Asp Tyr Ala Asp Ser Val 520 Glu Gly Arg Phe Thr 525 Ile Ser Arg
 Asp 530 Asn Ala Lys Asn Ser Leu 535 Tyr Leu Gln Met Asn 540 Ser Leu Arg Ala
 Glu 545 Asp Thr Ala Val Tyr 550 Tyr Cys Ala Lys Val 555 Ser Tyr Leu Ser Thr 560
 Ala Ser Ser Leu Asp 565 Tyr Trp Gly Lys Gly 570 Thr Leu Val Thr Val 575 Ser
 Ser Ala Ser Thr 580 Lys Gly Pro Ser Val 585 Phe Pro Leu Ala Pro 590 Ser Ser

A-1937-WO-PCT_ST25

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
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gggaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300
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tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1884
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1884

A-1937-WO-PCT_ST25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys 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
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tcctgcactg ggagcagttc caacatcggg gcagggttatg atgtacactg gtaccagcag 120
Page 1477

A-1937-WO-PCT_ST25

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aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggcccaag      540
agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc      600
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<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

A-1937-WO-PCT_ST25

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

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accaagggcc catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca	420
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tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	720
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A-1937-WO-PCT_ST25

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<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
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Gln Thr Lys Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val 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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggtcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcgaggg gaccaagggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttggtgtgc 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> 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

A-1937-WO-PCT_ST25

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 accatcgctcg 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 gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc	360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1893

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc	60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg	120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat	180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac	240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca	300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctcagcctc caccaagggc ccatcgtct tccccctggc accctcctcc	420
aagagcacct ctgggggac 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 tccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
ccatcccggg aggagatgac caagaaccag gtcagcctga 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 ggtggaggtt tgggtgcagcc ggggagatcg	1440
ctcaggctta gctgtgcggc atcgggggtt actttcgatg attatgcat gcattgggtc	1500
cggcaagcgc ctggaaaagg gctcagatgg 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 tgcctggtca aggactactt ccccgaaccg	1860

A-1937-WO-PCT_ST25

gtgacggtgt cgtggaactc aggcgccttg accagcggcg tgcacacctt cccggctgtc 1920
ctacagtcct caggactcta ctccctcgag agcgtggtga ccgtgccctc cagcagcttg 1980
ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 2040
aaagttgagc ccaaattctg t 2061

<210> 1894
<211> 687
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1894

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn
65 70 75 80

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 60

atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120

A-1937-WO-PCT_ST25

tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccg	180
gaatccgggg 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 tgttggtgtgc	420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccttc	480
caatcgggta actcccagga gagtgtcaca gacgaggaca gcaaggacag cacctacagc	540
ctcgagagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	600
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	660

<210> 1896
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<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

A-1937-WO-PCT_ST25

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 ctgaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<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

A-1937-WO-PCT_ST25

Tyr Asp Val₃₅ His Trp Tyr Gln Gln₄₀ Phe Pro Gly Thr Glu₄₅ Pro Lys Leu

Leu Ile₅₀ Gln Gly Asn Ser Asn₅₅ Arg Pro Ser Gly Val₆₀ Pro Asp Arg Phe

Ser Gly Ser Lys Ser Gly₇₀ Thr Ser Ala Ser Leu₇₅ Ala Ile Thr Gly Leu₈₀

Gln Ala Glu Asp Glu₈₅ Ala Asp Tyr Tyr Cys₉₀ Gln Ser Tyr Asp Ser₉₅ Ser

Leu Ser Gly Ser₁₀₀ Val Phe Gly Gly Gly₁₀₅ Thr Lys Leu Thr Val₁₁₀ Leu Gly

Gln Pro Lys₁₁₅ Ala Ala Pro Ser Val₁₂₀ Thr Leu Phe Pro Pro₁₂₅ Ser Ser Glu

Glu Leu₁₃₀ Gln Ala Asn Lys Ala₁₃₅ Thr Leu Val Cys Leu₁₄₀ Ile Ser Asp Phe

Tyr Pro Gly Ala Val Thr₁₅₀ Val Ala Trp Lys Ala₁₅₅ Asp Ser Ser Pro Val₁₆₀

Lys Ala Gly Val Glu₁₆₅ Thr Thr Thr Pro Ser₁₇₀ Lys Gln Ser Asn Asn₁₇₅ Lys

Tyr Ala Ala Lys₁₈₀ Ser Tyr Leu Ser Leu₁₈₅ Thr Pro Glu Gln Trp₁₉₀ Lys Ser

His Arg Ser₁₉₅ Tyr Ser Cys Gln Val₂₀₀ Thr His Glu Gly Ser₂₀₅ Thr Val Glu

Lys Thr₂₁₀ Val Ala Pro Thr Glu₂₁₅ Cys Ser

<210> 1899

<211> 2046

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1899

caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60

acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120

cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180

aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240

cagttctccc tgaagctgag ctctgtgact gccgcggaca cggtgtgta ttactgtgca 300

agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360

A-1937-WO-PCT_ST25

gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc accctcctcc	420
aagagcacct ctggggggcac agcgggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct	540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagtgt agcccaaadc ttgtgacaaa actcacacat gcccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc tccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc	1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1200
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg	1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg	1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt	1380
ggcggatccg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggggagtct	1440
ctgaagatct cctgtaagac ttctgaatac agctttacca gctactggat cggctgggtg	1500
cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcttgg tgactcagat	1560
accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgcagtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680
agaagtaact ggggtcttga ctactggggc aagggaaccc 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 gcttgggcac ccagacctac	1980
atctgcaacg tgaatcacia gccagcaac accaaggtgg acaagaaagt tgagcccaaa	2040
tcttgt	2046

<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggt 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

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
          20           25           30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Glu Pro Arg Leu Leu
          35           40           45

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

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A-1937-WO-PCT_ST25

<210> 1903
 <211> 2055
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 1903
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 agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
 cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
 gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
 cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
 tacttgtcta cagcttcgtc gctcgactat tggggtaag gaacgttggg caccgtctct 360
 agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 480
 tgggaagggtg 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
 ctcttggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 780
 tcccggaacc ctgaggtcac atgctgtgtg 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
 tccggggagg agatgacaa gaaccaggtc agcctgacct gcctgggtcaa aggccttctat 1140
 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200
 acgcctcccg tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac 1260
 aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcg tgatgcatga ggctctgcac 1320
 aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
 ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 1440
 tccctcacct gcgctgtcca tgggtgggtc 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 aggaaccct agtcaccgtc 1740
 tcctcagcct ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 1800

A-1937-WO-PCT_ST25

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 1860
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc 1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2040
gagcccaaat 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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> 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

A-1937-WO-PCT_ST25

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu 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 tgaccagtc 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 acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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

gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60

agctgtgctg catcggtgtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120

cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180

gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240

cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300

A-1937-WO-PCT_ST25

tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct	360
agtacggtgg ctgcaccatc tgtcttcac tttccgccat ctgatgagca gttgaaatct	420
ggaactgcct ctgttgtgtg cctgctgaat aactttctatc ccagagaggc caaagtacag	480
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac	540
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag	600
aaacacaaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaaag	660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa	720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac	780
tcccggaccc ctgaggtcac atgctgtgtg 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
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tcccgggagg agatgacaa gaaccaggtc agcctgacct gcctgggtcaa aggtctctat	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 gggaggtggc	1380
ggatcccagg tgcagctgca ggagtcgggc ccaggactgg tgaagccttc ggagaccctg	1440
tcctcacct gcactgtctc tgggtggctcc atcagtagtt acttctggag ctggattcgg	1500
cagccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacaaaa	1560
tacaaccct ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc	1620
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actgggagct actacggctt tgactactgg ggcaagggaa ccctgggtcac cgtctctca	1740
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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	1920
ggactctact ccctcgagag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	1980
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aaatcttgt	2049

<210> 1910
 <211> 683
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1910

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60
 Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val
 115 120 125
 Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 130 135 140
 Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 145 150 155 160
 Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 165 170 175
 Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys Ser Thr Leu
 180 185 190
 Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 195 200 205
 Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 210 215 220
 Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 225 230 235 240
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 245 250 255

A-1937-WO-PCT_ST25

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 260 265 270
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 275 280 285
 Val Glu Val His Asn Ala Lys Thr Lys Pro Cys Glu Glu Gln Tyr Gly
 290 295 300
 Ser Thr Tyr Arg Cys Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 305 310 315 320
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 325 330 335
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 340 345 350
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 355 360 365
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 405 410 415
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445
 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

A-1937-WO-PCT_ST25

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 tttactctca caatttccag cctgcagccc 240

gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300

gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggctct cccctggca 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420

ttcccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480

ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600

aaggtggaca agaaagttga gcccaaattct tgt

<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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
 atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
 tgggtaccagc agaaaccagg aaaggagcct aaactgtctca ttactgggc atctaccggt 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 tgttggtgtgc 420
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480
 caatcgggta actcccagga gagtgtcaca gacgaggaca 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

A-1937-WO-PCT_ST25

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 catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 420
ggaactgcct ctgttggttg cctgctgaat aacttctatc ccagagaggc caaagtagac 480
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 540
agcaaggaca gcacctacag cctcaagagc accctgacgc tgagcaaagc agactacgag 600
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcaciaaag 660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac 780
tcccggaacc ctgaggtcac atgctgtgtg gtggacgtga gccacgaaga ccctgaggtc 840

A-1937-WO-PCT_ST25

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgtgtgag 900
gagcagtacg gcagcacgta ccgttgtgtc agcgtcctca ccgtcctgca ccaggactgg 960
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag 1020
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1080
tccccgggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggtttctat 1140
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1200
acgcctcccc tgctggactc cgacgggtcc ttcttctct atagcaagct caccgtggac 1260
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcg tgatgcatga ggctctgcac 1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380
ggatcccagg tacagttgca ggagtcaggt ccaggactgg tgaagccctc ggagaccctc 1440
tcactcacct gtaccatctc cggggacagt gtctctacca acagtgttgc ttggaactgg 1500
attaggcagc ccccagggaaggccttgag 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
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 gcgtggtgac cgtgccctcc 1980
agcagcttgg gcaccagac 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgctcca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgctg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 1918
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1918

A-1937-WO-PCT_ST25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys 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 gagtgttaga agcagttact tagcctggta ccagcagaaa 120
Page 1516

A-1937-WO-PCT_ST25

cctggccagg agcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgaacggtg gctgcaccat ctgtcttcat cttcccggca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgtttgtg gcctgctgaa taactttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcaagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Lys
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1921

<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1921

gaggtgcagc	tggtgcagtc	tgagcagag	gtgaaaaagc	ccggggagtc	tctgaagatc	60
tcctgtaaga	cttctgaata	cagctttacc	agctactgga	tcggctgggt	gcgccagatg	120
cccgggaaaa	aactggagtg	gatggggatc	atctatcttg	gtgactcaga	taccagatac	180
agcccgctct	tccaaggcca	ggtcaccatc	tcagccgaca	agtccatcag	taccgcctac	240
ctgcagtgga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	gagaagtaac	300
tggggctctg	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
gtcttctctt	tcccccaaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgttgtg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	960
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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

A-1937-WO-PCT_ST25

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
 agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccca ggtgcagtta 1380
 cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgctgtgtc 1440
 catggtgggt ccttcagtgg ttactactgg aactggattc gccagccacc agggaagggg 1500
 ctagagtggg ttgggggaaat caatcatgct ggaaacacca actacaaccg gtccctcaag 1560
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 gtgaccgccg cggacacggc tgtgtattac tgtgagagag gatattgtag aagtaccacc 1680
 tgctactttg actactgggg caaggaacc ctagtcaccg tctcctcagc ctccaccaag 1740
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 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 1920
 ctcgagagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac 1980
 gtgaatcaca agcccagcaa caccaaggtg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser 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

