

SEQUENCE LISTING

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<120> Antibodies, Activatable Antibodies, Bispecific Antibodies, and
 Bispecific Activatable Antibodies and Methods of Use Thereof

<130> CYTM-055/001US 322001-2516

<150> 62/572,468
 <151> 2017-10-14

<150> 62/577,140
 <151> 2017-10-25

<150> 62/613,358
 <151> 2018-01-03

<150> 62/666,065
 <151> 2018-05-02

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<170> PatentIn version 3.5

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

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

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

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

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

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

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

Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

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

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

Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

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

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Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Ile Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
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Gly Thr Asn Lys Arg Ala Pro
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Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

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Thr Tyr Ala Met Asn
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Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

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His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
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Met	Met	Tyr	Cys	Gly	Gly	Asn	Glu	Val	Leu	Cys	Gly	Pro	Arg	Val
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Gly	Tyr	Arg	Trp	Gly	Cys	Glu	Trp	Asn	Cys	Gly	Gly	Ile	Thr	Thr
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Leu	Ser	Gly	Arg	Ser	Asp	Asn	His
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Leu Ser Gly Arg Ser Asp Asp His
1 5

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

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<400> 18

Leu Ser Gly Arg Ser Asp Asn His
1 5

<210> 19
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<400> 19

Leu Ser Gly Arg Ser Gly Asn His
1 5

<210> 20
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Thr Ser Thr Ser Gly Arg Ser Ala Asn Pro Arg Gly
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Ile Ser Ser Gly Leu Leu Ser Ser
1 5

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<400> 22

Gln Asn Gln Ala Leu Arg Met Ala
1 5

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<400> 23

Val His Met Pro Leu Gly Phe Leu Gly Pro
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<400> 24

Ala Val Gly Leu Leu Ala Pro Pro
1 5

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<400> 25

Leu Ser Gly Arg Ser Asp Asp His
1 5

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<400> 26

Leu Ser Gly Arg Ser Asp Ile His
1 5

<210> 27
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<400> 27

Leu Ser Gly Arg Ser Asp Gln His
1 5

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<400> 28

Leu Ser Gly Arg Ser Asp Thr His
1 5

<210> 29
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Leu Ser Gly Arg Ser Asp Tyr His
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Leu Ser Gly Arg Ser Asp Asn Pro
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Leu Ser Gly Arg Ser Ala Asn Pro
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Leu Ser Gly Arg Ser Ala Asn Ile
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Leu Ser Gly Arg Ser Asp Asn Ile
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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Gly Asn His
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Ala Val Gly Leu Leu Ala Pro Pro Ser Gly Arg Ser Ala Asn Pro Arg
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Gly

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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp His
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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ile His
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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln His
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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr His
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<400> 42

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Tyr His
1 5 10

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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro
1 5 10

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<400> 44

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro
1 5 10

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

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Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Ile
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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
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Asn His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Asp His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
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Ile His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
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Gln His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
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Thr His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Tyr His

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Asn Pro

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Ala
1 5 10 15

Asn Pro

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Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Ala
1 5 10 15

Asn Ile

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<400> 56

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
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Asn Ile

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Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
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Tyr Ala Ser Glu Ser Ile Ser
1 5

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Gln Gln Asn Asn Asn Trp Pro Thr Thr
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Asn Tyr Gly Val His
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Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
1 5 10 15

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Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
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<400> 63

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

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<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 64

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

Thr Leu Val Thr Val Ser Xaa
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<400> 65

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
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<223> Xaa may be Ser or Ala

<400> 66

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

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<222> (119)..(119)
<223> Xaa may be Ser or Ala

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<222> (299)..(299)
<223> Xaa can be any amino acid

<400> 67

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Xaa Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys

405

410

415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
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Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 68

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<222> (119)..(119)

<223> Xaa may be Ser or Ala

<400> 68

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
 20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
 50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 69
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> MISC_FEATURE
 <222> (119)..(119)
 <223> Xaa may be Ser or Ala

<220>

<221> misc_feature
<222> (236)..(236)
<223> Xaa can be any amino acid

<400> 69

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 70
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 70

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 71
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<220>
<221> misc_feature

<222> (237)..(237)

<223> Xaa can be any amino acid

<400> 71

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

195

200

205

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

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

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

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

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

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

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

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

Lys

<210> 72
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 72

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly

100

105

110

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 73
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<220>
<221> misc_feature
<222> (333)..(333)

<223> Xaa can be any amino acid

<400> 73

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Xaa Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 74
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 74

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 75
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 75

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 76
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 76

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
225 230 235 240

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 77
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa may be Ser or Ala

<400> 77

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60

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

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Xaa Val His Thr Phe Pro Ala Val Leu
115 120 125

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
130 135 140

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
145 150 155 160

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
165 170 175

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
180 185 190

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
195 200 205

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

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
225 230 235 240

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val
245 250 255

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
260 265 270

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

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
290 295 300

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
305 310 315 320

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
325 330 335

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
340 345 350

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
355 360 365

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
370 375 380

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
385 390 395 400

Lys

<210> 78

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 78

Leu Ser Cys Glu Gly Trp Ala Met Asn Arg Glu Gln Cys Arg Ala
1 5 10 15

<210> 79
<211> 15
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<220>
<223> synthetic

<400> 79

Pro	Pro	Leu	Glu	Cys	Asn	Thr	Lys	Ser	Met	Cys	Ser	Lys	His	Asp
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<400> 80

Asp	Arg	Asp	Cys	Arg	Gly	Arg	Arg	Ala	Arg	Cys	Gln	Gln	Glu	Gly
1				5					10					15

<210> 81
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<220>
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<400> 81

Phe	Thr	Cys	Glu	Gly	Trp	Ala	Met	Asn	Arg	Glu	Gln	Cys	Arg	Thr
1				5					10					15

<210> 82
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<220>
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<400> 82

Gly Arg Cys Pro Pro Ser Arg Asp Ile Arg Phe Cys Thr Tyr Met
1 5 10 15

<210> 83
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 83

Phe Ser Cys Glu Gly Trp Ala Met Asn Arg Ser Gln Cys Arg Thr
1 5 10 15

<210> 84
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 84

Phe Thr Cys Glu Gly Trp Ala Met Asn Arg Asp Gln Cys Arg Thr
1 5 10 15

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 85

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

<210> 86
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 86

Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly Pro Tyr Val Met
1 5 10

<210> 87

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 87

Cys Ile Ser Pro Arg Gly Cys
1 5

<210> 88

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 88

Gly Ser Gly Gly Ser
1 5

<210> 89

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 89

Gly Gly Gly Ser
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<210> 90

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 90

Gly Gly Ser Gly
1

<210> 91

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 91

Gly Gly Ser Gly Gly
1 5

<210> 92

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 92

Gly Ser Gly Ser Gly
1 5

<210> 93

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 93

Gly Ser Gly Gly Gly
1 5

<210> 94

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 94

Gly Gly Gly Ser Gly
1 5

<210> 95

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 95

Gly Ser Ser Ser Gly
1 5

<210> 96

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 96

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

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 97

Gly Gly Gly Ser
1

<210> 98

<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 98

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

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 99

Gly Gly Gly Gly Ser
1 5

<210> 100
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 100

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

<210> 101
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 101

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

Gly Gly Ser Gly Gly Gly Ser
20

<210> 102
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 102

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

Gly Gly Gly Ser Gly Gly Ser
20

<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 103

Gly Ser Ser Gly Thr
1 5

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 104

Gly Gly Gly Ser Ser Gly Gly Ser
1 5

<210> 105
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>

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<400> 105

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ggcggcgggtt ctgagaccgt ggtcacacag gagccctcac tgacagtgag ccctggcggg	180
accgtcacac tgacttgtcg cagttcaact ggcgccgtga ctaccagcaa ttacgctaac	240
tgggtccagc agaaaccagg acaggcacca cgaggactga tcggaggaac taataagaga	300
gcaccaggaa cccctgcaag gttctccgga tctctgctgg ggggaaaagc cgctctgaca	360
ctgagcggcg tgcagcctga ggacgaagct gagtactatt gcgcactgtg gtactccaac	420
ctgtgggtgt ttggcggggg aactaagctg accgtcctgg gaggaggagg aagcggagga	480
ggaggggagcg gaggaggagg atccgaagtg cagctggtcg agagcggagg aggactggtg	540
cagccaggag gatccctgaa gctgtcttgt gcagccagtg gcttcacctt caacacttac	600
gcaatgaact ggggtgcggca ggcacctggg aagggactgg aatgggtcgc ccggatcaga	660
tctaaataca ataactatgc cacctactat gctgacagtg tgaaggatag gttcaccatt	720
tcacgcgacg atagcaaaaa cacagcttat ctgcagatga ataacctgaa gaccgaggat	780
acagcagtgt actattgcgt cagacacggc aatttcggga actcttacgt gagttggttt	840
gcctattggg gacaggggac actggtcacc gtctcctcag gaggtggtgg atcccaggtg	900
cagctgaaac agagcggccc gggcctggtg cagccgagcc agagcctgag cattacctgc	960
accgtgagcg gctttagcct gaccaactat ggcgtgcatt ggggtgcgca gagcccgggc	1020
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tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtgtt ttttaaatg	1140
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gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc	1260
aaggggccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	1320
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	1380
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1440
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1500

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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      1560
gacaaaactc acacatgccc accgtgcccga gcacctgaac tcctgggggg accgtcagtc      1620
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca      1680
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      1740
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacca gagcacgtac      1800
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      1860
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa      1920
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag      1980
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc      2220
ctctccctgt ctccgggtaa a                                              2241

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<210> 106
<211> 747
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 106

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Gln Gly Gln Ser Gly Gln Met Met Tyr Cys Gly Gly Asn Glu Val Leu
1           5           10           15

