

SEQUENCE LISTING

<110> Eli Lilly and Company
 <120> BTLA Agonist Antibodies and Uses Thereof
 <130> X21261
 <140> 62/508510
 <141> 2017-05-19
 <160> 41
 <170> PatentIn version 3.5
 <210> 1
 <211> 449
 <212> PRT
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 <400> 1

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

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

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

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

Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
 65 70 75 80

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

Arg Gly Asp Tyr Tyr Asp Asp Tyr Val Tyr Val Tyr Ala Leu Asp Ile

100

105

110

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

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

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

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

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

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

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

Tyr Gly Pro Pro 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 Asp Val Ser Gln Glu
 260 265 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Glu 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 Leu
435 440 445

Gly

<210> 2
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

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 Gln Ala Ser Gln Ser Ile Ser Thr Ala
20 25 30

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

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

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

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

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

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

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

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

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

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

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

195

200

205

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 3

<211> 123

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<220>

<223> Synthetic Construct

<400> 3

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

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

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

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

Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
 65 70 75 80

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

Arg Gly Asp Tyr Tyr Asp Asp Tyr Val Tyr Val Tyr Ala Leu Asp Ile
 100 105 110

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

<210> 4

<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

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 Gln Ala Ser Gln Ser Ile Ser Thr Ala
20 25 30

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

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

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

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

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

<210> 5
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5

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

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

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

Gly Phe Ile Asn Tyr Gly Gly Ser Ala Tyr Tyr Ala Ser Arg Ala Lys
50 55 60

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

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

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

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

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

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

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

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

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

Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys

210

215

220

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

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

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
 260 265 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 275 280 285

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

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

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 325 330 335

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

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 355 360 365

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

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

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
 405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
420 425 430

Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 6
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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

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

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

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

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

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

Gly Ser Thr Ser Asp Asp Asn Pro Phe Gly Gly Gly Thr Lys Val Glu
100 105 110

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

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

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

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

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

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

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

<210> 7
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7

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

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

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

Gly Phe Ile Asn Tyr Gly Gly Ser Ala Tyr Tyr Ala Ser Arg Ala Lys
50 55 60

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

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

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

Val Ser Ser
115

<210> 8
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

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

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

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

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

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

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

Gly Ser Thr Ser Asp Asp Asn Pro Phe Gly Gly Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 9
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 9

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

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

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

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

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
65 70 75 80

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

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

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

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gln 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 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 Gly Leu Pro Ser Ser 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 Gln 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 Arg Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Glu 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 Leu Gly
 435 440 445

<210> 10

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 10

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 Gln Ala Ser Glu Asn Ile Tyr Asn Phe
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

35

40

45

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

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

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

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 11

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 11

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

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

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

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

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
65 70 75 80

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 12

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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

<210> 13
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 13

Gly Phe Ser Leu Ser Ser Tyr Gly Val Ser
1 5 10

<210> 14
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 14

Gly Phe Asp Ile Ser Lys Tyr Asn Ile Gln
1 5 10

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15

Gly Phe Ser Leu Ser Thr Tyr Ala Met Asn
1 5 10

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

<220>
<223> Synthetic Construct

<400> 16

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

<210> 17
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17

Phe Ile Asn Tyr Gly Gly Ser Ala Tyr Tyr Ala Ser Arg Ala Lys Gly
1 5 10 15

<210> 18
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

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

<210> 19

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 19

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

<210> 20

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

Gly	Leu	Ser	Asn	Ser	Asp	Leu
1			5			

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 21

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

1 5 10

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

Gln Ala Ser Gln Ser Ile Ser Thr Ala Leu Ala
1 5 10

<210> 23
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23

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

<210> 24
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

Gln Ala Ser Glu Asn Ile Tyr Asn Phe Leu Ala
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25