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cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc      60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag      120
tttccaggaa cagcccccaa actcctcatc caaggaataa gcaatcggcc ctgaggggtc      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 cttccccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg      540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      600
cccagcaaca ccaagggtga caagaaagt gagcccaaat cttgt                      645
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<210> 1924

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1924

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

A-1937-WO-PCT_ST25

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ser Val Phe Gly Glu Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
165 170 175

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 1925

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1925

gacatccaga tgaccagtc 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 acgaacggtg gctgcaccat ctgtcttcat cttcccgcc	360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1927
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
tggggtcttg actactgggg ccaggaacc ctggtcaccg tctctagtca gccaaggcc 360
aaccctactg tctctgtt 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 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 ctccaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag 1260
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ctggagtgga ttggctatat ctattacagt gggcagacca aatacaacct ctccctcaag 1560
agtcgagtca ccatatcaat agacacgtcc aagaaccagt tctccctgaa gctgagctct 1620
gtgaccgctg cggacacggc cgtgtattac tgtgcgagag aaactgggag ctactacggc 1680
tttgactact ggggcaaggg aaccctggtc accgtctcct cagcctccac caagggccca 1740
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 1800
tgcctgggtca aggactactt cccgaaccg gtgacggtgt cgtggaactc aggcgcctg 1860

A-1937-WO-PCT_ST25

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgag 1920
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 1980
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 60

tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

A-1937-WO-PCT_ST25

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagggttcg 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> 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt 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 gaccaaggtg gagatcaaac gaacggtggc 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> 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

A-1937-WO-PCT_ST25

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 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 accgccatgt attactgtgc gagaagtaac 300
tggggtcttg actactgggg ccaggaacc ctggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tcactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420

A-1937-WO-PCT_ST25

ctagtgtgtc	tgatcagtga	cttctacccg	ggagctgtga	cagtggcctg	gaaggcagat	480
ggcagccccg	tcaaggcggg	agtggagacc	accaaaccct	ccaaacagag	caacaacaag	540
tacgcggcca	agagctacct	gagcctgacg	cccagacagt	ggaagtccca	cagaagctac	600
agctgccagg	tcacgcatga	agggagcacc	gtggagaaga	cagtggcccc	tacagaatgt	660
tcagacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg	aactcctggg	gggaccgtca	720
gtcttcctct	tcccccaaaa	acccaaggac	accctcatga	tctcccggac	ccctgaggtc	780
acatgcgtgg	tggtggacgt	gagccacgaa	gaccctgagg	tcaagttcaa	ctggtacgtg	840
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgtgtg	aggagcagta	cggcagcacg	900
taccgtttgtg	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
tccgacgggt	ccttcttctt	ctatagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1260
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1320
agcctctccc	tgtctccggg	tggtggcgga	tcgggaggtg	gcggatccca	ggtacagttg	1380
caggagtcat	gtccaggact	ggtgaagccc	tcggagaccc	tctcactcac	ctgtaccatc	1440
tccggggaca	gtgtctctac	caacagtgtt	gcttggaact	ggattaggca	gccccaggg	1500
aaaggccttg	agtggatagg	aaggacatac	tacaggtcca	agtgggtataa	tgattatgca	1560
gtttctctga	aaagtcgagt	aaccatcagc	ccagacacat	ccaagaacca	gttctccctg	1620
aagctgagct	ctgtgactgc	cgcgacacg	gctgtgtatt	actgtgcaag	agaggatggg	1680
gatagctact	accgctacgg	tatggacgtc	tggggcaaa	ggaccacggt	caccgtctcc	1740
tcagcctcca	ccaagggccc	atcggtcttc	cccctggcac	cctcctccaa	gagcacctct	1800
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	1860
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tccgggctgt	cctacagtcc	1920
tcaggactct	actccctcga	gagcgtggtg	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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 cagccccaa 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 cagcgccct gggctgcctg	420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc	480
ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactcct 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

A-1937-WO-PCT_ST25

<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
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

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
caggtgcagt 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 cgcgacacg 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 acatgccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtctt 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

A-1937-WO-PCT_ST25

aatggcaagg agtacaagtg caaggtctcc 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
 cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260
 agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1320
 cactacacgc agaagagcct ctccctgtct ccgggtgggtg gcggatcggg aggtggcgga 1380
 tccgaggtac aactgggtga atcaggtgga ggtttgggtg agccggggag atcgctcagg 1440
 cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa 1500
 gcgcctggaa aagggtcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat 1560
 tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg 1620
 taccttcaga tgaactcact tcgcgcgga gataccgccg tatactactg cgccaaagtc 1680
 tcctacttgt ctacagcttc gtcgctcgac tattggggta aaggaacgtt ggtcaccgtc 1740
 tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctctc 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
 gagcccaaatt 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
625 630 635 640

Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val Val Thr Val Pro Ser Ser
645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
660 665 670

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
675 680 685

<210> 1941
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1941
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg 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> 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

A-1937-WO-PCT_ST25

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 ctccaggggctc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300

gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 1945
<211> 2040
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1945
caggtgcagt 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
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 540
aaggacagca cctacagcct caagagcacc ctgacgctga gcaaagcaga ctacgagaaa 600
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctgggggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc 780
cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggg acgtggacgg cgtggaggtg cataatgcca agacaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1080
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc 1140
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1200
cctcccgtgc tggactccga cggctccttc ttctctata gcaagctcac cgtggacaag 1260
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 ggtgcgccag 1500

A-1937-WO-PCT_ST25

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
 aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1800
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 1860
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1920
 tccctcgaga gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1980
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 2040

<210> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
450 455 460

Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys
465 470 475 480

Ile Ser Cys Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly
485 490 495

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile
500 505 510

Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln
515 520 525

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp
530 535 540

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser
545 550 555 560

Asn Trp Gly Leu Asp Tyr Trp Gly 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

A-1937-WO-PCT_ST25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1947
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 cttcggcgaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-W0-PCT_ST25

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 gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat 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> 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

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc

60

A-1937-WO-PCT_ST25

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc	120
ccaggttaaga aactggagtg gattggctat atctattaca gtgggcagac caaataacaac	180
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg	240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg	300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacgggtg	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 tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgctggtt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgtttgtg 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 cttcttctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtacaactgg tggaatcagg tggaggtttg gtgcagccgg ggagatcgct caggcttagc	1440
tgtgcggcat cggggtttac tttcgatgat tatgcatgc attgggtccg gcaagcgctt	1500
ggaaaagggc tcgagtgggt ttccgccatt acgtggaata gcggacacat cgattatgca	1560
gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt	1620
cagatgaact cacttcgcgc ggaagatacc gccgtatact actgcgcaa agtctcttac	1680
ttgtctacag cttcgtcgct cgactattgg ggtaaaggaa cgttgggtcac 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> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 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 gttcggcgaa 300

gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360

A-1937-WO-PCT_ST25

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttccccggtg 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccagcag 120
tttccaggaa cagagcccaa actcctcatc caaggtaaca gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactggggtc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtgggttcg 300
gtgttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcgggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggcccaag 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcacctg 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

A-1937-WO-PCT_ST25

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

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc 120

ccaggtaaga aactggagtg gattggctat atctattaca gtgggcagac caaatacaac 180

ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300

agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacggtg 360

gctgcacat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420

tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480

gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540

agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600

A-1937-WO-PCT_ST25

gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac	660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa 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 ctcattgtcc gtgatgcatg aggtcttgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccg gggagtctct gaagatctcc	1440
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gggaaaggcc tggagtggat ggggatcatc tatcttggtg actcagatac cagatacagc	1560
ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtac cgcctacctg	1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg	1680
ggtcttgact actggggcaa ggaaccctg gtcaccgtct ctagtgcttc caccaagggc	1740
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	1800
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	1860
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc	1920
gagagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	1980
aatcacaagc ccagcaacac caaggtggac aagaaagttg 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			

A-1937-WO-PCT_ST25

Phe Trp Ser₃₅ Trp Ile Arg Gln Pro₄₀ Pro Gly Lys Lys₄₅ Leu Glu Trp Ile

Gly Tyr₅₀ Ile Tyr Tyr Ser Gly₅₅ Gln Thr Lys Tyr Asn₆₀ Pro Ser Leu Lys

Ser₆₅ Arg Val Thr Ile Ser₇₀ Ile Asp Thr Ser Lys₇₅ Asn Gln Phe Ser Leu₈₀

Lys Leu Ser Ser₈₅ Val Thr Ala Ala Asp Thr₉₀ Ala Val Tyr Tyr Cys₉₅ Ala

Arg Glu Thr Gly₁₀₀ Ser Tyr Tyr Gly Phe₁₀₅ Asp Tyr Trp Gly Gln₁₁₀ Gly Thr

Leu Val Thr₁₁₅ Val Ser Ser Thr Val₁₂₀ Ala Ala Pro Ser Val₁₂₅ Phe Ile Phe

Pro Pro₁₃₀ Ser Asp Glu Gln Leu₁₃₅ Lys Ser Gly Thr Ala₁₄₀ Ser Val Val Cys

Leu₁₄₅ Leu Asn Asn Phe Tyr₁₅₀ Pro Arg Glu Ala Lys₁₅₅ Val Gln Trp Lys Val₁₆₀

Asp Asn Ala Leu Gln₁₆₅ Ser Gly Asn Ser Gln₁₇₀ Glu Ser Val Thr Glu₁₇₅ Gln

Asp Ser Lys Asp₁₈₀ Ser Thr Tyr Ser Leu₁₈₅ Lys Ser Thr Leu Thr₁₉₀ Leu Ser

Lys Ala Asp₁₉₅ Tyr Glu Lys His Lys₂₀₀ Val Tyr Ala Cys Glu₂₀₅ Val Thr His

Gln Gly₂₁₀ Leu Ser Ser Pro Val₂₁₅ Thr Lys Ser Phe Asn₂₂₀ Arg Gly Glu Cys

Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met

Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His

Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val

His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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 ccccttggca 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> 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 accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg

60

A-1937-WO-PCT_ST25

attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
 ggaaaagagc cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgctttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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
caggtagcagc tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480
gccaaagtac agtgaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660
cccgtcaca agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc 720
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac 780
accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa 840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900
aagccgtgtg aggagcagta cggcagcacg taccgttggt 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

A-1937-WO-PCT_ST25

aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctatagcaag	1260
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1320
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg tggtagcgga	1380
tcgggaggtg gcggatccga ggtacaactg gtggaatcag gtggaggttt ggtgcagccg	1440
gggagatcgc tcaggcttag ctgtgctggca tcgggggttta ctttcgatga ttatgcatg	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 gcttcgctgc tcgactattg gggtaaagga	1740
acgttgggtc ccgtctctag tgcctccacc aaggggccat cggctctccc cctggcacc	1800
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	1860
cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	1920
ccggctgtcc tacagtctc aggactctac tccctcgaga gcgtggtgac cgtgccctcc	1980
agcagcttgg gcaccagac 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaagggttct aaactgctca ttactgggc atctaccgg 180
gaatccgggg 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
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt 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