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Cys Gly Pro Arg Val Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20           25           30

```

```

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val
35           40           45

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```

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
50           55           60

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Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
100 105 110

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
115 120 125

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 107
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 107
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aatcatggca gtagcggtag ccagatcttg ctgaccaga gcccggtgat tctgagcgtg 180
agccccggcg aacgtgtgag ctttagctgc cgcgcgagcc agagcattgg caccaacatt 240
cattggtatc agcagcgcac caacggcagc ccgcgcctgc tgattaaata tgcgagcgaa 300
agcattagcg gcattccgag ccgctttagc ggcagcggca gcggcaccga ttttacctg 360
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tggccgacca ctttggcgc gggcaccaaa ctggaactga aacgtacggt ggctgcacca 480
tctgtcttca tcttcccgc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 540
tgcttgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 600
ctccaatcgg gtaactcca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
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tgt 783

<210> 108
<211> 261
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 108

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
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Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Leu Ser Gly Arg Ser Asp Asn His Gly Ser Ser Gly Thr Gln
35 40 45

Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly Glu
50 55 60

Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile
65 70 75 80

His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys
85 90 95

Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu
115 120 125

Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr
130 135 140

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

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
180 185 190

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
195 200 205

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 210 215 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 225 230 235 240

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 245 250 255

Asn Arg Gly Glu Cys
 260

<210> 109
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 109
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 ggcggcggtt ctcagaccgt ggtcacacag gagccctcac tgacagtgag ccctggcggg 180
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 tctaaatata ataactatgc cacctactat gctgacagtg tgaaggatag gttcaccatt 720
 tcacgcgacg atagcaaaaa cacagcttat ctgcagatga ataacctgaa gaccgaggat 780
 acagcagtgt actattgcgt cagacacggc aatttcggga actcttacgt gagttggttt 840

gcctattggg gacaggggac actggtcacc gtctcctcag gaggtggtgg atcccaggtg	900
cagctgaaac agagcggccc gggcctggtg cagccgagcc agagcctgag cattacctgc	960
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tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtgtt ttttaaaatg	1140
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gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc	1260
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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	1560
gacaaaactc acacatgccc accgtgcccga gcacctgaac tcctggggggg accgtcagtc	1620
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aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	2220
ctctccctgt ctccgggtaa a	2241

<210> 110
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 110

Gln Gly Gln Ser Gly Gln Met Met Tyr Cys Gly Gly Asn Glu Val Leu
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Cys Gly Pro Arg Val Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
100 105 110

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
115 120 125

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 111
<211> 774
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 111
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tacggctcga gcggtggcag cggtggctct ggtggctcag gtggaggctc gggcgggtggg 120
agcggcggtt ctgatatctt gctgaccag agcccgtga ttctgagcgt gagcccgggc 180
gaacgtgtga gctttagctg ccgcgcgagc cagagcattg gcaccaacat tcattggtat 240
cagcagcgca ccaacggcag cccgcgcctg ctgattaaat atgcgagcga aagcattagc 300
ggcattccga gccgctttag cggcagcggc agcggcaccg attttacct gagcattaac 360
agcgtggaaa gcgaagatat tgcggattat tattgccagc agaacaacaa ctggccgacc 420

acctttggcg cgggcaccaa actggaactg aaacgtacgg tggctgcacc atctgtcttc	480
atcttcccgcatcatgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	540
aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg	600
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	660
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	720
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt	774

<210> 112
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 112

Gln	Gly	Gln	Ser	Gly	Gln	Cys	Ile	Ser	Pro	Arg	Gly	Cys	Pro	Asp	Gly
1				5					10					15	

Pro	Tyr	Val	Met	Tyr	Gly	Ser	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly
			20					25					30		

Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Asp	Ile	Leu	Leu
		35					40					45			

Thr	Gln	Ser	Pro	Val	Ile	Leu	Ser	Val	Ser	Pro	Gly	Glu	Arg	Val	Ser
	50					55					60				

Phe	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	Ile	His	Trp	Tyr
65					70				75					80	

Gln	Gln	Arg	Thr	Asn	Gly	Ser	Pro	Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser
				85					90					95	

Glu	Ser	Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly
			100					105					110		

Thr	Asp	Phe	Thr	Leu	Ser	Ile	Asn	Ser	Val	Glu	Ser	Glu	Asp	Ile	Ala
		115					120					125			

Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala
130 135 140

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

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

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
180 185 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
210 215 220

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225 230 235 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 113
<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 113
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gttggctcga gcggtggcag cgggtggctct ggtggtatct cttccggact gctgtccggc 120
agatccgaca atcacggcgg cggttctcag accgtggtca cacaggagcc ctactgaca 180
gtgagccctg gcgggaccgt cacactgact tgtcgcagtt caactggcgc cgtgactacc 240

agcaattacg ctaactgggt ccagcagaaa ccaggacagg caccacgagg actgatcgga	300
ggaactaata agagagcacc aggaaccct gcaaggttct ccggatctct gctgggggga	360
aaagccgctc tgacactgag cggcgtgcag cctgaggacg aagctgagta ctattgcgca	420
ctgtggtact ccaacctgtg ggtgtttggc gggggaacta agctgaccgt cctgggagga	480
ggaggaagcg gaggaggagg gagcggagga ggaggatccg aagtgcagct ggtcgagagc	540
ggaggaggac tgggtgcagcc aggaggatcc ctgaagctgt cttgtgcagc cagtggcttc	600
accttcaaca cttacgcaat gaactgggtg cggcaggcac ctgggaaggg actggaatgg	660
gtcgcccgga tcagatctaa atacaataac tatgccacct actatgctga cagtgtgaag	720
gataggttca ccatttcacg cgacgatagc aaaaacacag cttatctgca gatgaataac	780
ctgaagaccg aggatacagc agtgtactat tgcgtcagac acggcaattt cgggaactct	840
tacgtgagtt ggtttgccta ttggggacag gggacactgg tcaccgtctc ctcaggaggt	900
ggtggatccc aggtgcagct gaaacagagc ggcccgggcc tgggtgcagcc gagccagagc	960
ctgagcatta cctgcaccgt gagcggcttt agcctgacca actatggcgt gcattgggtg	1020
cgccagagcc cgggcaaagg cctggaatgg ctgggcgtga tttggagcgg cggcaacacc	1080
gattataaca ccccgtttac cagccgcctg agcattaaca aagataacag caaaagccag	1140
gtgtttttta aaatgaacag cctgcaaagc caggataccg cgatttatta ttgcgcgcgc	1200
gcgctgacct attatgatta tgaatttgcg tattggggcc agggcaccct ggtgaccgtg	1260
agcgcggcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc	1320
tctgggggca cagcggccct gggctgcctg gtcaaggact acttcccga accggtgacg	1380
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	1440
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	1500
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaaggtgga caagaaagtt	1560
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg	1620
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1680
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1740
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	1800
taccagagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1860

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1920
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1980
 gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 2040
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 2100
 cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc 2160
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 2220
 tacacgcaga agagcctctc cctgtctccg ggtaaa 2256

<210> 114
 <211> 752
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 114

Gln Gly Gln Ser Gly Gln Met Met Tyr Cys Gly Gly Asn Glu Val Leu
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Cys Gly Pro Arg Val Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly
 35 40 45

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly
 50 55 60

Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
 65 70 75 80

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
 85 90 95

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg
 100 105 110

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

Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser
130 135 140

Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
165 170 175

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
180 185 190

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
195 200 205

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile
210 215 220

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
225 230 235 240

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
245 250 255

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

Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
275 280 285

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln
290 295 300

Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
305 310 315 320

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly
325 330 335

Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
340 345 350

Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
355 360 365

Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys
370 375 380

Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg
385 390 395 400

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr
405 410 415

Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
420 425 430

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
435 440 445

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
450 455 460

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
465 470 475 480

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
485 490 495

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
500 505 510

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
515 520 525

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
530 535 540

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
545 550 555 560

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
565 570 575

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
580 585 590

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val
595 600 605

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
610 615 620

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
625 630 635 640

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

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
660 665 670

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
675 680 685

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
690 695 700

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
705 710 715 720

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
725 730 735

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745 750

<210> 115

<211> 798

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 115
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agcggctcga gcgataatca tggcagtagc ggtaccaga tcttgctgac ccagagcccg 180
gtgattctga gcgtgagccc gggcgaacgt gtgagcttta gctgccgcgc gagccagagc 240
attggcacca acattcattg gtatcagcag cgcaccaacg gcagcccgcg cctgctgatt 300
aaatatgcga gcgaaagcat tagcggcatt ccgagccgct ttagcggcag cggcagcggc 360
accgatttta ccctgagcat taacagcgtg gaaagcgaag atattgcgga ttattattgc 420
cagcagaaca acaactggcc gaccaccttt ggcgcgggca ccaaactgga actgaaacgt 480
acgggtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 540
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 600
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 660
aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 720
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 780
ttcaacaggg gagagtgt 798