Ala Ala Ser Thr Leu Ala Ser
1 5

<210> 26

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

Arg Ala Ser Thr Leu Ala Ser
1 5

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27

Ser Ala Ser Thr Leu Ala Ser
1 5

<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

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

<210> 29
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29

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

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

Gln Gln Gly Ser Ser Asn Ser Asn Ile Asp Asn Pro
1 5 10

<210> 31
<211> 289
<212> PRT
<213> Homo sapiens

<400> 31

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

Phe Phe Leu Ile Pro Tyr Leu Asp Ile Trp Asn Ile His Gly Lys Glu
20 25 30

Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His Ser Ile
35 40 45

Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala
50 55 60

Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val
65 70 75 80

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

Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asp Asn Gly Ser
100 105 110

Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser
115 120 125

Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser
130 135 140

Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Arg Leu Leu Pro
145 150 155 160

Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys
165 170 175

Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala
180 185 190

Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr
195 200 205

Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly
210 215 220

Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser
225 230 235 240

Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val
245 250 255

Tyr Ala Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg Leu Ala
260 265 270

Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg
275 280 285

Ser

<210> 32
<211> 306
<212> PRT
<213> Mus musculus

<400> 32

Met Lys Thr Val Pro Ala Met Leu Gly Thr Pro Arg Leu Phe Arg Glu
1 5 10 15

Phe Phe Ile Leu His Leu Gly Leu Trp Ser Ile Leu Cys Glu Lys Ala
20 25 30

Thr Lys Arg Asn Asp Glu Glu Cys Glu Val Gln Leu Asn Ile Lys Arg
35 40 45

Asn Ser Lys His Ser Ala Trp Thr Gly Glu Leu Phe Lys Ile Glu Cys
50 55 60

Pro Val Lys Tyr Cys Val His Arg Pro Asn Val Thr Trp Cys Lys His
65 70 75 80

Asn Gly Thr Ile Trp Val Pro Leu Glu Val Gly Pro Gln Leu Tyr Thr
85 90 95

Ser Trp Glu Glu Asn Arg Ser Val Pro Val Phe Val Leu His Phe Lys
100 105 110

Pro Ile His Leu Ser Asp Asn Gly Ser Tyr Ser Cys Ser Thr Asn Phe
115 120 125

Asn Ser Gln Val Ile Asn Ser His Ser Val Thr Ile His Val Arg Glu
130 135 140

Arg Thr Gln Asn Ser Ser Glu His Pro Leu Ile Thr Val Ser Asp Ile
145 150 155 160

Pro Asp Ala Thr Asn Ala Ser Gly Pro Ser Thr Met Glu Glu Arg Pro
165 170 175

Gly Arg Thr Trp Leu Leu Tyr Thr Leu Leu Pro Leu Gly Ala Leu Leu
180 185 190

Leu Leu Leu Ala Cys Val Cys Leu Leu Cys Phe Leu Lys Arg Ile Gln
195 200 205

Gly Lys Glu Lys Lys Pro Ser Asp Leu Ala Gly Arg Asp Thr Asn Leu
210 215 220

Val Asp Ile Pro Ala Ser Ser Arg Thr Asn His Gln Ala Leu Pro Ser
225 230 235 240

Gly Thr Gly Ile Tyr Asp Asn Asp Pro Trp Ser Ser Met Gln Asp Glu
245 250 255

Ser Glu Leu Thr Ile Ser Leu Gln Ser Glu Arg Asn Asn Gln Gly Ile
260 265 270

Val Tyr Ala Ser Leu Asn His Cys Val Ile Gly Arg Asn Pro Arg Gln
275 280 285

Glu Asn Asn Met Gln Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val
290 295 300