A-1937-WO-PCT_ST25

Val₅₀ Pro Lys Leu Leu Ile Tyr₅₅ Trp Ala Ser Thr Arg₆₀ Glu Ser Gly Val

Pro Ser Arg Phe Ser Gly₇₀ Ser Gly Ser Gly Thr₇₅ Asp Phe Thr Leu Thr₈₀

Ile Ser Ser Leu Gln₈₅ Pro Glu Asp Val Ala₉₀ Thr Tyr Tyr Cys Gln₉₅ Gln

Tyr Tyr Lys Thr₁₀₀ Pro Leu Thr Phe Gly₁₀₅ Glu Gly Thr Lys Val₁₁₀ Glu Ile

Lys Arg Ala₁₁₅ Ser Thr Lys Gly Pro₁₂₀ Ser Val Phe Pro Leu₁₂₅ Ala Pro Ser

Ser Lys₁₃₀ Ser Thr Ser Gly Gly₁₃₅ Thr Ala Ala Leu Gly₁₄₀ Cys Leu Val Lys

Asp Tyr Phe Pro Glu Pro₁₅₀ Val Thr Val Ser Trp₁₅₅ Asn Ser Gly Ala Leu₁₆₀

Thr Ser Gly Val His₁₆₅ Thr Phe Pro Ala Val₁₇₀ Leu Gln Ser Ser Gly₁₇₅ Leu

Tyr Ser Leu Glu₁₈₀ Ser Val Val Thr Val₁₈₅ Pro Ser Ser Ser Leu₁₉₀ Gly Thr

Gln Thr Tyr₁₉₅ Ile Cys Asn Val Asn₂₀₀ His Lys Pro Ser Asn₂₀₅ Thr Lys Val

Asp Lys₂₁₀ Lys Val Glu Pro Lys₂₁₅ Ser Cys

<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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagagcccaa actcctcatc caaggttaaca 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

A-1937-WO-PCT_ST25

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggcccaag 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
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 cagccccag gaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180
 aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
 cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
 agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
 gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
 cagttgaaat ctggaactgc ctctgtttgtg 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 gtcttctct tcccccaaa acccaaggac 780
 accctcatga tctcccgga ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa 840
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 900
 aagccgtgtg aggagcagta cggcagcacg taccgtttgtg tcagcgtcct caccgtcctg 960
 caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca 1020
 gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1080
 accctgcccc catcccgga 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
 gaggtcttgc acaaccacta cacgcagaag agcctctccc tgtctccggg tgggtggcga 1380
 tcgggaggtg gcggatccga ggtgcagctg gtgcagctct gagcagaggt gaaaaagccc 1440
 ggggagtctc tgaagatctc ctgtaagact tctgaatata gctttaccag ctactggatc 1500
 ggctgggtgc gccagatgcc cgggaaaggc ctggagtggg tggggatcat ctatcttggg 1560
 gactcagata ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag 1620

A-1937-WO-PCT_ST25

tccatcagta cgcctacct gcagtggagc agcctgaagg cctcggacac cgccatgtat	1680
tactgtgcga gaagtaactg gggctcttgac tactggggca agggaaccct ggtcaccgtc	1740
tctagtgcct ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	1800
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1860
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag	1920
tcctcaggac tctactccct cgagagcgtg gtgaccgtgc cctccagcag cttgggcacc	1980
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	2040
gagcccaaat cttgt	2055

<210> 1970
 <211> 685
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polypeptide
 <400> 1970

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn	20 25 30
Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu	35 40 45
Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala	50 55 60
Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn	65 70 75 80
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

A-1937-WO-PCT_ST25

Ala Lys Val Gln Trp₁₆₅ Lys Val Asp Asn Ala₁₇₀ Leu Gln Ser Gly Asn₁₇₅ Ser

Gln Glu Ser Val₁₈₀ Thr Glu Gln Asp Ser₁₈₅ Lys Asp Ser Thr Tyr₁₉₀ Ser Leu

Lys Ser Thr₁₉₅ Leu Thr Leu Ser Lys₂₀₀ Ala Asp Tyr Glu Lys₂₀₅ His Lys Val

Tyr Ala₂₁₀ Cys Glu Val Thr His₂₁₅ Gln Gly Leu Ser Ser₂₂₀ Pro Val Thr Lys

Ser₂₂₅ Phe Asn Arg Gly Glu₂₃₀ Cys Asp Lys Thr His₂₃₅ Thr Cys Pro Pro Cys₂₄₀

Pro Ala Pro Glu Leu₂₄₅ Leu Gly Gly Pro Ser₂₅₀ Val Phe Leu Phe Pro₂₅₅ Pro

Lys Pro Lys Asp₂₆₀ Thr Leu Met Ile Ser₂₆₅ Arg Thr Pro Glu Val₂₇₀ Thr Cys

Val Val Val₂₇₅ Asp Val Ser His Glu₂₈₀ Asp Pro Glu Val Lys₂₈₅ Phe Asn Trp

Tyr Val₂₉₀ Asp Gly Val Glu Val₂₉₅ His Asn Ala Lys Thr₃₀₀ Lys Pro Cys Glu

Glu₃₀₅ Gln Tyr Gly Ser Thr₃₁₀ Tyr Arg Cys Val Ser₃₁₅ Val Leu Thr Val Leu₃₂₀

His Gln Asp Trp Leu₃₂₅ Asn Gly Lys Glu Tyr₃₃₀ Lys Cys Lys Val Ser₃₃₅ Asn

Lys Ala Leu Pro₃₄₀ Ala Pro Ile Glu Lys₃₄₅ Thr Ile Ser Lys Ala₃₅₀ Lys Gly

Gln Pro Arg₃₅₅ Glu Pro Gln Val Tyr₃₆₀ Thr Leu Pro Pro Ser₃₆₅ Arg Glu Glu

Met Thr₃₇₀ Lys Asn Gln Val Ser₃₇₅ Leu Thr Cys Leu Val₃₈₀ Lys Gly Phe Tyr

Pro₃₈₅ Ser Asp Ile Ala Val₃₉₀ Glu Trp Glu Ser Asn₃₉₅ Gly Gln Pro Glu Asn₄₀₀

Asn Tyr Lys Thr Thr₄₀₅ Pro Pro Val Leu Asp₄₁₀ Ser Asp Gly Ser Phe₄₁₅ Phe

Leu Tyr Ser Lys₄₂₀ Leu Thr Val Asp Lys₄₂₅ Ser Arg Trp Gln Gln₄₃₀ Gly Asn

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt      120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg      180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact      300
cctctcactt tcggcgaagg gaccaaggtg gagatcaaac gagcctccac caagggccca      360
tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggccctgggc      420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg      480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t              651

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<210> 1972

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1972

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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 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

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A-1937-WO-PCT_ST25

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
gatatccaaa tgacacaatc accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaaatccg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggt 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> 1974
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1974

A-1937-WO-PCT_ST25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys 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
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60

agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcattgggt ccggcaagcg 120

A-1937-WO-PCT_ST25

cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat	180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac	240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc	300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct	360
agtgcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggacacag 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
cctgaggtca catgctgggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtac	900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg	1260
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gtgcagttac agcagtcggg cgcaggactg ttgaagcctt cggagaccct gtccctcacc	1440
tgcgctgtcc atggtgggtc cttcagtgggt tactactgga actggattcg ccagccacca	1500
gggaaggggc tagagtggat tggggaaatc aatcatgctg gaaacaccaa ctacaaccg	1560
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agtaccacct gctactttga ctactggggc aagggaaacc tagtcaccgt ctctcaact	1740
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact	1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag	1860
gtggataacg ccctccaatc gggttaactc caggagagtg tcacagagca ggacagcaag	1920
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac	1980
aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc	2040
aacaggggag agtgt	2055

<210> 1976

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 1976

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val
35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

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

A-1937-WO-PCT_ST25

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
Arg₃₀₅ Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Gln₄₆₀ Val Gln Leu Gln
Gln₄₆₅ Ser Gly Ala Gly Leu₄₇₀ Leu Lys Pro Ser Glu₄₇₅ Thr Leu Ser Leu Thr₄₈₀
Cys Ala Val His Gly₄₈₅ Gly Ser Phe Ser Gly₄₉₀ Tyr Tyr Trp Asn Trp₄₉₅ Ile
Arg Gln Pro Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Ile Gly Glu Ile₅₁₀ Asn His

A-1937-WO-PCT_ST25

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 gagtggttaga agcagttact tagcctggta ccagcagaaa 120

cctggccagg aaccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gctcacctac cttcggccaa 300

gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420

A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctccaggactc tactccctca aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct tgt	633

<210> 1978
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1978

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Arg	Ser	Ser
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Glu	Pro	Arg	Leu	Leu
		35					40					45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80

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		

A-1937-WO-PCT_ST25

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 1979
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 1979
gatatccaaa tgacacaatc accatcgctg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtcca gggaatccgg aattacctg catggtatca gcaaaaaccc 120
ggaaaagcac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300
gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgaaag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 1980
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1980

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

A-1937-WO-PCT_ST25

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
85 90 95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys Arg 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
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgctta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtgccctcca ccaagggccc atcgggtctt cccctggcac cctcctcaa gagcacctct 420
gggggacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcaa aagcgtggtg accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

A-1937-WO-PCT_ST25

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cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgtgtga ggagcagtac 900
ggcagcacgt accgtttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
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gtgcagctgc aggagtcggg ccaggactg gtgaagcctt cggagaccct gtccctcacc 1440
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tccctcaaga gtcgagtcac catatcaata gacacgtcca agaaccagtt ctccctgaag 1620
ctgagctctg tgaccgtgc ggacacggcc gtgtattact gtgcgagaga aactgggagc 1680
tactacggct ttgactactg gggcaaggga accctggtca 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 cctgacgtg agcaaagcag actacgagaa acacaaagtc 1980
tacgcctgcg aagtcacca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 2040
ggagagtgt 2049

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<210> 1982
 <211> 683
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 1982

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt cccctcggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctgaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca 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 accatcgctcgt ctttcagcgt ctgttggcga ccgtgtgacg

60

A-1937-WO-PCT_ST25

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 cgctttacac attcggagaa 300
 gggacaaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 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 tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgctta cagcttcgtc gctcgactat tgggggtcaag gaacgttggt caccgtctct 360
agtgcctcca ccaagggccc 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
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccggacc 780
cctgaggtca catgctggtt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
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gagatgacca agaaccaggt cagcctgacc tgctgtgtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

A-1937-WO-PCT_ST25

gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg 1260
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 acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatcccag 1380
 gtacagttgc aggagtcagg tccaggactg gtgaagccct cggagaccct ctactcacc 1440
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 cccccagga 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 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> 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

A-1937-WO-PCT_ST25

Gln Gly Thr₁₁₅ Leu Val Thr Val Ser₁₂₀ Ser Ala Ser Thr Lys₁₂₅ Gly Pro Ser
Val Phe₁₃₀ Pro Leu Ala Pro Ser₁₃₅ Ser Lys Ser Thr Ser₁₄₀ Gly Gly Thr Ala
Ala₁₄₅ Leu Gly Cys Leu Val₁₅₀ Lys Asp Tyr Phe Pro₁₅₅ Glu Pro Val Thr Val₁₆₀
Ser Trp Asn Ser Gly₁₆₅ Ala Leu Thr Ser Gly₁₇₀ Val His Thr Phe Pro₁₇₅ Ala
Val Leu Gln Ser₁₈₀ Ser Gly Leu Tyr Ser₁₈₅ Leu Lys Ser Val Val₁₉₀ Thr Val
Pro Ser Ser₁₉₅ Ser Leu Gly Thr Gln₂₀₀ Thr Tyr Ile Cys Asn₂₀₅ Val Asn His
Lys Pro₂₁₀ Ser Asn Thr Lys Val₂₁₅ Asp Lys Lys Val Glu₂₂₀ Pro Lys Ser Cys
Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀
Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
Arg Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc 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 gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggtgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagccccaa actcctcatc caaggaataa 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 tctaccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480

A-1937-WO-PCT_ST25

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540
agctatctga gcctgacgcc tgagcagtgg 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
 agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
 tggggctcttg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tggggggacc 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
 aaggtctcca acaaagccct ccagcccc atcgagaaaa ccatctcaa 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
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 gggtccttca gtggttacta ctggaactgg attcgccagc caccagggaa ggggctagag 1500
 tggattgggg aaatcaatca tgctggaac accaactaca acccgctcct caagagtcga 1560
 gtcaccatat cattagacac gtccaagaac cagttctccc tgacgtgac ctctgtgacc 1620