<210> 116
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 116

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
1 5 10 15

Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly
35 40 45

Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser
50 55 60

Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser
65 70 75 80

Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro
85 90 95

Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser
100 105 110

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
115 120 125

Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn
130 135 140

Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
145 150 155 160

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
165 170 175

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
180 185 190

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
195 200 205

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
210 215 220

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
225 230 235 240

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
245 250 255

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
260 265

<210> 117
<211> 2133
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 117
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agccctggcg ggaccgtcac actgacttgt cgcagttcaa ctggcgccgt gactaccagc 120
aattacgcta actgggtcca gcagaaacca ggacaggcac cacgaggact gatcggagga 180
actaataaga gaggaccagg aacccttgca aggttctccg gatctctgct ggggggaaaa 240
gccgctctga cactgagcgg cgtgcagcct gaggacgaag ctgagtacta ttgcgcactg 300
tggtactcca acctgtgggt gtttggcggg ggaactaagc tgaccgtcct gggaggagga 360
ggaagcggag gaggaggag cggaggagga ggatccgaag tgcagctggt cgagagcgga 420
ggaggactgg tgcagccagg aggatccctg aagctgtctt gtgcagccag tggcttcacc 480
ttcaacactt acgcaatgaa ctgggtgcgg caggcacctg ggaagggact ggaatgggtc 540
gcccggatca gatctaaata caataactat gccacctact atgctgacag tgtgaaggat 600
aggttcacca tttcacgcga cgatagcaaa aacacagctt atctgcagat gaataacctg 660
aagaccgagg atacagcagt gtactattgc gtcagacacg gcaatttcgg gaactcttac 720
gtgagttggt ttgcctattg gggacagggg aactggtca ccgtctcctc aggaggtggt 780
ggatcccagg tgcagctgaa acagagcggc ccgggcctgg tgcagccgag ccagagcctg 840
agcattacct gcaccgtgag cggctttagc ctgaccaact atggcgtgca ttgggtgcgc 900
cagagcccgg gcaaaggcct ggaatggctg ggcgtgattt ggagcggcgg caacaccgat 960
tataacaccc cgtttaccag ccgcctgagc attaaciaag ataacagcaa aagccagggtg 1020
ttttttaaaa tgaacagcct gcaaagccag gataccgcga tttattattg cgcgcgcgcg 1080
ctgacctatt atgattatga atttgcgtat tggggccagg gcaccctggt gaccgtgagc 1140
gcggctagca ccaagggcc atcggctctt cccctggcac cctcctcaa gaggacctct 1200

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gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      1260
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgtg cctacagtcc      1320
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccag      1380
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      1440
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      1500
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc      1560
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      1620
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac      1680
cagagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      1740
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc      1800
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag      1860
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac      1920
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc      1980
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg      2040
tggcagcagg ggaacgtctt ctcattgctc gtgatgcatg aggtcttgca caaccactac      2100
acgcagaaga gcctctccct gtctccgggt aaa                                  2133

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<210> 118
 <211> 711
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 118

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

```

```

Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser
          20          25          30

```

