SEQUENCE LISTING

<110> Eli Lilly and Company
Zymeworks Inc.

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<130> X21099

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<151> 2017-07-10

<160> 51

<170> PatentIn version 3.5

<210> 1
<211> 290
<212> PRT
<213> Homo sapiens

<400> 1

Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15

Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
20 25 30

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

Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
50 55 60

Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65 70 75 80

Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
85 90 95

Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr

100 105 110

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

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
130 135 140

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

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
275 280 285

Glu Thr

290

<210> 2
<211> 288
<212> PRT
<213> Homo sapiens

<400> 2

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65 70 75 80

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

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
180 185 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
195 200 205

Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
210 215 220

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225 230 235 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
245 250 255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
260 265 270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
275 280 285

<210> 3
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 3

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

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

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

<210> 4
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 4

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 Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Gly Asn Ser Asn 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 Gln Ser Tyr Asp Ser Ser Leu
85 90 95

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

<210> 5
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (54)..(54)
<223> Xaa = M or S

<400> 5

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Xaa Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 6
<211> 120
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<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Ser Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 7
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 7

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Met Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 8

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

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

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

Ser 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 Ala Asn His Leu Pro Phe
85 90 95

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

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 9

Ser Leu Lys Ser Val
1 5

<210> 10
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 10

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
1 5 10 15

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Ser
20 25 30

<210> 11
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11

Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
1 5 10 15

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
20 25 30

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
35 40 45

Leu Asp Ser Asp Gly Ser Phe Ala Leu Val
50 55

<210> 12
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12

Val Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
1 5 10 15

Leu Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
20 25 30

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp
35 40 45

<210> 13
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13

Glu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
1 5 10 15

Cys Leu Val Thr Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
20 25 30

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

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 14

Ala Ala Glu Ser Glu Leu Ser
1 5

<210> 15
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15

Arg Val Gly Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
1 5 10 15

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
20 25 30

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Arg
35 40 45

<210> 16
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 16

Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1 5 10

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

<220>
<223> Synthetic construct

<400> 17

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

Gly

<210> 18
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 18

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

<210> 19
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 19

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

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 20

Tyr Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 21
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 21

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

<210> 22
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 22

Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1 5 10

<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 23

Leu Ile Ile Pro Ser Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 24

Leu Ile Ile Pro Met Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 25
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 25

Ala Arg Ala Glu His Ser Ser Thr Gly Thr Phe Asp Tyr
1 5 10

<210> 26
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 26

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 27

Ser Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 28

Gln Gln Ala Asn His Leu Pro Phe Thr
1 5

<210> 29
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 29

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Ser Pro Asp Tyr Ser Pro 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 Lys 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 Arg Val Glu Pro Lys
210 215 220

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

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

Val Ser Leu Leu 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 Leu Thr Trp
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> 30
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 30

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 Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Gly Asn Ser Asn 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 Gln Ser Tyr Asp Ser Ser Leu
85 90 95

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

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Glu Ser Glu 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 Ala Glu Cys Ser
210 215

<210> 31
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 31

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Ser Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Ala Glu His Ser Ser Thr Gly Thr 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 Glu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

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

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 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

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

Leu 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 Leu Thr Trp 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> 32
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 32

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Met Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Ala Glu His Ser Ser Thr Gly Thr 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 Glu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

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

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 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

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

Leu 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 Leu Thr Trp 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> 33
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 33

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Leu Ile Ile Pro Met Phe Asp Thr Ala Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Ala Glu His Ser Ser Thr Gly Thr 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 Glu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

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

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 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

Val Tyr Pro Pro Ser Arg Asp Glu Leu 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 Ala Leu Val 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> 34
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 34