A-1937-WO-PCT_ST25

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 taacgccttc 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

A-1937-WO-PCT_ST25

Gly Leu Tyr Ser₁₈₀ Leu Lys Ser Val₁₈₅ Val Thr Val Pro Ser₁₉₀ Ser Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val₂₁₅ Glu Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Leu Leu Gly₂₃₅ Gly Pro Ser Val₂₄₀ Phe
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr₂₅₀ Leu Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp₂₆₅ Val Ser His Glu Asp₂₇₀ Pro Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Cys Glu Glu Gln₂₉₅ Tyr Gly Ser Thr Tyr Arg₃₀₀ Cys Val Ser Val
 Leu₃₀₅ Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn₃₂₅ Lys Ala Leu Pro Ala₃₃₀ Pro Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu₃₄₅ Pro Gln Val Tyr Thr Leu₃₅₀ Pro Pro
 Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe₄₀₅ Leu Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp
 Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His
 Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly

A-1937-WO-PCT_ST25

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

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
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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 catcgggtctt ccccttgga      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc      540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

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<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

```

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Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
115          120          125

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A-1937-WO-PCT_ST25

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 ctgaggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact 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> 1998
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1998

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

A-1937-WO-PCT_ST25

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> 1999

<211> 2034

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 1999

gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cccggggagtc tctgaagatc 60

tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180

A-1937-WO-PCT_ST25

agcccgctcct	tccaaggcca	ggtcaccatc	tcagccgaca	agtccatcag	taccgcctac	240
ctgcagtggga	gcagcctgaa	ggcctcggac	accgccatgt	attactgtgc	gagaagtaac	300
tggggctcttg	actactgggg	ccaggggaacc	ctggtcaccg	tctctagtgc	ctccaccaag	360
ggcccatcgg	tcttccccct	ggcaccctcc	tccaagagca	cctctggggg	cacagcggcc	420
ctgggctgcc	tgggtcaagga	ctacttcccc	gaaccggtga	cgggtgtcgtg	gaactcaggc	480
gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	540
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gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaag	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaactcc	tgggggggacc	gtcagtcttc	720
ctcttcccc	caaaaccaa	ggacaccctc	atgatctccc	ggaccctga	ggtcacatgc	780
gtgggtgggtg	acgtgagcca	cgaagaccct	gaggtcaagt	tcaactggta	cgtggacggc	840
gtggaggtgc	ataatgcaa	gacaaagccg	tgtgaggagc	agtacggcag	cacgtaccgt	900
tgtgtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcaagga	gtacaagtgc	960
aaggtctcca	acaaagccct	cccagcccc	atcgagaaaa	ccatctccaa	agccaaaggg	1020
cagccccgag	aaccacaggt	gtacaccctg	cccccatccc	gggaggagat	gaccaagaac	1080
caggtcagcc	tgacctgcct	ggtcaaaggc	ttctatccca	gcgacatcgc	cgtggagtgg	1140
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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	attcggcagc	cccaggttaa	gggactggag	1500
tggattggct	atatctatta	cagtgggcag	accaaataca	accctccct	caagagtcga	1560
gtcaccatat	caatagacac	gtccaagaac	cagttctccc	tgaagctgag	ctctgtgacc	1620
gctgcggaca	cggccgtgta	ttactgtgcg	agagaaactg	ggagctacta	cggctttgac	1680
tactggggca	aggaaccct	ggtcaccgtc	tcctcaactg	tggctgcacc	atctgtcttc	1740
atcttcccg	catctgatga	gcagttgaaa	tctggaactg	cctctgttgt	gtgcctgctg	1800
aataacttct	atcccagaga	ggccaaagta	cagtgggaagg	tggataacgc	cctccaatcg	1860
ggtaactccc	aggagagtgt	cacagagcag	gacagcaagg	acagcaccta	cagcctcgaa	1920
agcaccctga	cgctgagcaa	agcagactac	gagaaacaca	aagtctacgc	ctgcgaagtc	1980
acccatcagg	gcctgagctc	gcccgtcaca	aagagcttca	acaggggaga	gtgt	2034

<210> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr
530 535 540

Ala Val Tyr Tyr Cys Ala Arg Glu Thr Gly Ser Tyr Tyr Gly Phe Asp
545 550 555 560

Tyr Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala
565 570 575

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
580 585 590

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
595 600 605

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
610 615 620

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
625 630 635 640

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
645 650 655

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
660 665 670

Phe Asn Arg Gly Glu Cys
675

<210> 2001
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2001
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcgggtctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540

A-1937-WO-PCT_ST25

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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 ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtcagc ccaaggctgc cccctcggtc 360
actctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccgaa 540
agctatctga gcctgacgcc tgagcagtg aagtcccaca gaagctacag ctgccaggtc 600
acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc a 651

<210> 2004
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 2004

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30
Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35 40 45
Leu Ile Gln Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60
Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

A-1937-WO-PCT_ST25

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
agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctctg actactgggg ccaggaacc ctggtcaccg tctctagtgc ctccaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcaaaagcg tggtgaccgt gccctccagc agcttgggca ccagacctc catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

A-1937-WO-PCT_ST25

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataatgcca 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 ggagccgga gaacaactac aagaccacgc ctcccgctgt ggactccgac 1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggtggtgg cggatcggga ggtggcggat cccaggtaca gttgcaggag 1380
tcaggtccag gactggtgaa gccctcggag accctctcac tcacctgtac catctccggg 1440
gacagtgtct ctaccaacag tgttgcttgg aactggatta ggcagccccc agggaaaggc 1500
cttgagtgga taggaaggac atactacagg tccaagtggg ataattgatta tgcagtttct 1560
ctgaaaagtc gagtaacat cagcccagac acatccaaga accagttctc cctgaagctg 1620
agctctgtga ctgccgcgga cacggctgtg tattactgtg caagagagga tggggatagc 1680
tactaccgct acggtatgga cgtctggggc aaagggacca cggtcaccgt ctctcaact 1740
gtggctgcac catctgtctt catcttccc ccatctgatg agcagttgaa atctggaact 1800
gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860
gtggataacg ccctccaatc gggtaactcc caggagagtgc tcacagagca ggacagcaag 1920
gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980
aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc 2040
aacaggggag agtgt 2055

<210> 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

A-1937-WO-PCT_ST25

Gly Ile Ile Tyr Leu Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Asn Trp Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser 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

A-1937-WO-PCT_ST25

Lys Val Ser Asn Lys₃₂₅ Ala Leu Pro Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro
 Ser Arg Glu₃₅₅ Glu Met Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe Leu₄₀₅ Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp
 Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His
 Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly
 Ser Gly₄₅₀ Gly Gly Gly Ser Gln₄₅₅ Val Gln Leu Gln Glu₄₆₀ Ser Gly Pro Gly
 Leu Val Lys Pro Ser Glu₄₇₀ Thr Leu Ser Leu Thr₄₇₅ Cys Thr Ile Ser Gly₄₈₀
 Asp Ser Val Ser Thr₄₈₅ Asn Ser Val Ala Trp₄₉₀ Asn Trp Ile Arg Gln₄₉₅ Pro
 Pro Gly Lys Gly₅₀₀ Leu Glu Trp Ile Gly₅₀₅ Arg Thr Tyr Tyr Arg₅₁₀ Ser Lys
 Trp Tyr Asn₅₁₅ Asp Tyr Ala Val Ser₅₂₀ Leu Lys Ser Arg Val₅₂₅ Thr Ile Ser
 Pro Asp₅₃₀ Thr Ser Lys Asn Gln₅₃₅ Phe Ser Leu Lys Leu₅₄₀ Ser Ser Val Thr
 Ala Ala Asp Thr Ala Val₅₅₀ Tyr Tyr Cys Ala Arg₅₅₅ Glu Asp Gly Asp Ser₅₆₀
 Tyr Tyr Arg Tyr Gly₅₆₅ Met Asp Val Trp Gly₅₇₀ Lys Gly Thr Thr Val₅₇₅ Thr
 Val Ser Ser Thr₅₈₀ Val Ala Ala Pro Ser₅₈₅ Val Phe Ile Phe Pro₅₉₀ Pro Ser

A-1937-WO-PCT_ST25

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
gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggaacct aaactgctca ttactgggc atctaccg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcgggtcttc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcttggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctg t 651

<210> 2008
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 2008

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

A-1937-WO-PCT_ST25

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> 2009

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide

<400> 2009

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttaga agcagttact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

A-1937-WO-PCT_ST25

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgag 300
gggacacgac tggagattaa acgaacgggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tgggtaccgcc tctgtttgtgt gcctgctgaa taactttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<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

A-1937-WO-PCT_ST25

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Glu
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 2011
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2011
caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat ccgccagcca 120
ccagggaaga agctagagtg gattggggaa atcaatcatg ctggaaacac caactacaac 180
ccgtccctca agagtcgagt caccatatca ttagacacgt ccaagaacca gttctccctg 240
acgctgacct ctgtgaccgc cgcgacacg gctgtgtatt actgtgagag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag 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 acaaaactca cacatgccc aacgtgcccag cacctgaact cctgggggga 720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 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
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

A-1937-WO-PCT_ST25

cagaagagcc tctccctgtc tccgggtggt ggcggatcgg gaggtggcgg atccgaggta 1380
 caactggtgg aatcagggtgg aggttttggtg cagccgggga gatcgctcag gcttagctgt 1440
 gcggcatcgg ggtttacttt cgatgattat gcgatgcatt ggggccggca agcgcctgga 1500
 aaagggctcg agtggggttc cgccattacg tggaatagcg gacacatcga ttatgcagac 1560
 agtgtggagg gcagattcac aatctcacga gacaatgcta agaacagcct gtaccttcag 1620
 atgaactcac ttcgcgcgga agataccgcc gtatactact gcgccaaagt ctcctacttg 1680
 tctacagctt cgtcgctcga ctattggggg aaaggaacgt tggtcaccgt ctctagtact 1740
 gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 1800
 gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt acagtggaag 1860
 gtggataacg ccctccaatc gggttaactcc caggagagtg tcacagagca ggacagcaag 1920
 gacagcacct acagcctcga aagcaccctg acgctgagca aagcagacta cgagaaacac 1980
 aaagtctacg cctgcgaagt caccatcag ggcctgagct cgcccgtcac aaagagcttc 2040
 aacaggggag agtgt 2055

<210> 2012
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 2012

Gln Val Gln Leu Gln Gln Ser Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30

Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu Trp Ile
 35 40 45

Gly Glu Ile Asn His Ala Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

Thr Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Tyr Cys Arg Ser Thr Thr Cys Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg 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> 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

A-1937-WO-PCT_ST25

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 ttgcagtgtg ttactgtcag cagtatggta gctcacctac cttcggcgag	300
gggacacgac tggagattaa acgaacggtg gctgcacat ctgtcttcat cttcccgcc	360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaaggtg 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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 2017
 caggtgcagt tacagcagtc gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
 acctgcgctg tccatggtgg gtccttcagt ggttactact 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
 ggacacagcg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcaaaag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgtgtgagga gcagtacggc 900
 agcacgtacc gttgtgtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccacgcagaa aaccatctcc 1020
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1080
 atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 1140