```

Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln
          35          40          45

```

Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg
50 55 60

Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys
65 70 75 80

Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr
85 90 95

Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly Gly Gly Thr
100 105 110

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

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

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

Phe Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

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

Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr
225 230 235 240

Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly
260 265 270

Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
275 280 285

Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
290 295 300

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
305 310 315 320

Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser
325 330 335

Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr
340 345 350

Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
370 375 380

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
385 390 395 400

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
405 410 415

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
420 425 430

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
435 440 445

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
450 455 460

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
465 470 475 480

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
485 490 495

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
500 505 510

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
515 520 525

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
530 535 540

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
545 550 555 560

Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
565 570 575

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
580 585 590

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
595 600 605

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
610 615 620

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
625 630 635 640

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
645 650 655

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
675 680 685

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
690 695 700

Leu Ser Leu Ser Pro Gly Lys
705 710

<210> 119
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 119
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agcgtgagcc cgggcgaacg tgtgagcttt agctgccgcg cgagccagag cattggcacc 120
aacattcatt ggtatcagca gcgcaccaac ggcagcccg ccttgctgat taaatatgcg 180
agcgaaagca ttagcggcat tccgagccgc tttagcggca gcggcagcgg caccgatttt 240
accctgagca ttaacagcgt ggaaagcgaa gatattgcgg attattattg ccagcagaac 300
aacaactggc cgaccacctt tggcgcgggc accaaactgg aactgaaacg tacggtggct 360
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 420
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 480
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 540
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 600
tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 660
ggagagtgt 669

<210> 120
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 120

Ser Asp Asn His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
1 5 10 15

Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
20 25 30

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
35 40 45

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

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

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
85 90 95

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
100 105 110

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

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

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

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

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

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

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

<210> 121
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 121
caaggccagt ctggatccgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact 60
acaggctcga gcggtggcag cgggtggctct ggtggctctga gcggccgttc cgataatcat 120
ggcggcgggtt ctcaaactgt agtaactcaa gaaccaagct tctccgtctc ccctggggga 180
acagtcacac ttacctgccg aagtagtaca ggtgctgtta cgaccagtaa ctatgccaat 240
tgggtacaac aaacgcctgg tcaggctccg cgcggattga taggaggcac gaataaacgg 300
gcacccgggtg tcccggacag attcagcggg agcatactcg gtaataaggc agctcttact 360
atcactggggg cccaagctga tgatgaaagt gattattatt gtgcgctctg gtacagcaac 420
ctctgggtgt ttgggggtgg cacgaaactt actgtcttgg gcggcggcgg atcaggggga 480
ggtggctctg gaggaggagg ctcagaagtc caactggctg aatccggggg agggctcgtg 540
cagccgggtg ggtccctcaa actctcttgt gcggcctcag ggtttacctt cagtacatac 600
gcgatgaatt gggtcggca ggccagtggg aaagggctcg aatgggtagg acgaatccga 660
tcaaaatata acaactacgc tacttattac gctgattccg tgaaggacag attcacaata 720
tcccgcgacg atagcaagaa tacggcatat cttcagatga attctcttaa aactgaggat 780
accgctgtgt attactgcac aagacatggg aattttggaa actcatatgt ctcttggttc 840
gcttattggg gacagggcac gttggttacc gtgtctagcg gaggtggtgg atcccaggtg 900
cagctgaaac agagcggccc gggcctgggtg cagccgagcc agagcctgag cattacctgc 960
accgtgagcg gctttagcct gaccaactat ggcgtgcatt ggggtgcgca gagcccgggc 1020
aaaggcctgg aatggctggg cgtgatttgg agcggcggca acaccgatta taacaccccg 1080
tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtgtt ttttaaaatg 1140
aacagcctgc aaagccagga taccgcgatt tattattgcg cgcgcgcgct gacctattat 1200
gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc 1260
aagggcccat cggctctccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 1320
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1380

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1440
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1500
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 1560
 gacaaaactc acacatgccc accgtgcccga gcacctgaat ttgaaggggg accgtcagtc 1620
 ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 1680
 tgcgtgggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1740
 ggctgggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa tagcacgtac 1800
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1860
 tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa 1920
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1980
 aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 2040
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 2100
 gacggctcct tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 2160
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 2220
 ctctccctgt ctccgggtaa atga 2244

<210> 122
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 122

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
 1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val
 35 40 45

Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

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

Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp
115 120 125

Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
705					710					715					720

Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				725					730					735	

Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
			740					745		

<210> 123
 <211> 2244
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 123

caaggccagt ctggatccgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact	60
acaggctcga gcggtggcag cgggtggctct ggtggctctga gcggccgttc cgataatcat	120
ggcggcggtt ctcaaactgt agtaactcaa gaaccaagct tctccgtctc ccctggggga	180
acagtcacac ttacctgccg aagtagtaca ggtgctgtta cgaccagtaa ctatgccaat	240
tgggtacaac aaacgcctgg tcaggctccg cgcggattga taggaggcac gaataaacgg	300
gcacccggtg tcccggacag attcagcggg agcatactcg gtaataaggc agctcttact	360
atcactgggg cccaagctga tgatgaaagt gattattatt gtgcgctctg gtacagcaac	420
ctctgggtgt ttgggggtgg cacgaaactt actgtcttgg gcggcggcgg atcaggggga	480
ggtggctctg gaggaggagg ctcagaagtc caactggtcg aatccggggg agggctcgta	540
cagccgggtg ggtccctcaa actctcttgt gcggcctcag ggtttacctt cagtacatac	600
gcgatgaatt gggtcggca ggccagtggg aaagggtcg aatgggtagg acgaatccga	660
tcaaaataca acaactacgc tacttattac gctgattccg tgaaggacag attcacaata	720
tcccgcgacg atagcaagaa tacggcatat cttcagatga attctcttaa aactgaggat	780
accgctgtgt attactgcac aagacatggg aattttggaa actcatatgt ctcttggttc	840
gcttattggg gacagggcac gttggttacc gtgtctagcg gaggtggtgg atcccaggtg	900
cagctgaaac agagcggccc gggcctggtg cagccgagcc agagcctgag cattacctgc	960

accgtgagcg gctttagcct gaccaactat ggcgtgcatt gggtagcgcca gagcccgggc	1020
aaaggcctgg aatggctggg cgtgatttgg agcggcggca acaccgatta taacacccccg	1080
tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtgtt ttttaaatg	1140
aacagcctgc aaagccagga taccgcgatt tattattgcg cgcgcgcgct gacctattat	1200
gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc	1260
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	1320
ggcctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	1380
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1440
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1500
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	1560
gacaaaactc acacatgccc accgtgcccga gcacctgaat ttgaaggggg accgtcagtc	1620
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	1680
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	1740
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtagca gagcacgtac	1800
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1860
tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa	1920
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag	1980
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag	2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	2220
ctctccctgt ctccgggtaa atga	2244

<210> 124
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 124

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

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

Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp
115 120 125

Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 125
<211> 2133
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 125
tccgatgatc atggcggcgg ttctcaaact gtagtaactc aagaaccaag cttctccgtc 60
tcccctgggg gaacagtcac acttacctgc cgaagtagta caggtgctgt tacgaccagt 120
aactatgcca attgggtaca acaaacgcct ggtcaggctc cgcgcggatt gataggaggc 180
acgaataaac gggcacccgg tgtcccggac agattcagcg gaagcatact cggtataaag 240
gcagctctta ctatcactgg ggcccaagct gatgatgaaa gtgattatta ttgtgcgctc 300
tggtacagca acctctgggt gtttgggggt ggcacgaaac ttactgtctt gggcggcggc 360
ggatcagggg gaggtggctc tggaggagga ggctcagaag tccaactggg cgaatccggg 420
ggagggtctg tacagccggg tgggtccctc aaactctctt gtgcggcctc agggtttacc 480
ttcagtacat acgcgatgaa ttgggtccgg caggccagtg ggaaagggct cgaatgggta 540

ggacgaatcc gatcaaaata caacaactac gctacttatt acgctgattc cgtgaaggac	600
agattcacaa tatcccgcgga cgatagcaag aatacggcat atcttcagat gaattctctt	660
aaaactgagg ataccgctgt gtattactgc acaagacatg gtaattttgg aaactcatat	720
gtctcttggt tcgcttattg gggacagggc acgttggtta ccgtgtctag cggaggtggt	780
ggatcccagg tgcagctgaa acagagcggc ccgggcctgg tgcagccgag ccagagcctg	840
agcattacct gcaccgtgag cggcttttagc ctgaccaact atggcgtgca ttgggtgcgc	900
cagagcccgg gcaaaggcct ggaatggctg ggcgtgattt ggagcggcgg caacaccgat	960
tataacaccc cgtttaccag ccgcctgagc attaacaaag ataacagcaa aagccaggtg	1020
ttttttaaaa tgaacagcct gcaaagccag gataccgcca ttattattg cgcgcgcgcg	1080
ctgacctatt atgattatga atttgcgtat tggggccagg gcaccctggt gaccgtgagc	1140
gcggttagca ccaagggccc atcggctctt cccctggcac cctcctcaa gagcacctct	1200
gggggcacag cggccctggg ctgcctggtc aaggactact tcccgaacc ggtgacggtg	1260
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	1320
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	1380
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	1440
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga atttgaaggg	1500
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	1560
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	1620
tggtagtggt acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	1680
cagagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	1740
aaggagtaca agtgcaaggc ctccaacaaa gccctcccag cctcaatcga gaaaaccatc	1800
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc atcccgggag	1860
gagatgacca agaaccaggc cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1920
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1980
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	2040
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	2100
acgcagaaga gcctctccct gtctccgggt aaa	2133

<210> 126
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 126

Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro
1 5 10 15

Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser
20 25 30

Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln
35 40 45

Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg
50 55 60

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

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

Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly Gly Gly Thr
100 105 110

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

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

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

Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly
165 170 175

Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp
195 200 205

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

Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr
225 230 235 240

Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly
260 265 270

Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
275 280 285

Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
290 295 300

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
305 310 315 320

Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser
325 330 335

Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr
340 345 350

Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
370 375 380

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
385 390 395 400

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
405 410 415

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
420 425 430

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
435 440 445

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
450 455 460

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
465 470 475 480

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
485 490 495

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
500 505 510

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
515 520 525

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
530 535 540

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
545 550 555 560

Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
565 570 575

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
580 585 590

Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
595 600 605

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
610 615 620

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
625 630 635 640

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
645 650 655

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
675 680 685

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
690 695 700

Leu Ser Leu Ser Pro Gly Lys
705 710

<210> 127
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 127
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agcgtgagcc cgggcgaacg tgtgagcttt agctgccgcg cgagccagag cattggcacc 120
aacattcatt ggtatcagca gcgcaccaac ggcagcccgc gcctgctgat taaatatgcg 180
agcgaaagca ttagcggcat tccgagccgc tttagcggca gcggcagcgg caccgatttt 240
accctgagca ttaacagcgt ggaaagcgaa gatattgcgg attattattg ccagcagaac 300
aacaactggc cgaccacctt tggcgcgggc accaaactgg aactgaaacg tacggtggct 360
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 420
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 480

aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 540
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 600
tacgcctgcg aagtcacca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 660
ggagagtgt 669

<210> 128
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 128

Ser Asp Asp His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
1 5 10 15

Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
20 25 30

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
35 40 45

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

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

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
85 90 95

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
100 105 110

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

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

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

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

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

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

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

<210> 129
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 129
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acaggctcga gcgggtggcag cgggtggctct ggtgggtctga gcggccgttc cgatgatcat 120
ggcggcggtt ctcaaactgt agtaactcaa gaaccaagct tctccgtctc ccctggggga 180
acagtcacac ttacctgccg aagtagtaca ggtgctgtta cgaccagtaa ctatgccaat 240
tgggtacaac aaacgcctgg tcaggctccg cgcggattga taggaggcac gaataaacgg 300
gcacccggtg tcccggacag attcagcggg agcatactcg gtaataaggc agctcttact 360
atcactgggg cccaagctga tgatgaaagt gattattatt gtgcgctctg gtacagcaac 420
ctctgggtgt ttgggggtgg cacgaaactt actgtcttgg gcggcggcgg atcaggggga 480
ggtggctctg gaggaggagg ctcagaagtc caactggtcg aatccggggg agggctcgtg 540
cagccgggtg ggtccctcaa actctcttgt gcggcctcag ggtttacctt cagtacatac 600
gcgatgaatt ggggtccggc ggccagtggg aaagggtcg aatgggtagg acgaatccga 660
tcaaaataca acaactacgc tacttattac gctgattccg tgaaggacag attcacaata 720

tcccgcgacg atagcaagaa tacggcatat cttcagatga attctcttaa aactgaggat	780
accgctgtgt attactgcac aagacatggg aattttggaa actcatatgt ctcttggttc	840
gcttattggg gacagggcac gttggttacc gtgtctagcg gaggtggtgg atcccagggtg	900
cagctgaaac agagcggccc gggcctggtg cagccgagcc agagcctgag cattacctgc	960
accgtgagcg gctttagcct gaccaactat ggcgtgcatt ggggtgcgcca gagccccggc	1020
aaaggcctgg aatggctggg cgtgatttgg agcggcggca acaccgatta taacacccccg	1080
tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtgtt ttttaaatg	1140
aacagcctgc aaagccagga taccgcgatt tattattgcg cgcgcgcgct gacctattat	1200
gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc	1260
aagggcccat cggctctccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	1320
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	1380
ggcgcccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1440
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	1500
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	1560
gacaaaactc acacatgccc accgtgcccga gcacctgaat ttgaaggggg accgtcagtc	1620
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	1680
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	1740
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtagca gagcacgtac	1800
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1860
tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa	1920
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag	1980
aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	2220
ctctccctgt ctccgggtaa a	2241

<210> 130
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 130

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

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

Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp
115 120 125

Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 131
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 131
caaggccagt ctggccaagg tcttagttgt gaaggttggg cgatgaatag agaacaatgt 60