Arg Ser
305

<211> 306
<212> PRT
<213> Mus musculus

<400> 33

Met Lys Thr Val Pro Ala Met Leu Gly Thr Pro Arg Leu Phe Arg Glu
1 5 10 15

Phe Phe Ile Leu His Leu Gly Leu Trp Ser Ile Leu Cys Glu Lys Ala
20 25 30

Thr Lys Arg Asn Asp Glu Glu Cys Pro Val Gln Leu Thr Ile Thr Arg
35 40 45

Asn Ser Lys Gln Ser Ala Arg Thr Gly Glu Leu Phe Lys Ile Gln Cys
50 55 60

Pro Val Lys Tyr Cys Val His Arg Pro Asn Val Thr Trp Cys Lys His
65 70 75 80

Asn Gly Thr Ile Cys Val Pro Leu Glu Val Ser Pro Gln Leu Tyr Thr
85 90 95

Ser Trp Glu Glu Asn Gln Ser Val Pro Val Phe Val Leu His Phe Lys
100 105 110

Pro Ile His Leu Ser Asp Asn Gly Ser Tyr Ser Cys Ser Thr Asn Phe
115 120 125

Asn Ser Gln Val Ile Asn Ser His Ser Val Thr Ile His Val Thr Glu
130 135 140

Arg Thr Gln Asn Ser Ser Glu His Pro Leu Ile Thr Val Ser Asp Ile
145 150 155 160

Pro Asp Ala Thr Asn Ala Ser Gly Pro Ser Thr Met Glu Glu Arg Pro
165 170 175

Gly Arg Thr Trp Leu Leu Tyr Thr Leu Leu Pro Leu Gly Ala Leu Leu
180 185 190

Leu Leu Leu Ala Cys Val Cys Leu Leu Cys Phe Leu Lys Arg Ile Gln
195 200 205

Gly Lys Glu Lys Lys Pro Ser Asp Leu Ala Gly Arg Asp Thr Asn Leu
210 215 220

Val Asp Ile Pro Ala Ser Ser Arg Thr Asn His Gln Ala Leu Pro Ser
225 230 235 240

Gly Thr Gly Ile Tyr Asp Asn Asp Pro Trp Ser Ser Met Gln Asp Glu
245 250 255

Ser Glu Leu Thr Ile Ser Leu Gln Ser Glu Arg Asn Asn Gln Gly Ile
260 265 270

Val Tyr Ala Ser Leu Asn His Cys Val Ile Gly Arg Asn Pro Arg Gln
275 280 285

Glu Asn Asn Met Gln Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val
290 295 300

Arg Ser
305

<210> 34
<211> 289
<212> PRT
<213> Macaca fascicularis

<400> 34

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

Val Phe Leu Ile Pro Tyr Leu Asp Ile Trp Asn Ile His Gly Lys Glu
20 25 30

Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Tyr His Ser Ile
35 40 45

Phe Ala Gly Asp Pro Phe Lys Leu Glu Cys Pro Val Lys Tyr Cys Ala
50 55 60

His Arg Pro Gln Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val
65 70 75 80

Lys Leu Glu Gly Arg His Thr Ser Trp Lys Gln Glu Lys Asn Leu Ser
85 90 95

Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Ser Asp Asn Gly Ser
100 105 110

Tyr Arg Cys Ser Ala Asn Phe Leu Ser Ala Ile Ile Glu Ser His Ser
115 120 125

Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser
130 135 140

Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Ser Leu Leu Pro
145 150 155 160

Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys
165 170 175

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

Gly Arg Glu Ile Thr Leu Val Asp Val Pro Phe Lys Ser Glu Gln Thr
195 200 205

Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly
210 215 220

Ile Tyr Asp Asn Glu Pro Asp Phe Cys Phe Arg Met Gln Glu Gly Ser

225 230 235 240

Tyr Ala Ser Leu Asn His Ser Ile Ile Gly Leu Asn Ser Arg Gln Ala
260 265 270

Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg
275 280 285

Ser

<220>
<223> Synthetic Construct

<400>	35						
caggtgcagc	tggatgcagtc	tggggctgag	gtgaagaagc	ctggggccctc	agtgaaggtt		60
tcctgcaagg	catctggatt	ctcccctcagt	agctatggag	tgagctgggt	gcgacaggcc		120
cctggacaag	ggcttgagt	gatgggagcc	attagttatg	atggtattac	atactacgcg		180
agctgggcga	aaagcagagt	caccatgacc	agggacacgt	ccacgagcac	agtctacatg		240
gagctgagca	gcctgagatc	tgaggacacg	gccgtgtatt	actgtgcgag	aggggactac		300
tacgatgatt	atgtttatgt	ttatgcttta	gacatctggg	gccagggcac	cctggtcacc		360
gtctcctcag	cttctacca	ggggcccatcg	gtcttcccg	tagcgccctg	ctccaggagc		420
acctccgaga	gcacagccgc	cctgggctgc	ctgggtcaagg	actactttccc	cgaaccggtg		480
acgggtgtcgt	ggaactcagg	cgccctgacc	agcggcgtgc	acacctttccc	ggctgtccta		540
cagtcctcag	gactctactc	cctcagcagc	gtgggtgaccg	tgccctccag	cagcttgggc		600
acgaagacct	acacctgcaa	cgtagatcac	aagcccagca	acaccaaggt	ggacaagaga		660

gttgagtcca aatatggtcc cccatgcccc ccctgcccag cacctgaggc cgccggggga	720
ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggaccct	780
gaggtcacgt gcgtgggtgg ggacgtgagc caggaagacc ccgaggtcca gttcaactgg	840
tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaacggcaag	960
gagtacaagt gcaaggtctc caacaaaggc ctcccgtcct ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag	1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctaccc cagcgacatc	1140
gccgtggagt gggaaaagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaggctaa ccgtggacaa gagcagggtg	1260
caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca	1320
cagaagagcc tctccctgtc tctgggt	1347

<210> 36
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 36	
gaaatttgtg tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgcc aggccagtca gagcattagt actgcattag cctggtacca gcagaaacct	120
ggccaggctc ccaggctcct catctatgct gcatccactc tggcatctgg catcccagac	180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct	240
gaagattttg cagtgtatta ctgtcaacag ggttatagta gtagtaatct tgataatgtt	300
ttcggcggag ggaccaaggt ggagatcaaa cggaccgtgg ctgcaccatc tgtcttcac	360
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat	420
aacttctatc ccagagaggc caaagtacag tggaagggtg ataacgccct ccaatcgggt	480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc	540
accctgacgc tgagcaaagc agactacgag aaacacaaaag tctacgcctg cgaagtcacc	600
catcagggcc tgagctcgcc cgtcacaaaag agcttcaaca ggggagagtg c	651

<210> 37
 <211> 1323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 37	
gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc	60
tcctgtgcag cctctggatt cgacatcagt aagtacaaca tccaatgggt ccgccaggct	120
ccagggaagg ggctggagtg ggttggcttc attaattatg gtggtagcgc atactacgcg	180
agccgggcga aaggcagatt caccatctca agagatgatt caaagaactc actgtatctg	240
caaatgaaca gcctgaaaac cgaggacacg gccgtgtatt actgtgctag aggactaagt	300
aatagcgacc tctggggcca gggcaccctg gtcaccgtct cctcagcttc taccaagggc	360
ccatcggctt tcccgtagc gccctgctcc aggagcacct ccgagagcac agccgccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttcccggt gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcacga agacctacac ctgcaacgta	600
gatcacaagc ccagcaacac caaggtggac aagagagttg agtccaaata tgggtcccca	660
tgcccaccct gcccagcacc tgaggccgcc gggggaccat cagtcttcct gttcccccca	720
aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac	780
gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat	840
aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc	900
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac	960
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag	1020

ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg	1080
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga aagcaatggg	1140
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc	1200
ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc	1260
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg	1320
ggt	1323