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200
 ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa cactacacg 1320
 cagaagagcc tctccctgtc tccgggtggg ggcggatcgg gaggtggcgg atccgaggtg 1380
 cagctggtgc agtctggagc agaggtgaaa aagcccgggg agtctctgaa gatctcctgt 1440
 aagacttctg aatacagctt taccagctac tggatcggct ggggtgcgcca gatgcccg 1500
 aaaggcctgg agtggatggg gatcatctat cttggtgact cagataccag atacagcccg 1560
 tccttccaag gccaggtcac catctcagcc gacaagtcca tcagtaccgc ctacctgcag 1620
 tggagcagcc tgaaggcctc ggacaccgcc atgtattact gtgcgagaag taactggggg 1680
 cttgactact ggggcaaggg aaccctggtc accgtctcta gtcagcccaa ggccaacccc 1740
 actgtcactc tgttcccgcc ctctctgag gagctccaag ccaacaaggc cacactagtg 1800
 tgtctgatca gtgacttcta cccgggagct gtgacagtgg cctggaaggc agatggcagc 1860

A-1937-WO-PCT_ST25

cccgtaagg cgggagtga gaccacaaa ccctccaaac agagcaacaa caagtacgcg 1920
gccgagagct acctgagcct gacgcccag cagtgggaagt cccacagaag ctacagctgc 1980
caggtcacgc atgaaggag 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Lys Thr Ser Glu Tyr Ser Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg
485 490 495

Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Leu Gly
500 505 510

Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile
515 520 525

Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu
530 535 540

Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ser Asn Trp Gly
545 550 555 560

Leu Asp Tyr Trp Gly 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 cagaaccaa actcctcatc caaggtaaca gcaatcggcc ctcaggggtc 180

A-1937-WO-PCT_ST25

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> 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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgag 300
gggaccaagc tggaaatcaa acgaacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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
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 catcgggtctt cccctgggca ccctcctcca agagcacctc tgggggcaca 420

A-1937-WO-PCT_ST25

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttag 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
taccgttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgaagg tctccaacaa agccctcca 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 ctaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtacaactg	1380
gtggaatcag gtggaggttt ggtgcagccg gggagatcgc tcaggcttag ctgtgcggca	1440
tcggggttta ctttcgatga ttatgcgatg cattgggtcc ggcaagcgcc tggaaaaggg	1500
ctcgagtggg tttccgcat tacgtggaat agcggacaca tcgattatgc agacagtgtg	1560
gagggcagat tcacaatctc acgagacaat gctaagaaca gcctgtacct tcagatgaac	1620
tcacttcgcg cggaagatac cgccgtatac tactgcgcca aagtctccta cttgtctaca	1680
gcttcgtcgc tcgactattg gggtaaagga acgttggtca ccgtctctag tactgtggct	1740
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct	1800
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat	1860
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc	1920
acctacagcc tcgaaagcac cctgacgtg agcaaagcag actacgagaa acacaaagtc	1980
tacgcctgcg aagtcacca tcagggcctg agctcgccc tcacaaagag cttcaacagg	2040
ggagagtgt	2049

<210> 2024
 <211> 683
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 2024

A-1937-WO-PCT_ST25

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 accatcgctc ctttcagcgt ctgttggcga ccgtgtgacg	60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc	120
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg	180
aggtttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc	240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa	300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccctggca	360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac	420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga gcccaaattct tgt	633

<210> 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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 2027
 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 acgaacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggtagcgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcgagag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 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

A-1937-WO-PCT_ST25

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 catcgggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cgggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca aaagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaatct 660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgga cctgaggtc 780
acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
taccgtttgtg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

A-1937-WO-PCT_ST25

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttct ctatagcaag ctaccctggg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccga ggtgcagctg 1380
gtgcagtctg gagcagaggt gaaaaagccc ggggagtctc tgaagatctc ctgtaagact 1440
tctgaataca gctttaccag ctactggatc ggctgggtgc gccagatgcc cgggaaaggc 1500
ctggagtga tggggatcat ctatcttggg gactcagata ccagatacag cccgtccttc 1560
caaggccagg tcaccatctc agccgacaag tccatcagta ccgcctacct gcagtggagc 1620
agcctgaagg cctcggacac cgccatgtat tactgtgcga gaagtaactg gggctcttgac 1680
tactggggca aggaaccct ggtcaccgtc tctagtcagc ccaaggccaa cccactgtc 1740
actctgttcc cgccctctc tgaggagctc caagccaaca aggccacact agtgtgtctg 1800
atcagtgact tctaccggg 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

A-1937-WO-PCT_ST25

Lys Leu Ser Ser Val₈₅ Thr Ala Ala Asp Thr₉₀ Ala Val Tyr Tyr Cys₉₅ Ala
 Arg Glu Thr Gly₁₀₀ Ser Tyr Tyr Gly Phe₁₀₅ Asp Tyr Trp Gly Gln₁₁₀ Gly Thr
 Leu Val Thr₁₁₅ Val Ser Ser Ala Ser₁₂₀ Thr Lys Gly Pro Ser₁₂₅ Val Phe Pro
 Leu Ala₁₃₀ Pro Ser Ser Lys Ser₁₃₅ Thr Ser Gly Gly Thr₁₄₀ Ala Ala Leu Gly
 Cys₁₄₅ Leu Val Lys Asp Tyr₁₅₀ Phe Pro Glu Pro Val₁₅₅ Thr Val Ser Trp Asn₁₆₀
 Ser Gly Ala Leu Thr₁₆₅ Ser Gly Val His Thr₁₇₀ Phe Pro Ala Val Leu₁₇₅ Gln
 Ser Ser Gly Leu₁₈₀ Tyr Ser Leu Lys Ser₁₈₅ Val Val Thr Val Pro₁₉₀ Ser Ser
 Ser Leu Gly₁₉₅ Thr Gln Thr Tyr Ile₂₀₀ Cys Asn Val Asn His₂₀₅ Lys Pro Ser
 Asn Thr₂₁₀ Lys Val Asp Lys Lys₂₁₅ Val Glu Pro Lys Ser₂₂₀ Cys Asp Lys Thr
 His₂₂₅ Thr Cys Pro Pro Cys₂₃₀ Pro Ala Pro Glu Leu₂₃₅ Leu Gly Gly Pro Ser₂₄₀
 Val Phe Leu Phe Pro₂₄₅ Pro Lys Pro Lys Asp₂₅₀ Thr Leu Met Ile Ser₂₅₅ Arg
 Thr Pro Glu Val₂₆₀ Thr Cys Val Val Val₂₆₅ Asp Val Ser His Glu₂₇₀ Asp Pro
 Glu Val Lys₂₇₅ Phe Asn Trp Tyr Val₂₈₀ Asp Gly Val Glu Val₂₈₅ His Asn Ala
 Lys Thr₂₉₀ Lys Pro Cys Glu Glu₂₉₅ Gln Tyr Gly Ser Thr₃₀₀ Tyr Arg Cys Val
 Ser Val₃₀₅ Leu Thr Val Leu₃₁₀ His Gln Asp Trp Leu₃₁₅ Asn Gly Lys Glu Tyr₃₂₀
 Lys Cys Lys Val Ser₃₂₅ Asn Lys Ala Leu Pro₃₃₀ Ala Pro Ile Glu Lys₃₃₅ Thr
 Ile Ser Lys Ala₃₄₀ Lys Gly Gln Pro Arg₃₄₅ Glu Pro Gln Val Tyr₃₅₀ Thr Leu

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccagcag 120
tttccaggaa cagaaccaa 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 tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat cttgt 645

<210> 2032
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 2032

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Glu Pro Lys Leu
35 40 45

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgctg 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 tcggcgaggg gaccaaggtg gagatcaaac gaacggtggc tgcaccatct 360
gtcttcactt tcccgccatc tgatgagcag ttgaaatctg gtaccgcctc tgttgtgtgc 420

A-1937-WO-PCT_ST25

ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 480
 caatcgggta actcccagga gagtgtcaca gacgaggaca 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

A-1937-WO-PCT_ST25

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 2035
<211> 2070
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2035
caggtacagt tgcaggagtc aggtccagga ctggtgaagc cctcggagac cctctcactc 60
acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggatcagg 120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gcccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
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gtcaccgtct cctcagcctc caccaagggc ccatcggctt tccccctggc accctcctcc 420
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc 600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
aagaaagttg agcccaaact ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
gaactcctgg ggggaccgtc agtcttctc tccccccaa 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 cacaggtgta caccctgccc 1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1200
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gctcaccgtg 1260
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtggtggcgg atcgggaggt 1380
ggcggatccg aggtacaact ggtggaatca ggtggaggtt tgggtgcagcc ggggagatcg 1440
ctcaggctta gctgtgcggc atcggggttt actttcgatg attatgcat gcattgggtc 1500
cggcaagcgc ctggaaaagg gctcagatgg gtttccgcca ttacgtggaa tagcggacac 1560

A-1937-WO-PCT_ST25

atcgattatg cagacagtgt ggagggcaga ttcacaatct cactgagacaa tgctaagaac 1620
 agcctgtacc ttcagatgaa ctacttcgc gcggaagata cgcgcgtata ctactgcgcc 1680
 aaagtctcct acttgtctac agcttcgtcg ctcgactatt ggggtaaagg aacgttggtc 1740
 accgtctcta gtactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 1800
 ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaata acttctatcc cagagaggcc 1860
 aaagtacagt ggaaggtgga taacgccctc caatcgggta actcccagga gagtgtcaca 1920
 gagcaggaca gcaaggacag cacctacagc ctcgaaagca ccctgacgct gagcaaagca 1980
 gactacgaga aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 2040
 gtcacaaaga 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly 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 gcaaaaaccc 120
 ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt 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 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

A-1937-WO-PCT_ST25

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 aaaggttcct aaactgctca tttactgggc atctaccgga 180
gaatccgggg 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 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> 2040
<211> 220
<212> PRT
<213> Artificial Sequence

A-1937-WO-PCT_ST25

<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

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 ccatcggctt tccccctggc accctcctcc	420
aagagcacct ctgggggac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
ccggtgacgg tgtcgtgga ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct	540
gtcctacagt cctcaggact ctactccctc aaaagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagaaagttg agcccaaact ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttctc tttccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag	840
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgtgt	900
gaggagcagt acggcagcac gtaccgttgt gtcagcgtcc tcaccgtcct gcaccaggac	960
tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agccccatc	1020
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc	1080
ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggg caaaggcttc	1140
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag	1200
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gtcaccgtg	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 gcccgctcctt ccaaggccag gtcaccatct cagccgacaa gtccatcagt	1620
accgcctacc tgacgtggag cagcctgaag gcctcggaca ccgcatgta ttactgtgcg	1680
agaagtaact ggggtcttga ctactggggc aagggaaccc tggtcaccgt ctctagtcag	1740
cccaaggcca accccactgt cactctgttc ccgccctcct ctgaggagct ccaagccaac	1800
aaggccacac tagtgtgtct gatcagtac ttctaccgg gagctgtgac agtggcctgg	1860
aaggcagatg gcagccccgt caaggcggga gtggagacca ccaaaccctc caaacagagc	1920
aacaacaagt acgcggccga gagctacctg agcctgacgc ccgagcagtg gaagtccac	1980

A-1937-WO-PCT_ST25

agaagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct 2040
acagaatggt 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

A-1937-WO-PCT_ST25

Asn Val₂₁₀ Asn His Lys Pro Ser₂₁₅ Asn Thr Lys Val₂₂₀ Asp Lys Lys Val Glu
 Pro Lys Ser Cys Asp Lys₂₃₀ Thr His Thr Cys Pro₂₃₅ Pro Cys Pro Ala Pro₂₄₀
 Glu Leu Leu Gly Gly₂₄₅ Pro Ser Val Phe Leu₂₅₀ Phe Pro Pro Lys Pro₂₅₅ Lys
 Asp Thr Leu Met₂₆₀ Ile Ser Arg Thr Pro₂₆₅ Glu Val Thr Cys Val₂₇₀ Val Val
 Asp Val Ser₂₇₅ His Glu Asp Pro Glu₂₈₀ Val Lys Phe Asn Trp₂₈₅ Tyr Val Asp
 Gly Val₂₉₀ Glu Val His Asn Ala₂₉₅ Lys Thr Lys Pro Cys₃₀₀ Glu Glu Gln Tyr
 Gly₃₀₅ Ser Thr Tyr Arg Cys₃₁₀ Val Ser Val Leu Thr₃₁₅ Val Leu His Gln Asp₃₂₀
 Trp Leu Asn Gly Lys₃₂₅ Glu Tyr Lys Cys Lys₃₃₀ Val Ser Asn Lys Ala₃₃₅ Leu
 Pro Ala Pro Ile₃₄₀ Glu Lys Thr Ile Ser₃₄₅ Lys Ala Lys Gly Gln₃₅₀ Pro Arg
 Glu Pro Gln₃₅₅ Val Tyr Thr Leu Pro₃₆₀ Pro Ser Arg Glu Glu₃₆₅ Met Thr Lys
 Asn Gln₃₇₀ Val Ser Leu Thr Cys₃₇₅ Leu Val Lys Gly Phe₃₈₀ Tyr Pro Ser Asp
 Ile Ala Val Glu Trp Glu₃₉₀ Ser Asn Gly Gln Pro₃₉₅ Glu Asn Asn Tyr Lys₄₀₀
 Thr Thr Pro Pro Val₄₀₅ Leu Asp Ser Asp Gly₄₁₀ Ser Phe Phe Leu Tyr₄₁₅ Ser
 Lys Leu Thr Val₄₂₀ Asp Lys Ser Arg Trp₄₂₅ Gln Gln Gly Asn Val₄₃₀ Phe Ser
 Cys Ser Val₄₃₅ Met His Glu Ala Leu₄₄₀ His Asn His Tyr Thr₄₄₅ Gln Lys Ser
 Leu Ser₄₅₀ Leu Ser Pro Gly Gly₄₅₅ Gly Gly Ser Gly Gly₄₆₀ Gly Gly Ser Glu
 Val₄₆₅ Gln Leu Val Gln Ser₄₇₀ Gly Ala Glu Val Lys₄₇₅ Lys Pro Gly Glu Ser₄₈₀