cgagccggag gtggctcgag cggcggctct atctcttccg gactgctgtc cggcagatcc 120
gaccagcacg gcggaggatc ccaaactctg ctgacacagt ctcctgtcat actgagtgtc 180
tccccggcg agagagtctc tttctcatgt cgggccagtc agtctattgg gactaacata 240
cactggtacc agcaacgcac caacggaagc ccgcgcctgc tgattaaata tgcgagcgaa 300

agcattagcg gcattccgag ccgctttagc ggcagcggca gcggcaccga ttttacctg	360
agcattaaca gcgtggaaag cgaagatatt gcggattatt attgccagca gaacaacaac	420
tggccgacca ctttggcgc gggcaccaaa ctggaactga aacgtacggt ggctgcacca	480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg	540
tgcttgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc	600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac	660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc	720
tgcgaaagtca cccatcaggg cctgagctcg cccgtcacia agagcttcaa caggggagag	780
tgt	783

<210> 132
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 132

Gln	Gly	Gln	Ser	Gly	Gln	Gly	Leu	Ser	Cys	Glu	Gly	Trp	Ala	Met	Asn
1				5					10					15	

Arg	Glu	Gln	Cys	Arg	Ala	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ile	Ser
			20					25					30		

Ser	Gly	Leu	Leu	Ser	Gly	Arg	Ser	Asp	Gln	His	Gly	Gly	Gly	Ser	Gln
		35					40					45			

Ile	Leu	Leu	Thr	Gln	Ser	Pro	Val	Ile	Leu	Ser	Val	Ser	Pro	Gly	Glu
	50					55					60				

Arg	Val	Ser	Phe	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	Ile
65					70					75					80

His	Trp	Tyr	Gln	Gln	Arg	Thr	Asn	Gly	Ser	Pro	Arg	Leu	Leu	Ile	Lys
			85						90					95	

Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu
115 120 125

Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr
130 135 140

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

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
180 185 190

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
195 200 205

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
225 230 235 240

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
245 250 255

Asn Arg Gly Glu Cys
260

<210> 133
<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 133
caaggccagt ctggatccgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact

acaggctcga gcggtggcag cggtggctct ggtggtatat cgagtggatt gctgtctggc	120
agatctgacg atcacggcgg cggttctcaa actgtagtaa ctcaagaacc aagcttctcc	180
gtctcccctg ggggaacagt cacacttacc tgccgaagta gtacaggtgc tgttacgacc	240
agtaactatg ccaattgggt acaacaaacg cctggtcagg ctccgcgcgg attgatagga	300
ggcacgaata aacgggcacc cggtgtcccg gacagattca gcggaagcat actcggtaat	360
aaggcagctc ttactatcac tggggcccaa gctgatgatg aaagtgatta ttattgtgcg	420
ctctggtaca gcaacctctg ggtgtttggg ggtggcacga aacttactgt cttgggcggc	480
ggcggatcag ggggaggtgg ctctggagga ggaggctcag aagtccaact ggtcgaatcc	540
gggggagggc tcgtacagcc ggggtgggtcc ctcaaactct cttgtgcggc ctcagggttt	600
accttcagta catacgcat gaattgggtc cggcaggcca gtgggaaagg gctcgaatgg	660
gtaggacgaa tccgatcaaa atacaacaac tacgctactt attacgctga ttccgtgaag	720
gacagattca caatatcccg cgacgatagc aagaatacgg catatcttca gatgaattct	780
cttaaaactg aggataccgc tgtgtattac tgcacaagac atggtaattt tggaaactca	840
tatgtctctt gggtcgctta ttggggacag ggcacgttgg ttaccgtgtc tagcggaggt	900
ggtggatccc aggtgcagct gaaacagagc ggcccgggcc tgggtgcagcc gagccagagc	960
ctgagcatta cctgcaccgt gagcggcttt agcctgacca actatggcgt gcattgggtg	1020
cgccagagcc cgggcaaagg cctggaatgg ctgggcgtga tttggagcgg cggcaacacc	1080
gattataaca ccccgtttac cagccgcctg agcattaaca aagataacag caaaagccag	1140
gtgtttttta aaatgaacag cctgcaaagc caggataccg cgatttatta ttgcgcgcgc	1200
gcgctgacct attatgatta tgaatttgcg tattggggcc agggcaccct ggtgaccgtg	1260
agcgcggcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc	1320
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1380
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag	1440
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	1500
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	1560
gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaatttgaa	1620
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccg	1680

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1740
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1800
 taccagagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1860
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcctcaat cgagaaaacc 1920
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1980
 gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 2040
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 2100
 cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc 2160
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 2220
 tacacgcaga agagcctctc cctgtctccg ggtaaa 2256

<210> 134
 <211> 752
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 134

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
 1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly
 35 40 45

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly
 50 55 60

Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
 65 70 75 80

Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg
 85 90 95

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg
100 105 110

Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly
115 120 125

Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
130 135 140

Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
165 170 175

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
180 185 190

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn
195 200 205

Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile
210 215 220

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
225 230 235 240

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
245 250 255

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

Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
275 280 285

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln
290 295 300

Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
305 310 315 320

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly
325 330 335

Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
340 345 350

Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
355 360 365

Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys
370 375 380

Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg
385 390 395 400

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr
405 410 415

Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
420 425 430

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
435 440 445

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
450 455 460

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
465 470 475 480

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
485 490 495

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
500 505 510

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
515 520 525

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
530 535 540

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
545 550 555 560

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
565 570 575

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
580 585 590

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val
595 600 605

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
610 615 620

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
625 630 635 640

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

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
660 665 670

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
675 680 685

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
690 695 700

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
705 710 715 720

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
725 730 735

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745 750

<210> 135
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 135
caaggccagt ctggccagt catctcacct cgtggttgtc cggacggccc atacgtcatg 60
tacggctcga gcggtggcag cggtggctct ggtggatccg gtctgagcgg ccgttccgat 120
gatcatggca gtagcggtag ccagatcttg ctgaccaga gcccggtgat tctgagcgtg 180
agcccgggag aacgtgtgag ctttagctgc cgcgcgagcc agagcattgg caccaacatt 240
cattggtatc agcagcgcac caacggcagc ccgcgcctgc tgattaaata tgcgagcgaa 300
agcattagcg gcattccgag ccgctttagc ggcagcggca gcggcaccga ttttaccctg 360
agcattaaca gcgtggaaag cgaagatatt gcggattatt attgccagca gaacaacaac 420
tggccgacca ctttggcgc gggcaccaaa ctggaactga aacgtacggt ggctgcacca 480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 540
tgctgtctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcaagtca cccatcaggg cctgagctcg cccgtcacia agagcttcaa caggggagag 780
tgt 783

<210> 136
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 136

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
1 5 10 15

Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Leu Ser Gly Arg Ser Asp Asp His Gly Ser Ser Gly Thr Gln
35 40 45

Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly Glu
50 55 60

Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile
65 70 75 80

His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys
85 90 95

Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu
115 120 125

Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr
130 135 140

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

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
180 185 190

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
195 200 205

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 225 230 235 240

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 245 250 255

Asn Arg Gly Glu Cys
 260

<210> 137
 <211> 2244
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 137
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 acaggctcga gcggtggcag cggtggctct ggtggtctga gcggccgttc cgatgatcat 120
 ggcggcgggtt ctcaaactgt agtaactcaa gaaccaagct tctccgtctc ccctggggga 180
 acagtcacac ttacctgccg aagtagtaca ggtgctgtta cgaccagtaa ctatgccaat 240
 tgggtacaac aaacgcctgg tcaggctccg cgcggattga taggaggcac gaataaacgg 300
 gcacccgggtg tcccggacag attcagcggg agcatactcg gtaataaggc agctcttact 360
 atcactggggg cccaagctga tgatgaaagt gattattatt gtgcgctctg gtacagcaac 420
 ctctgggtgt ttgggggtgg cacgaaactt actgtcttgg gcggcggcgg atcaggggga 480
 ggtggctctg gaggaggagg ctcagaagtc caactggtcg aatccggggg agggctcgtg 540
 cagccgggtg ggtccctcaa actctcttgt gcggcctcag ggtttacctt cagtacatac 600
 gcgatgaatt ggggccggca ggccagtggg aaagggtcg aatgggtagg acgaatccga 660
 tcaaaataca acaactacgc tacttattac gctgattccg tgaaggacag attcacaata 720
 tcccgcgacg atagcaagaa tacggcatat cttcagatga attctcttaa aactgaggat 780
 accgctgtgt attactgcac aagacatggg aattttggaa actcatatgt ctcttggttc 840
 gcttattggg gacagggcac gttggttacc gtgtctagcg gaggtggtgg atcccaagtg 900
 accctgagag agtctggccc tgccctcgtg aagcctaccc agaccctgac actgacctgc 960
 accttcagcg gcttcagcct gagcaccagc ggcatgtctg tgggctggat cagacagcct 1020

cctggcaagg ccctggaatg gctggccgac atttggtggg acgacaagaa ggactacaac	1080
cccagcctga agtcccggct gaccatcagc aaggacacca gcaagaacca ggtggtgctg	1140
aaagtgacca acatggaccc cgccgacacc gccacctact actgcgccag atccatgac	1200
accaactggt acttcgacgt gtggggagcc ggcaccaccg tgacagtgtc atctgctagc	1260
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca	1320
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	1380
tcaggcggcc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	1440
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc	1500
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc	1560
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aatttgaagg gggaccgtca	1620
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	1680
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	1740
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta ccagagcacg	1800
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1860
aagtgcaagg tctccaacaa agccctcca gcctcaatcg agaaaaccat ctcaaagcc	1920
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1980
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	2040
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	2100
tccgacggct ctttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag	2160
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	2220
agcctctccc tgtctccggg taaa	2244

<210> 138
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 138

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

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

Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp
115 120 125

Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Arg Glu
290 295 300

Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys
305 310 315 320

Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
325 330 335

Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp
340 345 350

Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr
355 360 365

Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn
370 375 380

Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile
385 390 395 400

Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val
405 410 415

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
420 425 430

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
435 440 445

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
450 455 460

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
465 470 475 480

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
485 490 495

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
500 505 510

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
515 520 525

Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe
530 535 540

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
545 550 555 560

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
565 570 575

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
580 585 590

Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr
595 600 605

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
610 615 620

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
625 630 635 640

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
645 650 655

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
660 665 670

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
675 680 685

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

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
705 710 715 720

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
725 730 735

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 139
<211> 639
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 139
gacatccaga tgaccagag ccccagcaca ctgagcgcca gcgtgggcga cagagtgacc 60
atcacatgca agtgccagct gagcgtgggc tacatgcact ggtatcagca gaagcccggc 120
aaggcccca agctgctgat ctacgacacc agcaagctgg cctccggcgt gcccagcaga 180
ttttctggca gcggctccgg caccgagttc accctgacaa tcagcagcct gcagcccgac 240
gacttcgcca cctactactg ttttcaaggc tccggctacc ctttcacctt cggcggaggc 300
accaagctgg aaatcaagcg gacggtggct gcaccatctg tcttcatctt cccgccatct 360
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag 480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg 600

agctcgccccg tcacaaagag cttcaacagg ggagagtgt

639

<210> 140
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 140

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

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
20 25 30

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 141
<211> 2259
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 141
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acaggctcga gcggtggcag cgggtggctct ggtggtatat cgagtggatt gctgtctggc 120
agatctgacg atcacggcgg cggttctcaa actgtagtaa ctcaagaacc aagcttctcc 180
gtctcccctg ggggaacagt cacacttacc tgccgaagta gtacaggtgc tgttacgacc 240
agtaactatg ccaattgggt acaacaaacg cctggtcagg ctccgcgcgg attgatagga 300
ggcacgaata aacgggcacc cgggtgtccg gacagattca gcggaagcat actcggtaat 360
aaggcagctc ttactatcac tggggcccaa gctgatgatg aaagtgatta ttattgtgcg 420
ctctggtaca gcaacctctg ggtgtttggg ggtggcacga aacttactgt cttgggcggc 480
ggcggatcag ggggaggtgg ctctggagga ggaggctcag aagtccaact ggtcgaatcc 540
gggggagggc tcgtacagcc gggtgggtcc ctcaaactct cttgtgcggc ctcagggttt 600
accttcagta catacgcgat gaattgggtc cggcaggcca gtgggaaagg gctcgaatgg 660
gtaggacgaa tccgatcaaa atacaacaac tacgctactt attacgtga ttccgtgaag 720
gacagattca caatatcccg cgacgatagc aagaatacgg catatcttca gatgaattct 780
cttaaaaactg aggataccgc tgtgtattac tgcacaagac atggtaattt tggaaactca 840
tatgtctctt ggttcgctta ttggggacag ggcacgttgg ttaccgtgtc tagcggaggt 900

ggtggatccc aagtgaccct gagagagtct ggccctgccc tcgtgaagcc taccagacc	960
ctgacactga cctgcacctt cagcggcttc agcctgagca ccagcggcat gtctgtgggc	1020
tggatcagac agcctcctgg caaggccctg gaatggctgg ccgacatttg gtgggacgac	1080
aagaaggact acaaccccag cctgaagtcc cggctgacca tcagcaagga caccagcaag	1140
aaccagggtgg tgctgaaagt gaccaacatg gaccccgccg acaccgccac ctactactgc	1200
gccagatcca tgatcaccaa ctggtacttc gacgtgtggg gagccggcac caccgtgaca	1260
gtgtcatctg ctagcaccaa gggcccatcg gtcttcccc tggcacctc ctccaagagc	1320
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg	1380
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta	1440
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	1500
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa	1560
gttgagccca aatcttgtga caaaactcac acatgccac cgtgcccagc acctgaattt	1620
gaagggggac cgtcagtctt cctcttcccc caaaaccca aggacaccct catgatctcc	1680
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag	1740
ttcaactggg acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag	1800
cagtaccaga gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg	1860
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagctc aatcgagaaa	1920
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc	1980
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	2040
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	2100
cctcccgtgc tggactccga cggctccttc ttctctaca gcaagctcac cgtggacaag	2160
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	2220
cactacacgc agaagagcct ctccctgtct ccgggtaaa	2259

<210> 142
 <211> 753
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 142

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly
35 40 45

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly
50 55 60

Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
65 70 75 80

Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg
85 90 95

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg
100 105 110

Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly
115 120 125

Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
130 135 140

Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
165 170 175

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
180 185 190

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn
195 200 205

Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile
210 215 220

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
225 230 235 240

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
245 250 255

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

Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
275 280 285

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln
290 295 300

Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr
305 310 315 320

Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly
325 330 335

Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp
340 345 350

Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu
355 360 365

Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
370 375 380

Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys
385 390 395 400

Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
405 410 415

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
420 425 430

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
435 440 445

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
450 455 460

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
465 470 475 480

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
485 490 495

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
500 505 510

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
515 520 525

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro
530 535 540

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