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 35
<211> 787
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 35
cagtccgtcc tgactcagcc accttccgct agcggtaccc ccggccagag agtgacaatc 60

tcatgctccg gttccagctc taacattggc tctaacactg tcaattggta ccagcagctg 120

ccaggaaccg caccaaagct gctgatctat ggaaactcaa ataggcctag cggggtgcca 180

gaccggttta gcggatctaa aagtgggact tcagcttccc tggcaatttc tggactgcag 240

agtgaggacg aagctgatta ctattgccag tcctacgata gttcactgag cggttccgtg 300

ttcggcggag ggatcaagct gacagtcctg ggccagccca aggtgagttc tagaggatcc 360

atctgggata agcatgctgt tttctgtctg tccctaacat gccctgtgat tatccgcaaa 420

caacacaccc aagggcagaa ctttgttact taaacaccat cctgtttgct tctttcctca 480

ggccgctcct tccgtgactc tgtttccccc ttccagcgag gaactgcagg ccaataaggc 540

caccctggtg tgcctgatta gcgacttcta tcctggagct gtgacagtcg catggaaggc 600

cgattctagt ccagtgaaag caggggtcga gaccacaact ccctccaagc agagcaacaa 660

caagtacgca gccgagtctg aactgagtct gaccccagaa cagtggaagt cccacaggag 720

ttattcatgc caggtgaccc atgagggctc cacagtggag aagaccgtgg cccctgctga 780

gtgtagc 787

<210> 36
<211> 642
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 36
gacattcaga tgacccagag cccaagcagc gtgagcgcca gcgtcgggga ccgagtgacc 60

atcacatgca gggccagcca gggtatttct agttggctgg cttggtacca gcagaagcca 120

ggcaaagcac ccaagctgct gatctccgcc gcttcaagcc tgcagtccgg agtgccctct 180

cgattctctg gtagtggctc aggaacagac tttactctga ccatttcctc tctgcagcct 240

gaggatttcg ctacttacta ttgccagcag gcaaaccacc tgccattcac ctttggcgga 300

gggacaaaag tggagatcaa gagaaccgtc gcggcgccca gtgtcttcat ttttccccct 360

agcgacgaac agctgaagtc tgggacagcc agagtgggct gtctgctgaa caacttctac 420

cctagagagg ctaaagtgca gtggaaggtc gataacgcac tgcagtccgg aaattctcag 480

gagagtgtga ctgaacagga ctcaaaagat agcacctatt ccctgagaag cacactgact 540

ctgagcaagg ccgactacga gaagcataaa gtgtatgctt gtgaagtcac ccaccagggg 600

ctgagttcac cagtcacaaa atcattcaac agaggggagt gc 642

<210> 37
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 37
caggtccagc tggtgcagag cggagccgaa gtgaagaaac ccggtagcag cgtcaaagtg 60