A-1937-WO-PCT_ST25

Leu Lys Ile Ser Cys₄₈₅ Lys Thr Ser Glu Tyr₄₉₀ Ser Phe Thr Ser Tyr₄₉₅ Trp

Ile Gly Trp Val₅₀₀ Arg Gln Met Pro Gly₅₀₅ Lys Gly Leu Glu Trp₅₁₀ Met Gly

Ile Ile Tyr₅₁₅ Leu Gly Asp Ser Asp₅₂₀ Thr Arg Tyr Ser Pro₅₂₅ Ser Phe Gln

Gly Gln Val Thr Ile Ser Ala₅₃₅ Asp Lys Ser Ile Ser₅₄₀ Thr Ala Tyr Leu

Gln Trp Ser Ser Leu Lys₅₅₀ Ala Ser Asp Thr Ala₅₅₅ Met Tyr Tyr Cys Ala₅₆₀

Arg Ser Asn Trp Gly₅₆₅ Leu Asp Tyr Trp Gly₅₇₀ Lys Gly Thr Leu Val₅₇₅ Thr

Val Ser Ser Gln₅₈₀ Pro Lys Ala Asn Pro₅₈₅ Thr Val Thr Leu Phe₅₉₀ Pro Pro

Ser Ser Glu₅₉₅ Glu Leu Gln Ala Asn₆₀₀ Lys Ala Thr Leu Val₆₀₅ Cys Leu Ile

Ser Asp₆₁₀ Phe Tyr Pro Gly Ala₆₁₅ Val Thr Val Ala Trp₆₂₀ Lys Ala Asp Gly

Ser Pro Val Lys Ala Gly₆₃₀ Val Glu Thr Thr Lys₆₃₅ Pro Ser Lys Gln Ser₆₄₀

Asn Asn Lys Tyr Ala₆₄₅ Ala Glu Ser Tyr Leu₆₅₀ Ser Leu Thr Pro Glu₆₅₅ Gln

Trp Lys Ser His₆₆₀ Arg Ser Tyr Ser Cys₆₆₅ Gln Val Thr His Glu₆₇₀ Gly Ser

Thr Val Glu₆₇₅ Lys Thr Val Ala Pro₆₈₀ Thr Glu Cys Ser

<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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagaaccaa actcctcatc caaggaataca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 2045
<211> 2064
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2045
gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt 60
agctgtgcgg catcgggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag 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
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgata 780
tcccggaccc ctgaggtcac atgctgtgtg 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 ttcttctct atagcaagct caccgtggac 1260
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1320
aaccactaca cgcagaagag cctctccctg tctccgggtg gtggcggatc gggaggtggc 1380

A-1937-WO-PCT_ST25

ggatcccagg tgcagttaca gcagtcgggc gcaggactgt tgaagccttc ggagaccctg 1440
 tccctcacct gcgctgtcca tgggtgggtcc ttcagtgggt 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
 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> 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-W0-PCT_ST25

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 gagtggttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg aaccagggt cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggg gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattc 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

A-1937-WO-PCT_ST25

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
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggagaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt cccctggca 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> 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

A-1937-WO-PCT_ST25

<220>

<223> Synthetic polynucleotide

<400> 2051

gaggtacaac tgggtggaatc aggtggaggt ttggtgcagc cggggagatc gctcaggctt	60
agctgtgcgg catcgggggtt tacttttcgat gattatgcga tgcatctgggt ccggcaagcg	120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat	180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac	240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc	300
tacttgtcta cagcttcgtc gctcgactat tgggggtcaag gaacgttgggt caccgtctct	360
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
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag	660
agcttcaaca ggggagagtg tgacaaaact cacacatgcc caccgtgccc agcacctgaa	720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac	780
tcccggaccc ctgaggtcac atgctgtgtg 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 aggccttctat	1140
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1200
acgcctcccg tgctggactc cgacggctcc ttcttctctt 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
cagccccccag gtaagggact ggagtggatt ggctatatct attacagtgg gcagacccaa	1560
tacaaccctt ccctcaagag tcgagtcacc atatcaatag acacgtccaa gaaccagttc	1620
tccctgaagc tgagctctgt gaccgtgcg gacacggccg tgtattactg tgcgagagaa	1680
actgggagct actacggctt tgactactgg ggcaagggaa ccctgggtcac cgtctcctca	1740
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga	1800
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg	1860
aagggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc	1920

A-1937-WO-PCT_ST25

aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa 1980
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 2040
 ttcaacaggg gagagtgt 2058

<210> 2052
 <211> 686
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 2052

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Lys Leu Glu Trp Val
 35 40 45

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 165 170 175

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120

gggaaagaac ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

A-1937-WO-PCT_ST25

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt ccccctggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttccccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcacca 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

A-1937-WO-PCT_ST25

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 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
aggtttagcg 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 gcccaaattc 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

A-1937-WO-PCT_ST25

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
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agctgtgcgg catcggggtt tactttcgat gattatgcga tgcattgggt ccggcaagcg 120
cctggaaaaa agctcgagtg ggtttccgcc attacgtgga atagcggaca catcgattat 180
gcagacagtg tggagggcag attcacaatc tcacgagaca atgctaagaa cagcctgtac 240
cttcagatga actcacttcg cgcggaagat accgccgtat actactgcgc caaagtctcc 300
tacttgtcta cagcttcgtc gctcgactat tggggtaag gaacgttggt caccgtctct 360
agtacggtgg ctgcaccatc tgtcttcac ttcccgcac ctgatgagca gttgaaatct 420

A-1937-WO-PCT_ST25

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	ggggagagt	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	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	ttcttctctt	atagcaagct	caccgtggac	1260
aagagcaggt	ggcagcaggg	gaacgtcttc	tcattgctccg	tgatgcatga	ggctctgcac	1320
aaccactaca	cgcagaagag	cctctccctg	tctccgggtg	gtggcggatc	gggaggtggc	1380
ggatcccagg	tacagttgca	ggagtcaggt	ccaggactgg	tgaagccctc	ggagaccctc	1440
tcactcacct	gtaccatctc	cggggacagt	gtctctacca	acagtgttgc	ttggaactgg	1500
attaggcagc	ccccagggaa	aggccttgag	tggataggaa	ggacatacta	caggtccaag	1560
tggtataatg	attatgcagt	ttctctgaaa	agtcgagtaa	ccatcagccc	agacacatcc	1620
aagaaccagt	tctccctgaa	gctgagctct	gtgactgccg	cggacacggc	tgtgtattac	1680
tgtgcaagag	aggatgggga	tagctactac	cgctacggta	tggacgtctg	gggcaaaggg	1740
accacgggtca	ccgtctcctc	aactgtggct	gcaccatctg	tcttcatctt	cccgccatct	1800
gatgagcagt	tgaatctgg	aactgcctct	gttgtgtgcc	tgctgaataa	cttctatccc	1860
agagaggcca	aagtacagt	gaagggtgat	aacgccctcc	aatcgggtaa	ctcccaggag	1920
agtgtcacag	agcaggacag	caaggacagc	acctacagcc	tcgaaagcac	cctgacgctg	1980
agcaaagcag	actacgagaa	acacaaagtc	tacgcctgcg	aagtcaccca	tcagggcctg	2040
agctcgcccc	tcacaaagag	cttcaacagg	ggagagtgt			2079

<210> 2058
 <211> 693
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic polypeptide
 <400> 2058

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 tgaccagtc 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 gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcttggtca aggactactt ccccgaaccg gtgacggtgt 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

A-1937-WO-PCT_ST25

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
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 ccaggaacc ctggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tctactgttt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtcca cagaagctac 600
agctgccagg tcacgcatga agggagcacc gtggagaaga cagtggcccc tacagaatgt 660
tcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

A-1937-WO-PCT_ST25

gacggcgtgg aggtgcataa tgccaagaca aagccgtgtg aggagcagta cggcagcacg 900
taccgtttgtg 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 ctttcttctt ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cagcagaag 1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatccca ggtgcagtta 1380
cagcagtcgg gcgcaggact gttgaagcct tcggagaccc tgtccctcac ctgcgctgtc 1440
catggtgggt ccttcagtgg 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gagtgttaga agcagttact tagcctggta ccagcagaaa 120
cctggccagg aaccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagtatggta gctcacctac cttcggccaa 300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca 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> 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

A-1937-WO-PCT_ST25

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 gcagggttatg atgtacactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc caaggaataca gcaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

A-1937-WO-PCT_ST25

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> 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

A-1937-WO-PCT_ST25

Leu Glu Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 2069
<211> 2040
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2069
gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac 180
agccccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac 300
tggggctcttg actactgggg ccagggaaacc ctgggtcaccg tctctagtca gcccaaggcc 360
aaccctactg tctactctgtt cccgccctcc tctgaggagc tccaagccaa caaggccaca 420
ctagtgtgtc tgatcagtga cttctacccg ggagctgtga cagtggcctg gaaggcagat 480
ggcagccccg tcaaggcggg agtggagacc accaaaccct ccaaacagag caacaacaag 540
tacgcggcca agagctacct gagcctgacg cccgagcagt ggaagtccca cagaagctac 600
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
gagtgaggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttct ctatagcaag ctaccctggg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg tgggtggcggg tcgggaggtg gcggatccca ggtgcagctg 1380

A-1937-WO-PCT_ST25

caggagtcgg gcccaggact ggtgaagcct tcggagaccc tgtccctcac ctgcactgtc 1440
tctggtggct ccatcagtag ttacttctgg agctggattc ggcagccccc aggtaagggg 1500
ctggagtggg 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 ggaaggtgga 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser 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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
 gggaaagaac ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggccaa 300
 gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt cccctcggca 360
 ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcacca 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

A-1937-WO-PCT_ST25

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 cagccccaa actcctcatc caaggaataa gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca cttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2074
<211> 215
<212> PRT
<213> Artificial Sequence

A-1937-WO-PCT_ST25

<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 ccggggagtc tctgaagatc	60
tcctgtaaga cttctgaata cagctttacc agctactgga tcggctgggt gcgccagatg	120
cccgggaaaa aactggagtg gatggggatc atctatcttg gtgactcaga taccagatac	180
agcccgctcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac	240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaagtaac	300
tggggctcttg actactgggg ccaggaacc 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 ccgagcagc ggaagtcca 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 tctccaaca agccctcca gccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc ccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttct ctatagcaag ctaccctgtg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggtctgtc acaaccacta cacgcagaag	1320
agcctctccc tgtctccggg tgggtggcga tcgggaggtg gcggatcca ggtacagttg	1380
caggagtcag gtccaggact ggtgaagccc tcggagaccc tctcactcac ctgtaccatc	1440
tccggggaca gtgtctctac caacagtgtt gcttggaact ggattaggca gccccaggg	1500
aaaggccttg agtggatagg aaggacatac tacaggcca agtggtataa tgattatgca	1560
gtttctctga aaagtcgagt aaccatcagc ccagacacat ccaagaacca gttctccctg	1620
aagctgagct ctgtgactgc cgcggacacg gctgtgtatt actgtgcaag agaggatggg	1680
gatagctact accgctacgg tatggacgtc tggggcaaag ggaccacggt caccgtctcc	1740
tcaactgtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct	1800
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag	1860
tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac	1920
agcaaggaca gcacctacag cctcgaaagc accctgacgc tgagcaaagc agactacgag	1980

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

gacatccaga tgaccagtc 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

A-1937-WO-PCT_ST25

atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcggagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctccccaag agcacctctg ggggcacagc ggcctgggc 420
tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcaaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t 651

<210> 2078

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2078

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys
35 40 45

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

A-1937-WO-PCT_ST25

