

SEQUENCE LISTING

<110> Eli Lilly and Company

<120> GDF15 Agonists and Uses Thereof

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<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

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

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 2

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 2

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
35 40 45

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
50 55 60

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
65 70 75 80

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
85 90 95

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
100 105 110

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
115 120 125

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
145 150 155 160

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Gln Leu Glu Ser
165 170 175

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

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

Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ala Pro Ala Pro Ala Pro
210 215 220

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gly Gly
225 230 235 240

Gly Gly Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
245 250 255

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
260 265 270

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
275 280 285

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
290 295 300

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
305 310 315 320

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
325 330 335

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
340 345 350

<210> 3

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 3

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 4
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

Gln Thr Asn Asn Cys Thr Tyr Leu Arg Glu Gln Cys Leu Arg Asp Ala
1 5 10 15

Asn Gly Cys Lys His Ala Trp Arg Val Met Glu Asp Ala Cys Asn Asp
20 25 30

Ser Asp Pro Gly Asp Pro Cys Lys Met Arg Asn Ser Ser Tyr Cys Asn
35 40 45

Leu Ser Ile Gln Tyr Leu Val Glu Ser Asn Phe Gln Phe Lys Glu Cys
50 55 60

Leu Cys Thr Asp Asp Phe Tyr Cys Thr Val Asn Lys Leu Leu Gly Lys
65 70 75 80

Lys Cys Ile Asn Lys Ser Asp Asn Val Lys Glu Asp Lys Phe Lys Trp
85 90 95

Asn Leu Thr Thr Arg Ser His His Gly Phe Lys Gly Met Trp Ser Cys
100 105 110

Leu Glu Val Ala Glu Ala Cys Val Gly Asp Val Val Cys Asn Ala Gln
115 120 125

Leu Ala Ser Tyr Leu Lys Ala Cys Ser Ala Asn Gly Asn Pro Cys Asp
130 135 140

Leu Lys Gln Cys Gln Ala Ala Ile Arg Phe Phe Tyr Gln Asn Ile Pro
145 150 155 160

Phe Asn Ile Ala Gln Met Leu Ala Phe Cys Asp Cys Ala Gln Ser Asp
165 170 175

Ile Pro Cys Gln Gln Ser Lys Glu Ala Leu His Ser Lys Thr Cys Ala
180 185 190

Val Asn Met Val Pro Pro Pro Thr Cys Leu Ser Val Ile Arg Ser Cys
195 200 205

Gln Asn Asp Glu Leu Cys Arg Arg His Tyr Arg Thr Phe Gln Ser Lys
210 215 220

Cys Trp Gln Arg Val Thr Arg Lys Cys His Glu Asp Glu Asn Cys Ile
225 230 235 240

Ser Thr Leu Ser Lys Gln Asp Leu Thr Cys Ser Gly Ser Asp Asp Cys
245 250 255

Lys Ala Ala Tyr Ile Asp Ile Leu Gly Thr Val Leu Gln Val Gln Cys
260 265 270

Thr Cys Arg Thr Ile Thr Gln Ser Glu Glu Ser Leu Cys Lys Ile Phe
275 280 285

Gln His Met Leu His Arg Lys Ser Cys Phe Asn Tyr Pro Thr Leu Ser
290 295 300

Asn Val Lys Gly Met Ala Leu Tyr Thr Arg Lys His Ala Asn Lys His
305 310 315 320

His His His His His
325

<210> 5
<211> 616
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5

Glu Arg Lys Ser Ser Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

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

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

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

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

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Arg Lys Ser Ser
260 265 270

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
275 280 285

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
290 295 300

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
305 310 315 320

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
325 330 335

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
340 345 350

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
355 360 365

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
370 375 380

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
405 410 415

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
420 425 430

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
435 440 445

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
450 455 460

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
465 470 475 480

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
485 490 495

Gly Ser Gly Gly Gly Gly Ala Ser Ala Arg Asn Gly Asp His Cys Pro
500 505 510

Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu
515 520 525

Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln
530 535 540

Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn
545 550 555 560

Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr
565 570 575

Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu
580 585 590

Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu
595 600 605

Leu Ala Lys Asp Cys His Cys Ile
610 615

<210> 6

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Ala Leu Gly Gly
1 5 10 15

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
20 25 30

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
35 40 45

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
50 55 60

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
65 70 75 80

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
85 90 95

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
100 105 110

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
115 120 125

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
130 135 140

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
145 150 155 160

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
180 185 190

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
195 200 205

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
210 215 220

Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asn Gly Thr His Cys
245 250 255

Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser
260 265 270

Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val
275 280 285

Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala
290 295 300

Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp
305 310 315 320

Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val
325 330 335

Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp
340 345 350

Leu Leu Ala Lys Asp Cys His Cys Ile
355 360

<210> 7
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7

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

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Gln Leu
165 170 175

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Gln Gly Gly Gly
210 215 220

Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly
225 230 235 240

Gln Gly Gly Gly Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys
245 250 255

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
260 265 270

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
275 280 285

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr
290 295 300

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
305 310 315 320

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
325 330 335

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
340 345 350

Ile

<210> 8
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 9
<211> 353
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 9

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

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Gln Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Gln Gly Gly Gly
210 215 220

Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly
225 230 235 240

Gln Gly Gly Gly Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys
245 250 255

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
260 265 270

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
275 280 285

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr
290 295 300

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
305 310 315 320

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
325 330 335

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
340 345 350

Ile

<210> 10
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10

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

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Gln Gly Gly Gly
210 215 220

Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly
225 230 235 240

Gln Gly Gly Gly Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys
245 250 255

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
260 265 270

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
275 280 285

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr
290 295 300

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
305 310 315 320

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
325 330 335

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
340 345 350

Ile

<210> 11
<211> 355
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11

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

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

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Gln Leu
165 170 175

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Gly Gly Gly Gly Ser Ala Pro Ala
210 215 220

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
225 230 235 240

Pro Gly Gly Gly Gly Ser Gly Asp His Cys Pro Leu Gly Pro Gly Arg
245 250 255

Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp
260 265 270

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

Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile
290 295 300

Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys
305 310 315 320

Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp
325 330 335

Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys
340 345 350

His Cys Ile
355

<210> 12
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

Gly Gly Gly Gly Gln Gly Gly Gly Gly Gln Gly Gly Gly Gly Gln Gly
1 5 10 15

Gly Gly Gly Gln Gly Gly Gly Gly Gln
20 25

<210> 13
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 13

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro
20

<210> 14

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 14

Gly Gly Gly Gly Ser
1 5

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 15

Gly Gly Gly Gly
1

<210> 16

<211> 1053

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 16

gaggccgccg ggggaccatc agtcttcctg ttcccccaa aaccaagga cactctcatg 60

atctcccgga cccctgaggt cacgtgcgtg gtggtggacg tgagccagga agaccccgag 120

gtccagttca actggtacgt ggatggcgtg gaggtgcata atgccaagac aaagccgcgg	180
gaggagcagt tcaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac	240
tggctgaacg gcaaggagta caagtgaag gtctccaaca aaggcctccc gtcctccatc	300
gagaaaacca tctccaaagc caaagggcag ccccgagagc cacaggtgta caccctgccc	360
ccatcccagg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	420
taccccagcg acatcgccgt ggagtgggaa agcaatgggc agccggagaa caactacaag	480
accacgcctc ccgtgctgga ctccgacggc tccttcagc tcgagagcag gctaaccgtg	540
gacaagagca ggtggcagga ggggaatgtc ttctcatgct ccgtgatgca tgaggctctg	600
cacaaccact acacacagaa gaggcctctcc ctgtctctgg gtggcggtgg tggagctcca	660
gccccagctc ctgctcctgc accagcacct gccccgctc cagcaccgc acctggagga	720
gggggcggtg accactgtcc cctggggcct ggccggtgtt gcagactgca tacagtccgg	780
gcctccctgg aagacctggg ttgggcagat tgggtgctct cacctcgca ggttcaggtg	840
accatgtgca ttggggcttg tccctcaca tttcgcgag ctaacatgca cgcccaaadc	900
aaaacctccc tgcaccggct taaaccggat actgttcctg ctccctgctg cgtgccagca	960
tcctacaacc ccatggtgct gatccagaag acggatacag gggtgtcact gcagacctat	1020
gatgacctcc tggccaaaga ttgccactgt atc	1053

<210> 17
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 17

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Ala	Leu	Ala	Gly
1				5				10					15		

Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
			20					25					30		

Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
		35					40					45			

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225