tcatgtaaag cctcaggggg aacattctcc agctacgcca tctcctgggt gagacaggct 120

ccaggacagg gactggagtg gatgggagga atcatcccta tcttcggcac cgccaactac 180

gctcagaagt ttcagggccg cgtgaccatc acagccgaca agagcacctc tacagcttat 240

atggagctgt cttccctgag aagcgaggat acagccgtgt actattgcgc tcgctccccc 300

gactacagcc cttactatta ctatggcatg gacgtgtggg gccagggcac cacagtgacc 360

gtgagctctg ctagcacaaa gggcccatcc gtgttcccac tggctccatc cagcaagtcc 420

accagcggag gaacagccgc tctgggctgt ctggtgaagg actatttccc agagccagtg 480

accgtgtcct ggaacagcgg cgccctgacc tctggagtgc acacatttcc cgctgtgctg 540

cagtcttccg gcctgtactc tctgaagtcc gtggtgaccg tgcctagctc ttccctgggc 600

acccagacat atatctgcaa cgtgaatcac aagccttcca atacaaaggt ggacaagagg 660

gtggagccaa agagctgtga taagacccat acatgccccc cttgtcctgc tccagaggct 720

gctggaggac caagcgtgtt cctgtttcca cccaagccca aggacaccct gatgatctct 780

aggacccctg aggtgacatg cgtggtggtg tccgtgtccc acgaggaccc agaggtgaag 840

tttaactggt acgtggatgg cgtggaggtg cataatgcta agaccaagcc tagggaggag 900

cagtacaaca gcacctatcg ggtggtgtct gtgctgacag tgctgcatca ggattggctg 960

aacggcaagg agtataagtg caaggtgtct aataaggccc tgcccgctcc tatcgagaag 1020

accatctcca aggccaaggg ccagcctagg gagccacagg tgtacgtgct gcctccaagc 1080

cgggacgagc tgacaaagaa ccaggtgtct ctgctgtgcc tggtgaaggg cttctatcca 1140

tctgatatcg ctgtggagtg ggagtccaat ggccagcccg agaacaatta cctgacctgg 1200

ccccctgtgc tggacagcga tggctctttc tttctgtatt ccaagctgac agtggataag 1260

agccggtggc agcagggcaa cgtgttctcc tgttctgtga tgcacgaggc actgcacaat 1320

cattacaccc agaaatccct gtcactgagc cccggcaag 1359

<210> 38
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 38
caggtccagc tggtgcagag cggggcagag gtcaagaaac ccggtagctc cgtgaaggtc 60

agctgcaagg cttccggcgg aaccttctct agttacgcca tcagctgggt gagacaggct 120

cctggccagg gactggaatg gatgggcctg atcattccat cttttgatac cgctggctac 180

gcacagaagt ttcagggacg ggtggcaatt acagtcgatg agtcaaccag cacagcctat 240

atggagctgt caagcctgcg gtccgaagac actgccgtgt actattgcgc aagggccgaa 300

cactcctcta ctggaacctt cgattactgg gggcagggta ccctggtgac agtcagttca 360

gccagcacta agggacccag cgtgtttcca gaggcccccc ctagtaaatc cacttctgga 420

ggcaccgctg cactgggctg tctggtgacc gattacttcc cagagcccgt cacagtgagc 480

tggaactccg gggccctgac cagcggagtc catacatttc ctgctgtgct ggagtcaagc 540

gggctgtact ccctgtcctc tgtggtcacc gtgccaagtt caagcctggg aactcagacc 600

tatatctgca acgtgaatca caagccttca aatacaaaag ttgacaaacg tgtggaaccc 660

aagagttgtg ataaaaccca tacatgcccc ccttgtccgg cgccagaggc tgcaggagga 720

ccaagcgtgt tcctgtttcc acccaagcct aaagacacac tgatgatttc ccgaaccccc 780

gaagtcacat gcgtggtcgt gtctgtgagt cacgaggacc ctgaagtcaa gttcaactgg 840

tacgtggatg gcgtcgaggt gcataatgcc aagactaaac ctagggagga acagtacaac 900

tcaacctatc gcgtcgtgag cgtcctgaca gtgctgcacc aggattggct gaacggcaaa 960

gaatataagt gcaaagtgag caataaggcc ctgcccgctc ctatcgagaa aaccatttcc 1020

aaggctaaag ggcagcctcg cgaaccacag gtctacgtgc tgcctccatc ccgggacgag 1080

ctgacaaaga accaggtctc tctgctgtgc ctggtgaaag gcttctatcc atcagatatt 1140

gctgtggagt gggaaagcaa tgggcagccc gagaacaatt acctgacttg gccccctgtg 1200

ctggactctg atgggagttt ctttctgtat tctaagctga ccgtggataa aagtaggtgg 1260

cagcagggaa atgtctttag ttgttcagtg atgcatgaag ccctgcataa ccactacacc 1320

cagaaaagcc tgtccctgtc ccccggaaaa 1350

<210> 39
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 39
caggtccagc tggtgcagag cggggcagag gtcaagaaac ccggtagctc cgtgaaggtc 60