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
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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagcccccaa actcctcatc caaggaataa gcaatcggcc ctcagggggtc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg aagggaacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcgggtc 360
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttcccggc tgtcctacag tcctcaggac tctactccct cgaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 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

A-1937-WO-PCT_ST25

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
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acctgcgctg tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120
ccaggaaga agctagagt gattggggaa atcaatcatg ctggaacac caactacaac 180
ccgtccctca agatcgagt caccatatca ttagacacgt ccaagaacca gttctcctg 240
acgctgacct ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgag aggatattgt 300
agaagtacca cctgctactt tgactactgg ggccagggaa ccctagtcac cgtctcctca 360
acggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 420
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 480

A-1937-WO-PCT_ST25

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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 ccaaaccaca aggacaccct catgatctcc      780
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccg 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 ttctctata gcaagctcac cgtggacaag      1260
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac     1320
cactacacgc agaagagcct ctccctgtct ccgggtggtg gcggatcggg aggtggcgga      1380
tccgaggtac aactggtgga atcaggtgga ggtttggtgc agccggggag atcgctcagg      1440
cttagctgtg cggcatcggg gtttactttc gatgattatg cgatgcattg ggtccggcaa      1500
gcgcttgga aagggctcga gtgggtttcc gccattacgt ggaatagcgg acacatcgat      1560
tatgcagaca gtgtggaggg cagattcaca atctcacgag acaatgctaa gaacagcctg      1620
taccttcaga tgaactcact tcgcgcggaa gataccgccg tatactactg cgccaaagtc      1680
tcctacttgt ctacagcttc gtcgctcgac tattggggta aaggaacggt ggtcacgctc      1740
tctagtactg tggctgcacc atctgtcttc atcttccgc catctgatga gcagttgaaa      1800
tctggaactg cctctgttgt gtgcctgctg aataacttct atcccagaga ggccaaagta      1860
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag      1920
gacagcaagg acagcaccta cagcctcgaa agcaccctga cgctgagcaa agcagactac      1980
gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctgagctc gcccgtcaca      2040
aagagcttca acaggggaga gtgt                                     2064

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<210> 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

A-1937-WO-PCT_ST25

Thr Leu Ser Leu Thr Cys Ala Val His Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 accatcgctcg ctttcagcgt ctgttggcga ccgtgtgacg 60
attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt cccctggca 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
aagggtggaca agaaagttga gcccaaattct tgt 633

<210> 2084
<211> 211

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 2084

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Glu Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Lys
 100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 115 120 125

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

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacctac cttcggcgaa      300
gggacacgac tggagattaa acgagcctcc accaagggcc catcggtctt cccctggca      360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggg caaggactac      420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc      480
ttcccggtg tcctacagtc ctcaggactc tactccctcg aaagcgtggg gaccgtgccc      540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc      600
aaggtggaca agaaagttga gcccaaattct tgt                                633

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<210> 2086

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2086

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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1           5           10          15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Ser
          20          25          30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35          40          45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
          50          55          60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65          70          75          80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
          85          90          95

Thr Phe Gly Glu Gly Thr Arg Leu Glu Ile Lys Arg Ala Ser Thr Lys
          100         105         110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
          115         120         125

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A-1937-WO-PCT_ST25

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 tccatggtgg gtccttcagt ggttactact ggaactggat tcgccagcca 120
ccaggaaga agctagagt 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
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
caciaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt caciaagagc 660
ttcaacaggg gagagtgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 720
ctggggggac cgtcagtcct cctcttcccc ccaaaccaca aggacaccct catgatctcc 780
cggacccttg aggtcacatg cgtgggtggtg gacgtgagcc acgaagacc tgaggtcaag 840
ttcaactggt acgtggacgg cgtggaggtg cataatgcc aagacaaagcc gtgtgaggag 900
cagtacggca gcacgtaccg ttgtgtcagc gtcctcaccg tcctgcacca ggactggctg 960
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1020

A-1937-WO-PCT_ST25

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1080
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 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 cttccaagg ccaggtcacc atctcagccg acaagtccat cagtaccgcc 1620
 tacctgcagt ggagcagcct gaaggcctcg gacaccgcca tgtattactg tgcgagaagt 1680
 aactggggtc ttgactactg gggcaaggga accctggtca ccgtctctag tcagcccaag 1740
 gccaaccca ctgtcactct gttcccgcc tcctctgagg agctccaagc caacaaggcc 1800
 aactagtgt gtctgatcag tgacttctac ccgggagctg tgacagtggc ctggaaggca 1860
 gatggcagcc ccgtcaaggc gggagtggag accaccaaac cctccaaaca gagcaacaac 1920
 aagtacgcg ccgagagcta cctgagcctg acgcccagc 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

A-1937-WO-PCT_ST25

Thr Leu Thr Ser Val₈₅ Thr Ala Ala Asp Thr₉₀ Ala Val Tyr Tyr Cys₉₅ Ala
 Arg Gly Tyr Cys₁₀₀ Arg Ser Thr Thr Cys₁₀₅ Tyr Phe Asp Tyr Trp₁₁₀ Gly Gln
 Gly Thr Leu₁₁₅ Val Thr Val Ser Ser₁₂₀ Thr Val Ala Ala Pro Ser Val Phe
 Ile Phe₁₃₀ Pro Pro Ser Asp Glu₁₃₅ Gln Leu Lys Ser Gly₁₄₀ Thr Ala Ser Val
 Val₁₄₅ Cys Leu Leu Asn Asn₁₅₀ Phe Tyr Pro Arg Glu₁₅₅ Ala Lys Val Gln Trp₁₆₀
 Lys Val Asp Asn Ala₁₆₅ Leu Gln Ser Gly Asn₁₇₀ Ser Gln Glu Ser Val₁₇₅ Thr
 Glu Gln Asp Ser₁₈₀ Lys Asp Ser Thr Tyr₁₈₅ Ser Leu Lys Ser Thr₁₉₀ Leu Thr
 Leu Ser Lys₁₉₅ Ala Asp Tyr Glu Lys₂₀₀ His Lys Val Tyr Ala₂₀₅ Cys Glu Val
 Thr His₂₁₀ Gln Gly Leu Ser Ser₂₁₅ Pro Val Thr Lys Ser₂₂₀ Phe Asn Arg Gly
 Glu₂₂₅ Cys Asp Lys Thr His₂₃₀ Thr Cys Pro Pro Cys₂₃₅ Pro Ala Pro Glu Leu₂₄₀
 Leu Gly Gly Pro Ser₂₄₅ Val Phe Leu Phe Pro₂₅₀ Pro Lys Pro Lys Asp Thr₂₅₅
 Leu Met Ile Ser₂₆₀ Arg Thr Pro Glu Val₂₆₅ Thr Cys Val Val Val₂₇₀ Asp Val
 Ser His Glu₂₇₅ Asp Pro Glu Val Lys₂₈₀ Phe Asn Trp Tyr Val₂₈₅ Asp Gly Val
 Glu Val₂₉₀ His Asn Ala Lys Thr₂₉₅ Lys Pro Cys Glu Glu₃₀₀ Gln Tyr Gly Ser
 Thr Tyr Arg Cys Val Ser₃₁₀ Val Leu Thr Val Leu₃₁₅ His Gln Asp Trp Leu₃₂₀
 Asn Gly Lys Glu Tyr₃₂₅ Lys Cys Lys Val Ser₃₃₀ Asn Lys Ala Leu Pro₃₃₅ Ala
 Pro Ile Glu Lys₃₄₀ Thr Ile Ser Lys Ala₃₄₅ Lys Gly Gln Pro Arg₃₅₀ Glu Pro

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
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tttccaggaa cagaaccaa 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 tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagt gagcccaaat 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

A-1937-WO-PCT_ST25

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

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtggttaga agcagttact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtta ttactgtcag cagtatggta gctcacctac cttcggcgaa	300
gggacacgac tggagattaa acgagcctcc accaagggcc catcgggtctt ccccttgga	360
ccctcctcca agagcacctc tggggggcaca gcggccctgg gctgcctggt caaggactac	420

A-1937-WO-PCT_ST25

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc	480
ttcccggctg tcctacagtc ctccaggactc tactccctcg aaagcgtggt gaccgtgccc	540
tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc	600
aaggtggaca agaaagttga 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		

A-1937-WO-PCT_ST25

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 caaatataac 180
ccctccctca agagtcgagt caccatatca atagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agaaactggg 300
agctactacg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcaacgggtg 360
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc 420
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg 480
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac 540
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa 600
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccggacc 780
cctgagggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag 900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca cctgcccc atcccgggag 1080
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttctc tatagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca 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

A-1937-WO-PCT_ST25

gacagtgtgg agggcagatt cacaatctca cgagacaatg ctaagaacag cctgtacctt 1620
cagatgaact cacttcgcg c ggaagatacc gccgtatact actgcgcca agtctctctac 1680
ttgtctacag cttcgtcgct cgactattgg ggtaaaggaa cgttgggtcac cgtctctagt 1740
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 1800
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggcca agtacagtgg 1860
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 1920
aaggacagca cctacagcct cgaaagcacc ctgacgctga gcaaagcaga ctacgagaaa 1980
caciaagtct acgcctgcga agtcacccat cagggcctga gctcgcccg caciaagagc 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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide

<400> 2095
 gatatccaaa tgacacaatc accatcgtcg ctttcagcgt ctgttggcga ccgtgtgacg 60
 attacctgtc gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
 ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
 aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
 gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
 gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
 cctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
 ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
 ttcccggtg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
 tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
 aaggtggaca agaaagttga gcccaaattc 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

A-1937-W0-PCT_ST25

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 tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagagacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 300
gggaccaagc tggaaatcaa acgagcctcc accaagggcc catcggtctt cccctggca 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctcg aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct 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

A-1937-WO-PCT_ST25

acctgcactg tctctggtgg ctccatcagt agttacttct ggagctggat tcggcagccc	120
ccaggttaaga 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 ctcaacgggtg	360
gctgcaccat ctgtcttcat cttcccgcga tctgatgagc agttgaaatc tggaactgcc	420
tctgttgtgt gcctgctgaa taacttctat cccagagagg ccaaagtaca gtggaagggtg	480
gataacgccc tccaatcggg taactcccag gagagtgtca cagagcagga cagcaaggac	540
agcacctaca gcctcaagag caccctgacg ctgagcaaag cagactacga gaaacacaaa	600
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac	660
aggggagagt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgctgggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgtgtga ggagcagtag	900
ggcagcacgt accgttgtgt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1080
gagatgacca agaaccaggt cagcctgacc tgcttgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttctc tatagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggtcttgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggtggcggat cgggaggtgg cggatccgag	1380
gtgcagctgg tgcagtctgg agcagaggtg aaaaagcccg gggagtctct gaagatctcc	1440
tgtaagactt ctgaatacag ctttaccagc tactggatcg gctgggtgag ccagatgccc	1500
gggaaaggcc tggagtggat ggggatcatc tatcttgggtg actcagatac cagatacagc	1560
ccgtccttcc aaggccaggt caccatctca gccgacaagt ccatcagtag cgcctacctg	1620
cagtggagca gcctgaaggc ctcggacacc gccatgtatt actgtgagag aagtaactgg	1680
ggtcttgact actggggcaa gggaaccctg gtcaccgtct ctagtcagcc caaggccaac	1740
cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta	1800
gtgtgtctga tcagtactt 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

A-1937-WO-PCT_ST25

Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
 Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
 Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
 His Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Cys Glu Glu Gln Tyr₃₀₀ Gly Ser Thr Tyr
 Arg₃₀₅ Cys Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
 Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Tyr Thr Leu₃₅₅ Pro Pro Ser Arg Glu₃₆₀ Glu Met Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Thr₃₇₀ Cys Leu Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Tyr Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Ser Gly₄₅₅ Gly Gly Gly Ser Glu₄₆₀ Val Gln Leu Val
 Gln₄₆₅ Ser Gly Ala Glu Val₄₇₀ Lys Lys Pro Gly Glu₄₇₅ Ser Leu Lys Ile Ser₄₈₀
 Cys Lys Thr Ser Glu₄₈₅ Tyr Ser Phe Thr Ser₄₉₀ Tyr Trp Ile Gly Trp₄₉₅ Val
 Arg Gln Met Pro₅₀₀ Gly Lys Gly Leu Glu₅₀₅ Trp Met Gly Ile Ile₅₁₀ Tyr Leu

A-1937-WO-PCT_ST25

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

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tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

tttccaggaa cagaaccaa 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 caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg 420

A-1937-WO-PCT_ST25

gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
 ggcgtgcaca ccttcccggc tgtcctacag tcctcaggac tctactccct caaaagcgtg 540
 gtgaccgtgc cctccagcag cttggggcacc cagacctaca tctgcaacgt gaatcacaag 600
 cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2102
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide

<400> 2102

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15

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

A-1937-WO-PCT_ST25

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys
210 215

<210> 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 ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctcggac gttcggcgaa 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 tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtaggaca agaaagttga gcccaaattct tgt 633

<210> 2104
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 2104

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

A-1937-WO-PCT_ST25

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Arg
85 90 95

Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg Ala Ser Thr Lys
100 105 110

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
115 120 125

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
130 135 140

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
145 150 155 160

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Glu Ser Val
165 170 175

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
180 185 190

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
195 200 205

Lys Ser Cys
210

<210> 2105
<211> 2079
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2105
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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg 120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat 180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac 240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca 300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg 360
gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 420
cagttgaaat ctggaactgc ctctgttggtg tgcctgctga ataacttcta tcccagagag 480
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc 540
acagagcagg acagcaagga cagcacctac agcctcaaga gcaccctgac gctgagcaaa 600
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 660

A-1937-WO-PCT_ST25

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cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc      720
ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac      780
accctcatga tctcccggac ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa      840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca      900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg      960
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca     1020
gcccccatcg agaaaacat ctccaaagcc 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 tgggtggcggA     1380
tcgggagggtg gcggatccga ggtacaactg gtggaatcag gtggagggtt ggtgcagccg     1440
gggagatcgc tcaggcttag ctgtgcgga tcgggggtta ctttcgatga ttatgcatg     1500
cattgggtcc ggcaagcgcc tggaaaagg 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 tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc     1860
agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag     1920
agtgtcacag agcaggacag caaggacagc acctacagcc tcgaaagcac cctgacgctg     1980
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg     2040
agctcgcccc tcacaaagag cttcaacagg ggagagtgt      2079

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<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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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 gcgcgtccca gggaatccgg aattacctcg catggtatca gcaaaaaccc 120
ggaaaagaac cgaagctcct gatctatgcc gcctcgactc ttcagagtgg tgtgccgtcg 180
aggttttagcg ggtccgggtc aggtacggac tttactctca caatttccag cctgcagccc 240
gaagatgtag ctacctatta ctgccagaga tacaaccgag cgccttacac attcggacaa 300
gggacaaaag tcgagatcaa gcgtgcctcc accaagggcc catcgggtctt ccccttgga 360
ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 420
ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 480
ttcccggctg tcctacagtc ctcaggactc tactccctca aaagcgtggt gaccgtgccc 540
tccagcagct tgggcacca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 600
aaggtggaca agaaagttga gcccaaattct tgt 633

<210> 2108
<211> 211
<212> PRT
<213> Artificial Sequence

A-1937-WO-PCT_ST25

<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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gacatccaga tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc      60
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tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg      180
gaatccgggg 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
tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccttg      480
accagcggcg tgcacacctt cccggtgtc ctacagtcct caggactcta ctccctcgaa      540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga cctacatctg caacgtgaat      600
cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattcttg t          651

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<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

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A-1937-WO-PCT_ST25

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

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acctgtacca tctccgggga cagtgtctct accaacagtg ttgcttgga ctggattagg	120
cagccccag ggaaaaaact tgagtggata ggaaggacat actacaggtc caagtggat	180
aatgattatg cagtttctct gaaaagtcga gtaaccatca gccagacac atccaagaac	240
cagttctccc tgaagctgag ctctgtgact gccgcggaca cggctgtgta ttactgtgca	300
agagaggatg gggatagcta ctaccgctac ggtatggacg tctggggcca agggaccacg	360
gtcaccgtct cctcaacggt ggctgcacca tctgtcttca tcttcccgcc atctgatgag	420
cagttgaaat ctggaactgc ctctgtttgtg 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
cccgtcacaa agagcttcaa caggggagag tgtgacaaaa ctcacacatg cccaccgtgc	720
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac	780
accctcatga tctcccgac ccctgaggtc acatgcgtgg tggatggacgt gagccacgaa	840
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	900
aagccgtgtg aggagcagta cggcagcacg taccgttgtg tcagcgtcct caccgtcctg	960
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctcca	1020
gccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1080

A-1937-WO-PCT_ST25

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aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1200
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag 1260
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tcgggaggtg gcggatccga ggtgcagctg gtgcagtctg gagcagaggt gaaaaagccc 1440
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tactgtgcga gaagtaactg gggctctgac tactggggca agggaaccct ggtcaccgtc 1740
tctagtcagc ccaaggccaa cccactgtc actctgttcc cgccctcctc tgaggagctc 1800
caagccaaca aggccacact agtgtgtctg atcagtgact tctaccggg agctgtgaca 1860
gtggcctgga aggcatgga cagccccgtc aaggcgggag tggagaccac caaacctcc 1920
aaacagagca acaacaagta cgcggccgag agctacctga gcctgacgcc cgagcagtgg 1980
aagtcccaca gaagctacag ctgccaggtc acgcatgaag ggagcaccgt ggagaagaca 2040
gtggccccta cagaatgttc a 2061

<210> 2112

<211> 687

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 2112

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Val Ser Thr Asn
20 25 30

Ser Val Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Lys Leu Glu
35 40 45

Trp Ile Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Leu Lys Ser Arg Val Thr Ile Ser Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
85 90 95

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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

A-1937-WO-PCT_ST25

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
cagtctgtgc tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60
tcctgcactg ggagcagttc caacatcggg gcaggttatg atgtacactg gtaccagcag 120
tttccaggaa cagaacccaa actcctcatc caaggttaaca gcaatcggcc ctcaggggctc 180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240
caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggttcg 300
gtgttcggcg gagggacaa gctgaccgtc ctaggtgcct ccaccaaggg cccatcggtc 360
ttccccctgg caccctcctc caagagcacc tctgggggca cagcggccct gggctgcctg 420
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc 480
ggcgtgcaca ctttccggc tgtcctacag tcctcaggac tctactcct caaaagcgtg 540
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag 600
cccagcaaca ccaaggtgga caagaaagtt gagcccaaat cttgt 645

<210> 2114
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<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

A-1937-WO-PCT_ST25

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 tgaccagtc tccaagctcc ctgtctgcgt ctgtgggcga tagggtcacc 60
atcacttgca ggtccagcca gagtgtgtta tacagctcca acaataagaa ctacttagtt 120
tggtaccagc agaaaccagg aaaggttcct aaactgctca ttactgggc atctaccgg 180
gaatccgggg tccctagtcg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcagcctga agatgtggca acttattact gtcagcaata ttataagact 300
cctctcactt tcggcgaagg gaccaaggtg gagatcaaac gagcctccac caagggccca 360
tcggtcttcc ccctggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 420
tgcctgggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgcctg 480

A-1937-WO-PCT_ST25

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcgaa 540
agcgtggtga ccgtgccctc cagcagcttg ggcaccaga 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
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> 2117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 2117
 gctgcatcca gtttgcaaag t 21

<210> 2118
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 2118
 caacagagtt acagtacccc tcggacg 27

<210> 2119
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 2119
 aggtccagcc agagtgtgtt atacagctcc aacaataaga actacttagt t 51

<210> 2120
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 2120
 tgggcatcta cccgggaatc c 21

<210> 2121
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 2121
 cagcaatatt ataagactcc tctcact 27

<210> 2122
 <211> 15

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2122
 gattatgcga tgcac 15

<210> 2123
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2123
 gccattacgt ggaatagcgg acacatcgat tatgcagaca gtgtggaggg c 51

<210> 2124
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2124
 gtctctact tgcctacagc ttcgtcgctc gactat 36

<210> 2125
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2125
 agctactgga tcggc 15

<210> 2126
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2126
 atcatctatc ttggtgactc agataccaga tacagcccgt ccttccaagg c 51

<210> 2127
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide
 <400> 2127
 agtaactggg gtcttgacta c 21

<210> 2128
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 2128
 ggttactact ggaac 15

<210> 2129
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 2129
 gaaatcaatc atgctggaaa caccaactac aaccctgtccc tcaagagt 48

<210> 2130
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 2130
 ggatattgta gaagtaccac ctgctacttt gactac 36

<210> 2131
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 2131
 agttacttct ggagc 15

<210> 2132
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 2132
 tatatctatt acagtgggca gaccaaatac aaccctctccc tcaagagt 48

<210> 2133
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic oligonucleotide

<400> 2133
gaaactggga gctactacgg ctttgactac

30

<210> 2134

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 2134
accaacagtg ttgcttgga c

21

<210> 2135

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 2135
aggacatact acaggtccaa gtggtataat gattatgcag tttctctgaa aagt

54

<210> 2136

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 2136
gaggatgggg atagtacta ccgctacggt atggacgtc

39