545 550 555 560

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
565 570 575

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
580 585 590

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val
595 600 605

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
610 615 620

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys
625 630 635 640

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

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
660 665 670

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
675 680 685

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
705 710 715 720

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
725 730 735

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
740 745 750

Lys

<210> 143
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 143

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
165 170 175

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
180 185 190

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln
195 200 205

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
210 215 220

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
245

<210> 144
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 144

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
145 150 155 160

Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
165 170 175

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
180 185 190

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
195 200 205

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
210 215 220

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
245

<210> 145
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 145

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Ile Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
145 150 155 160

Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg
165 170 175

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
180 185 190

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln
195 200 205

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
210 215 220

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
245

<210> 146
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 146

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

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

Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp
115 120 125

Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 147
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 147
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gttggctcga gcggtggcag cgggtggctct ggtgggtctga gcggccgttc cgataatcat 120
ggcggcggtt ctgagaccgt ggtcacacag gagccctcac tgacagttag ccctggcggg 180
accgtcacac tgacttgtcg cagttcaact ggcgccgtga ctaccagcaa ttacgctaac 240
tgggtccagc agaaaccagg acaggcacca cgaggactga tcggagggaac taataagaga 300
gcaccaggaa cccctgcaag gttctccgga tctctgctgg ggggaaaagc cgctctgaca 360
ctgagcggcg tgcagcctga ggacgaagct gagtactatt gcgcactgtg gtactccaac 420
ctgtgggtgt ttggcggggg aactaagctg accgtcctgg gaggaggagg aagcggagga 480
ggaggggagcg gaggaggagg atccgaagtg cagctggctg agagcggagg aggactgggtg 540
cagccaggag gatccctgaa gctgtcttgt gcagccagtg gcttcacctt caacacttac 600
gcaatgaact ggggtgcggca ggcacctggg aagggactgg aatgggtcgc ccggatcaga 660
tctaaataca ataactatgc cacctactat gctgacagtg tgaaggatag gttcaccatt 720

tcacgcgacg atagcaaaaa cacagcttat ctgcagatga ataacctgaa gaccgaggat	780
acagcagtgt actattgcgt cagacacggc aatttcggga actcttacgt gagttggttt	840
gcctattggg gacaggggac actggtcacc gtctcctcag gaggtggtgg atcccaagtg	900
accctgagag agtctggccc tgcctcgtg aagcctacc agaccctgac actgacctgc	960
accttcagcg gcttcagcct gagcaccagc ggcatgtctg tgggctggat cagacagcct	1020
cctggcaagg ccctggaatg gctggccgac atttggtggg acgacaagaa ggactacaac	1080
cccagcctga agtcccggct gaccatcagc aaggacacca gcaagaacca ggtggtgctg	1140
aaagtgacca acatggaccc cgccgacacc gccacctact actgcgccag atccatgac	1200
accaactggt acttcgacgt gtggggagcc ggcaccaccg tgacagtgtc atctgctagc	1260
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca	1320
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	1380
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	1440
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc	1500
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc	1560
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	1620
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	1680
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	1740
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta ccagagcacg	1800
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1860
aagtgcaagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc	1920
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc	1980
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	2040
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	2100
tccgacggct ctttcttct ctacagcaag ctaccgtgg acaagagcag gtggcagcag	2160
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	2220
agcctctccc tgtctccggg taaa	2244

<210> 148
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 148

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Ala Val Val
35 40 45

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
100 105 110

Ile Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp
115 120 125

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
180 185 190

Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
195 200 205

Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn
210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu
245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe
260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln
290 295 300

Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys
305 310 315 320

Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg
325 330 335

Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly
340 345 350

Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn
355 360 365

Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln
370 375 380

Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr
385 390 395 400

Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
405 410 415

Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

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

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 149
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 149

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 150
<211> 249
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 150

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

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

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

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Ile Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Ala
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg
165 170 175

Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp
180 185 190

Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr Leu Gln
 195 200 205

Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg
 210 215 220

His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 151
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 151
 caaggccagt ctggttctgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact 60
 acaggctcga gcggtggcag cgggtggctct ggtggctcga gcggccgttc cgatgatcat 120
 ggcggcggat cccagacggt agtgactcag gagccatcat tttctgtctc tcctggaggt 180
 actgtgacac tcacatgtag aagctcaact ggtgcagtca ccacttcaaa ttacgcgaat 240
 tgggtccagc agaccctgg gcaggctccg agagggttga ttggaggtag taacaaacgg 300
 gcaccgggag tgcctgatag gttttccggt tctattctcg gaaacaaggc ggctctcacg 360
 atcacgggtg cgcaggccga cgatgaatca gactattact gcgctttgtg gtactcaaac 420
 ctgtgggtat tcggaggggg caccaagctg acggtgttgg gtgggggggg ctctggggga 480
 gggggaagcg gaggtggggg cagcgagggt cagcttggtg aaagtgggtg cggactcgta 540
 caaccgggtg gaagtcttag actctcatgt gcagcatctg gatttacttt ttctacttat 600
 gctatgaact gggtgaagaca ggcaccgggg aaagggtg aatgggttgc acgcattcga 660
 tctaaatata ataactatgc tacatactac gccgatagtg ttaaggatcg attcactata 720
 tctcgggacg acagtaagaa ctcactttac ctgcagatga attccttgaa aactgaggac 780
 acggccgttt attattgtgt acggcacggg aatttcggca attcttacgt ttcctggttc 840
 gcctattggg ggcaaggtag gctggtcacg gtgtctagcg gaggtgggtg atcccagggtg 900

cagctgaaac agagcggccc gggcctggtg cagccgagcc agagcctgag cattacctgc	960
accgtgagcg gcttttagcct gaccaactat ggcgtgcatt ggggtgcgcca gagcccgggc	1020
aaaggcctgg aatggctggg cgtgatttgg agcggcggca acaccgatta taacaccccg	1080
tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccaggtggt ttttaaatg	1140
aacagcctgc aaagccagga taccgcgatt tattattgcg cgcgcgcgct gacctattat	1200
gattatgaat ttgcgtattg gggccagggc accctggtga ccgtgagcgc ggctagcacc	1260
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	1320
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	1380
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1440
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1500
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	1560
gacaaaactc acacatgccc accgtgcccga gcacctgaat ttgaaggggg accgtcagtc	1620
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	1680
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	1740
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtagca gagcacgtac	1800
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1860
tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa	1920
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag	1980
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag	2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	2220
ctctccctgt ctccgggtaa a	2241

<210> 152
 <211> 2241
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 152

caaggccagt ctggatccgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact	60
acaggctcga gcggtggcag cgggtggctct ggtggtctga gcggccgttc cgatgatcat	120
ggcggcggtt ctcaggccgt tgttacacaa gagccttcac ttactgtgtc tccaggaggc	180
actgtgacac ttacgtgccg atcctctacg ggtgccgtga ccacaagcaa ctatgccaac	240
tgggtccagc agaagccagg tcaagcgcct cgaggtctga tcgggggcac gaataaacga	300
gctcctggaa ctccggccag attttctggg agtcttattg gtggcaaggc ggcgttgacc	360
ctgagtggag cccaaccgga agacgaggcc gagtactact gcgccttggt gtattccaat	420
ttgtgggtct tcggaggcgg aacaaagctc acagtactgg gaggtggagg tagcgggggc	480
ggaggctccg ggggagggtg ttccgaagtc cagcttggtg aatcagggtg gggcttggtg	540
caaccagggtg gttcactgaa gttgtcctgt gcagcgtccg gatttacatt tagtacgtat	600
gctatgaact gggtcaggca ggccagtggg aaaggtctcg aatgggttggt ccggataagg	660
tcaaagtaca ataattacgc aacctactac gcggattccg tgaaagacag gttcactatt	720
tcacgagatg atagcaaaaa tactgcgtat ctccaaatga atagtcttaa aactgaagac	780
actgccgtat attattgcac taggcacggc aactttggta actcttatgt ttcttggttc	840
gcatactggg gacaaggaac tttggtcact gtctcatctg gaggtgggtg atcccagggtg	900
cagctgaaac agagcggccc gggcctgggtg cagccgagcc agagcctgag cattacctgc	960
accgtgagcg gctttagcct gaccaactat ggcgtgcatt ggggtgcgcca gagcccgggc	1020
aaaggcctgg aatggctggg cgtgatttggt agcggcggca acaccgatta taacaccccg	1080
tttaccagcc gcctgagcat taacaaagat aacagcaaaa gccagggtgtt ttttaaatg	1140
aacagcctgc aaagccagga taccgcgatt tattattgctg cgcgcgcgct gacctattat	1200
gattatgaat ttgcgtattg gggccagggc accctgggtga ccgtgagcgc ggctagcacc	1260
aaggggcccat cggctttccc cctggcacc cctccaaga gcacctctgg gggcacagcg	1320
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	1380
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1440
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1500
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	1560

gacaaaactc acacatgccc accgtgccc gcacctgaat ttgaaggggg accgtcagtc 1620
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 1680
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1740
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacca gagcacgtac 1800
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1860
tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa 1920
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1980
aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 2040
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 2100
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 2160
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 2220
ctctccctgt ctccgggtaa a 2241

<210> 153
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 153

Met Met Tyr Cys Gly Gly Asn Glu Val Leu Cys Gly Pro Arg Val Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
35 40 45

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
100 105 110

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
195 200 205

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
245 250 255

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val
290 295 300

Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
305 310 315 320

Leu Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly
325 330 335

Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
340 345 350

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
355 360 365

Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr
370 375 380

Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp
385 390 395 400

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
405 410 415

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
420 425 430

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
435 440 445

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
450 455 460

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
465 470 475 480

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
485 490 495

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
500 505 510

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
515 520 525

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
530 535 540

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
545 550 555 560

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
565 570 575

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln
580 585 590

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
595 600 605

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
610 615 620

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
625 630 635 640

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
645 650 655

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
660 665 670

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
675 680 685

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
690 695 700

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
705 710 715 720

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
725 730 735

Ser Leu Ser Pro Gly Lys
740

<210> 154
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (180)..(180)
<223> Xaa may be any amino acid

<400> 154

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 Xaa 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 Glu Glu
225 230 235 240

Met 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> 155
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 155

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 Gln 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 Glu Glu
225 230 235 240

Met 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> 156
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (117)..(117)
<223> Xaa can be any amino acid

<400> 156

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 Xaa 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 Glu Glu
225 230 235 240

Met 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> 157
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<400> 157

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

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

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

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

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

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

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

Lys

<210> 158
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa may be Ser or Ala

<220>
<221> MISC_FEATURE
<222> (237)..(237)
<223> Xaa may be any amino acid

<400> 158

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

340

345

350

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

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

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

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

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

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

Lys

<210> 159

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 159

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 Glu 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 Glu Glu
 225 230 235 240

Met 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> 160
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<220>
<221> MISC_FEATURE
<222> (214)..(214)
<223> Xaa can be any amino acid

<400> 160

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 Xaa 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 Glu Glu
 225 230 235 240

Met 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> 161
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 161

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 Ser 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 Glu Glu
225 230 235 240

Met 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> 162
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 162

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 Phe Glu 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 Ser 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 Glu Glu
 225 230 235 240

Met 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> 163
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 163

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 Phe Glu 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 Gln 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 Ser 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 Glu Glu
 225 230 235 240

Met 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> 164
<211> 2133
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 164
tccgataatc atggcggcgg ttctcaaact gtagtaactc aagaaccaag cttctccgtc 60
tcccctgggg gaacagtcac acttacctgc cgaagtagta caggtgctgt tacgaccagt 120
aactatgcca attgggtaca acaaacgcct ggtcaggctc cgcgcggatt gataggaggc 180
acgaataaac gggcacccgg tgtcccggaac agattcagcg gaagcatact cggtataaag 240
gcagctctta ctatcactgg ggcccaagct gatgatgaaa gtgattatta ttgtgcgctc 300
tggtacagca acctctgggt gtttgggggt ggcacgaaac ttactgtctt gggcggcggc 360
ggatcagggg gaggtggctc tggaggagga ggctcagaag tccaactggg cgaatccggg 420
ggagggctcg tacagccggg tgggtccctc aaactctctt gtgcggcctc agggtttacc 480
ttcagtacat acgcgatgaa ttgggtccgg caggccagtg ggaaagggct cgaatgggta 540
ggacgaatcc gatcaaaata caacaactac gctacttatt acgctgattc cgtgaaggac 600
agattcacia tatcccgca cgatagcaag aatacggcat atcttcagat gaattctctt 660
aaaactgagg ataccgctgt gtattactgc acaagacatg gtaattttgg aaactcatat 720

gtctcttggt tcgcttattg gggacagggc acgttggtta ccgtgtctag cggaggtggt	780
ggatcccagg tgcagctgaa acagagcggc ccgggcctgg tgcagccgag ccagagcctg	840
agcattacct gcaccgtgag cggcttttagc ctgaccaact atggcgtgca ttgggtgcgc	900
cagagcccgg gcaaaggcct ggaatggctg ggcgtgattt ggagcggcgg caacaccgat	960
tataacaccc cgtttaccag ccgcctgagc attaacaaag ataacagcaa aagccagggtg	1020
ttttttaaaa tgaacagcct gcaaagccag gataccgcga tttattattg cgcgcgcgcg	1080
ctgacctatt atgattatga atttgcgtat tggggccagg gcaccctggt gaccgtgagc	1140
gcggctagca ccaagggccc atcggctctt cccctggcac cctcctcaa gagcacctct	1200
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg	1260
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc	1320
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	1380
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	1440
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga atttgaaggg	1500
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	1560
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tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	1680
cagagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	1740
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cctcaatcga gaaaaccatc	1800
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggag	1860
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac	1920
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1980
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	2040
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	2100
acgcagaaga gcctctccct gtctccgggt aaa	2133

<210> 165
 <211> 711
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 165

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

Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser
20 25 30

Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln
35 40 45

Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg
50 55 60

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

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

Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly Gly Gly Thr
100 105 110

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

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

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

Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly
165 170 175

Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
180 185 190

Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp

195

200

205

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

Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr
 225 230 235 240

Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 245 250 255

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly
 260 265 270

Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
 275 280 285

Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
 290 295 300

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
 305 310 315 320

Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser
 325 330 335

Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr
 340 345 350

Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
 355 360 365

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
 370 375 380

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 385 390 395 400

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 405 410 415

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
420 425 430

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
435 440 445

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
450 455 460

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
465 470 475 480

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
485 490 495

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
500 505 510

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
515 520 525

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
530 535 540

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
545 550 555 560

Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
565 570 575

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
580 585 590

Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
595 600 605

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
610 615 620

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

625 630 635 640

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 645 650 655

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

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 675 680 685

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 690 695 700

Leu Ser Leu Ser Pro Gly Lys
705 710

<210> 166
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 166
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agcgtgagcc cgggcgaacg tgtgagcttt agctgccgcg cgagccagag cattggcacc 120
aacattcatt ggtatcagca gcgcaccaac ggcagcccg cgcctgctgat taaatatgcg 180
agcgaaagca ttagcggcat tccgagccgc tttagcggca gcggcagcgg caccgatttt 240
accctgagca ttaacagcgt ggaaagcgaa gatattgcgg attattattg ccagcagaac 300
aacaactggc cgaccacctt tggcgcgggc accaaactgg aactgaaacg tacggtggct 360
gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 420
gttgtgtgcc tgctgaataa cttctatccc agagaggcca aagtacagtg gaaggtggat 480
aacgccctcc aatcgggtaa ctcccaggag agtgtcacag agcaggacag caaggacagc 540
acctacagcc tcagcagcac cctgacgctg agcaaagcag actacgagaa acacaaagtc 600
tacgcctgcg aagtcacca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 660

<210> 167
 <211> 223
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 167

Ser Asp Asn His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
 1 5 10 15

Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
 20 25 30

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
 35 40 45

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

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

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
 85 90 95

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
 100 105 110

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

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

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp

165

170

175

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

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

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

<210> 168

<211> 2256

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 168

caaggccagt ctggatccgg ttatctgtgg ggttgcgagt ggaattgcgg agggatcact	60
acaggctcga gcggtggcag cgggtggctct ggtggtatat cgagtggatt gctgtctggc	120
agatctgacc aacacggcgg cggttctcaa actgtagtaa ctcaagaacc aagcttctcc	180
gtctcccctg ggggaacagt cacacttacc tgccgaagta gtacaggtgc tgttacgacc	240
agtaactatg ccaattgggt acaacaaacg cctggtcagg ctccgcgcgg attgatagga	300
ggcacgaata aacgggcacc cgggtgtcccg gacagattca gcggaagcat actcggtaat	360
aaggcagctc ttactatcac tggggcccaa gctgatgatg aaagtgatta ttattgtgcg	420
ctctggtaca gcaacctctg ggtgttttggg ggtggcacga aacttactgt cttgggcggc	480
ggcggatcag ggggaggtgg ctctggagga ggaggctcag aagtccaact ggtcgaatcc	540
gggggagggc tcgtacagcc gggtgggtcc ctcaaactct cttgtgcggc ctcagggttt	600
accttcagta catacgcgat gaattgggtc cggcaggcca gtgggaaagg gctcgaatgg	660
gtaggacgaa tccgatcaaa atacaacaac tacgctactt attacgtga ttccgtgaag	720
gacagattca caatatcccg cgacgatagc aagaatacgg catatcttca gatgaattct	780
cttaaaaactg aggataccgc tgtgtattac tgcacaagac atggtaattt tggaaactca	840
tatgtctctt ggttcgctta ttggggacag ggcacgttgg ttaccgtgtc tagcggaggt	900

ggtggatccc aggtgcagct gaaacagagc ggcccgggcc tggtgcagcc gagccagagc	960
ctgagcatta cctgcaccgt gagcggcctt agcctgacca actatggcgt gcattgggtg	1020
cgccagagcc cgggcaaagg cctggaatgg ctgggcgtga tttggagcgg cggcaacacc	1080
gattataaca ccccgtttac cagccgcctg agcattaaca aagataacag caaaagccag	1140
gtgtttttta aaatgaacag cctgcaaagc caggataaccg cgatttatta ttgcgcgcgc	1200
gcgctgacct attatgatta tgaatttgcg tattggggcc agggcacct ggtgaccgtg	1260
agcgcggcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc	1320
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1380
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag	1440
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	1500
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	1560
gagcccaaat cttgtgaaa aactcacaca tgcccaccgt gcccagcacc tgaatttgaa	1620
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1680
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1740
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	1800
taccagagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat	1860
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcctcaat cgagaaaacc	1920
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1980
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	2040
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	2100
cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc	2160
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	2220
tacacgcaga agagcctctc cctgtctccg ggtaaa	2256

<210> 169
 <211> 752
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 169

Gln Gly Gln Ser Gly Ser Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys
1 5 10 15

Gly Gly Ile Thr Thr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln His Gly Gly Gly
35 40 45

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly
50 55 60

Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
65 70 75 80

Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg
85 90 95

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg
100 105 110

Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly
115 120 125

Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser
130 135 140

Asn Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
165 170 175

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys
180 185 190

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn
195 200 205

Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val Gly Arg Ile
210 215 220

Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys
225 230 235 240

Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu
245 250 255

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

Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp
275 280 285

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln
290 295 300

Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
305 310 315 320

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly
325 330 335

Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
340 345 350

Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
355 360 365

Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys
370 375 380

Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg
385 390 395 400

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr
405 410 415

Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro

420

425

430

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 435 440 445

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 450 455 460

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 465 470 475 480

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 485 490 495

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 500 505 510

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 515 520 525

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser
 530 535 540

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 545 550 555 560

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 565 570 575

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 580 585 590

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val
 595 600 605

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 610 615 620

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr
 625 630 635 640

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

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
660 665 670

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
675 680 685

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
690 695 700

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
705 710 715 720

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
725 730 735

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745 750

<210> 170
<211> 798
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 170
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tctggcagat ctgaccaaca cggcagtagc ggtaccaga tcttgctgac ccagagcccg 180
gtgattctga gcgtgagccc gggcgaacgt gtgagcttta gctgccgcgc gagccagagc 240
attggcacca acattcattg gtatcagcag cgcaccaacg gcagcccgcg cctgctgatt 300
aaatatgcga gcgaaagcat tagcggcatt ccgagccgct ttagcggcag cggcagcggc 360
accgatttta ccctgagcat taacagcgtg gaaagcgaag atattgcgga ttattattgc 420
cagcagaaca acaactggcc gaccaccttt ggcgcgggca ccaaactgga actgaaacgt 480

acggtggctg caccatctgt cttcatcttc ccgcatctg atgagcagtt gaaatctgga 540
 actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 600
 aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 660
 aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 720
 cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 780
 ttcaacaggg gagagtgt 798

<210> 171
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 171

Gln Gly Gln Ser Gly Gln Cys Ile Ser Pro Arg Gly Cys Pro Asp Gly
 1 5 10 15

Pro Tyr Val Met Tyr Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
 20 25 30

Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln His Gly
 35 40 45

Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser
 50 55 60

Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser
 65 70 75 80

Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro
 85 90 95

Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser
 100 105 110

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
 115 120 125

Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn
130 135 140

Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
145 150 155 160

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
165 170 175

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
180 185 190

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
195 200 205

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
210 215 220

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
225 230 235 240

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
245 250 255

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
260 265

<210> 172
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 172
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ggcggcggtt ctcagaccgt ggtcacacag gagccctcac tgacagtgag ccctggcggg 180
accgtcacac tgacttgtcg cagttcaact ggcgccgtga ctaccagcaa ttacgctaac 240

tggtccagc agaaaccagg acaggcacca cgaggactga tcggaggaac taataagaga	300
gcaccaggaa cccctgcaag gttctccgga tctctgctgg ggggaaaagc cgctctgaca	360
ctgagcggcg tgcagcctga ggacgaagct gagtactatt gcgcactgtg gtactccaac	420
ctgtgggtgt ttggcggggg aactaagctg accgtcctgg gaggaggagg aagcggagga	480
ggagggagcg gaggaggagg atccgaagtg cagctggtcg agagcggagg aggactggtg	540
cagccaggag gatccctgaa gctgtcttgt gcagccagtg gcttcacctt caacacttac	600
gcaatgaact gggcgcggca ggcacctggg aagggactgg aatgggtcgc ccgcatcaga	660
tctaaataca ataactatgc cacctactat gctgacagtg tgaaggatag gttcaccatt	720
tcacgcgacg atagcaaaaa cacagcttat ctgcagatga ataacctgaa gaccgaggat	780
acagcagtgt actattgcgt cagacacggc aatttcggga actcttacgt gagttggttt	840
gcctattggg gacaggggac actggtcacc gtctcctcag gaggtggtgg atcccaagtg	900
accctgagag agtctggccc tgcctcctg agacacctgac actgacctgc	960
accttcagcg gcttcagcct gagcaccagc ggcatgtctg tgggctggat cagacagcct	1020
cctggcaagg ccctggaatg gctggccgac atttggtggg acgacaagaa ggactacaac	1080
cccagcctga agtcccggct gaccatcagc aaggacacca gcaagaacca ggtggtgctg	1140
aaagtgacca acatggaccc cgccgacacc gccacctact actgcgccag atccatgac	1200
accaactggt acttcgacgt gtggggagcc ggcaccaccg tgacagtgtc atctgctagc	1260
accaagggcc catcggctct cccctggca ccctcctcca agagcacctc tgggggcaca	1320
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	1380
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	1440
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	1500
tgcaacgtga atcacaagcc cagcaacacc aagggtgaca agaaagtga gcccaaattc	1560
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	1620
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	1680
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	1740
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta ccagagcacg	1800
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	1860

aagtgaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1920
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 1980
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 2040
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tccgacggct ctttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 2160
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 2220
agcctctccc tgtctccggg taaa 2244

<210> 173
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 173

Gln Gly Gln Ser Gly Gln Met Met Tyr Cys Gly Gly Asn Glu Val Leu
1 5 10 15

Cys Gly Pro Arg Val Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val
35 40 45

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
50 55 60

Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
65 70 75 80

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
85 90 95

Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
100 105 110

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp

115

120

125

Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe
 130 135 140

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Gly
 145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 165 170 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
 180 185 190

Ser Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala
 195 200 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
 210 215 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
 225 230 235 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
 245 250 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
 260 265 270

Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu
 275 280 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Arg Glu
 290 295 300

Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys
 305 310 315 320

Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
 325 330 335

Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp
340 345 350

Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr
355 360 365

Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn
370 375 380

Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile
385 390 395 400

Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val
405 410 415

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
420 425 430

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
435 440 445

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
450 455 460

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
465 470 475 480

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
485 490 495

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
500 505 510

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
515 520 525

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
530 535 540

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val

545		550		555		560									
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
				565					570					575	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
			580					585					590		
Arg	Glu	Glu	Gln	Tyr	Gln	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
		595					600					605			
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
	610						615				620				
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
625					630					635					640
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg
				645					650					655	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
			660					665					670		
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		675					680					685			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
	690					695					700				
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln
705					710					715					720
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
				725					730					735	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
			740					745							

<210> 174
 <211> 639
 <212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 174

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aaggcccca agctgctgat ctacgacacc agcaagctgg cctccggcgt gcccagcaga      180
ttttctggca gcggctccgg caccgagttc accctgacaa tcagcagcct gcagcccgac      240
gacttcgcca cctactactg ttttcaaggc tccggctacc cttcacctt cggcggaggc      300
accaagctgg aaatcaagcg gacggtggct gcaccatctg tcttcatctt cccgccatct      360
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc      420
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag      480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg      540
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg      600
agctcgcccc tcacaaagag cttcaacagg ggagagtgt      639
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<210> 175

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 175

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