agctgcaagg cttccggcgg aaccttctct agttacgcca tcagctgggt gagacaggct 120

cctggccagg gactggaatg gatgggcctg atcattccaa tgttcgacac cgctggctac 180

gcacagaagt ttcagggacg ggtggcaatt acagtcgatg agtcaaccag cacagcctat 240

atggagctgt caagcctgcg gtccgaagac actgccgtgt actattgcgc aagggccgaa 300

cactcctcta ctggaacctt cgattactgg gggcagggta ccctggtgac agtcagttca 360

gccagcacta agggacccag cgtgtttcca gaggcccccc ctagtaaatc cacttctgga 420

ggcaccgctg cactgggctg tctggtgacc gattacttcc cagagcccgt cacagtgagc 480

tggaactccg gggccctgac cagcggagtc catacatttc ctgctgtgct ggagtcaagc 540

gggctgtact ccctgtcctc tgtggtcacc gtgccaagtt caagcctggg aactcagacc 600

tatatctgca acgtgaatca caagccttca aatacaaaag ttgacaaacg tgtggaaccc 660

aagagttgtg ataaaaccca tacatgcccc ccttgtccgg cgccagaggc tgcaggagga 720

ccaagcgtgt tcctgtttcc acccaagcct aaagacacac tgatgatttc ccgaaccccc 780

gaagtcacat gcgtggtcgt gtctgtgagt cacgaggacc ctgaagtcaa gttcaactgg 840

tacgtggatg gcgtcgaggt gcataatgcc aagactaaac ctagggagga acagtacaac 900

tcaacctatc gcgtcgtgag cgtcctgaca gtgctgcacc aggattggct gaacggcaaa 960

gaatataagt gcaaagtgag caataaggcc ctgcccgctc ctatcgagaa aaccatttcc 1020

aaggctaaag ggcagcctcg cgaaccacag gtctacgtgt atcctccaag ccgggacgag 1080

ctgacaaaga accaggtctc cctgacttgt ctggtgaaag ggttttaccc tagtgatatc 1140

gctgtggagt gggaatcaaa tggacagcca gagaacaatt ataagactac ccccccctgtg 1200

ctggacagtg atgggtcatt cgcactggtc tccaagctga cagtggacaa atctcggtgg 1260

cagcagggaa atgtcttttc atgtagcgtg atgcatgaag cactgcacaa ccattacacc 1320

cagaagtcac tgtcactgtc accaggaaaa 1350

<210> 40
<211> 330
<212> PRT
<213> Homo sapiens

<400> 40

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 41
<211> 280
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 41

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Lys
1 5 10 15

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

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
35 40 45

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
50 55 60

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

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
85 90 95

Val Ser Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
100 105 110

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
115 120 125

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
130 135 140

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

165 170 175

Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu Leu Thr
180 185 190

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
210 215 220

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Val
225 230 235 240

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
245 250 255

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
260 265 270

Ser Leu Ser Leu Ser Pro Gly Lys
275 280

<210> 42
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Glu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Thr Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Glu Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Ser Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Val Tyr Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Ala
275 280 285

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 43
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 43

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Glu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Thr Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Glu Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Ser Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu

225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 44
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 44

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Lys Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Ser Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Val Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Leu Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Leu Thr Trp Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 45
<211> 105
<212> PRT
<213> Homo sapiens

<400> 45

Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu
1 5 10 15

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 46
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46

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

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

Tyr Ala Ala Glu Ser Glu Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Ala Glu Cys Ser
100 105

<210> 47
<211> 107
<212> PRT
<213> Homo sapiens

<400> 47

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 48
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 48

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Arg Val Gly Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Arg Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 49
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 49

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Ser Pro Asp Tyr Ser Pro 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 Lys 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 Arg Val Glu Pro Lys
210 215 220

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

Ala 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 Ser 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 Asn 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 Val Tyr Pro Pro Ser Arg Asp Glu Leu 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 Ala Leu Val 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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cctgggaccg ctccaaagct gctgatctat ggcaactcca atcgaccatc tggagtgcct 180

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gcaggagtcg agaccacaac tccatcaaag cagagcaaca acaagtacgc agccgagagc 540

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