<210> 38
 <211> 663
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 38	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc aggccagtca gagcattagt agttggttat cctggatatca gcagaaacca	120
gggaaagccc ctaagctcct gatctacagg gcatccactc tggcatctgg ggtcccatca	180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct	240
gaagatattg caacatatta ctgtcaatcc acttatgggtg gtgttggttg cagtactagt	300
gatgataatc ctttcggcgg agggaccaag gtggagatca aacggaccgt ggctgcacca	360
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg	420
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc	480
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac	540
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc	600
tgcgaagtca cccatcaggg cctgagctcg cccgtcaca agagcttcaa caggggagag	660
tgc	663

<210> 39
 <211> 1341
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39

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tcctgcaagg	catctggatt	ctccctcagt	acctatgcaa	tgaactgggt	gcgacaggcc	120
cctggacaag	ggcttgagtg	gatgggaatc	attagtgatg	atggtaccac	atactacgcg	180
acctgggcga	aaggcagagt	cacatgacc	agggacacgt	ccacgagcac	agtctacatg	240
gagctgagca	gcctgagatc	tgaggacacg	gccgtgtatt	actgtgcgag	agatgctggt	300
gctggtggtg	tccaagacta	cttaaccttg	tggggccagg	gcaccctggt	caccgtctcc	360
tcagcttcta	ccaagggccc	atcggctctc	ccgctagcgc	cctgctccag	gagcacctcc	420
gagagcacag	ccgccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtggtg	accgtgccct	ccagcagctt	gggcacgaag	600
acctacacct	gcaacgtaga	tcacaagccc	agcaacacca	aggtggacaa	gagagttgag	660
tccaaatatg	gtcccccatg	cccaccctgc	ccagcacctg	aggccgccgg	gggaccatca	720
gtcttcctgt	tcccccaaaa	acccaaggac	actctcatga	tctcccggac	ccctgaggtc	780
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gatggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg	aggagcagtt	caacagcacg	900
taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaacgg	caaggagtac	960
aagtgcaagg	tctccaacaa	aggcctcccc	tcctccatcg	agaaaaccat	ctccaaagcc	1020
aaagggcagc	cccagagacc	acagggtgtac	accctgcccc	catcccagga	ggagatgacc	1080
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	acccagcga	catcgccgtg	1140
gagtgggaaa	gcaatgggca	gccggagaac	aactacaaga	ccacgcctcc	cgtgctggac	1200
tccgacggct	ccttcttcct	ctacagcagg	ctaaccgtgg	acaagagcag	gtggcaggag	1260
gggaatgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacacagaag	1320

agcctctccc tgtctctggg t

1341

<210> 40

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc	60
atcaactgcc aggccagtga gaatatattac aacttttttg cctggtacca gcagaaacca	120
ggacagcctc ctaagctgct catttactct gcatccactc tggcatctgg ggtccctgac	180
cgattcagtg gcagcgggtc tgggacagat ttactctca ccatcagcag cctgcaggct	240
gaagatgtgg cagtttatta ctgtcaacag ggttctagta atagtaatat tgataatcct	300
ttcggcggag ggaccaaggt ggagatcaaa cggaccgtgg ctgcaccatc tgtcttcatc	360
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat	420
aacttctatc ccagagaggc caaagtacag tggaagggtg ataacgccct ccaatcgggt	480
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc	540
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc	600
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg c	651

<210> 41

<211> 283

<212> PRT

<213> Homo sapiens

<400> 41

Met	Glu	Pro	Pro	Gly	Asp	Trp	Gly	Pro	Pro	Pro	Trp	Arg	Ser	Thr	Pro
1				5				10						15	

Lys	Thr	Asp	Val	Leu	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala
			20				25						30		

Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
35 40 45

Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
50 55 60

Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65 70 75 80

Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
85 90 95

Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
100 105 110

Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
115 120 125

Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
130 135 140

Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
145 150 155 160

Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
165 170 175

Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
180 185 190

Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
195 200 205

Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
210 215 220

Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
225 230 235 240

Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
245 250 255

Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
260 265 270

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
275 280