```
Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
20           25           30
```

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 176
caaggccagt ctggccaa

<210> 177

<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 177
atgatgtatt gcggtgggaa tgaggtgttg tgcgggccgc gggttggctc gagcgggtggc 60
agcgggtggct ctggtggtct gagcggccgt tccgataatc atggcggcgg ttctcagacc 120
gtggtcacac aggagccctc actgacagtg agccctggcg ggaccgtcac actgacttgt 180
cgcagttcaa ctggcgccgt gactaccagc aattacgcta actgggtcca gcagaaacca 240
ggacaggcac cagcaggact gatcggagga actaataaga gagcaccagg aacccttgca 300
aggttctccg gatctctgct ggggggaaaa gccgctctga cactgagcgg cgtgcagcct 360
gaggacgaag ctgagtacta ttgcgcactg tggtactcca acctgtgggt gtttggcggg 420
ggaactaagc tgaccgtcct gggaggagga ggaagcggag gaggaggag cggaggagga 480
ggatccgaag tgcagctggc cgagagcggg ggaggactgg tgcagccagg aggatccctg 540
aagctgtctt gtgcagccag tggcttcacc ttcaacactt acgcaatgaa ctgggtgcgg 600
caggcacctg ggaagggact ggaatgggtc gcccgatca gatctaaata caataactat 660
gccacctact atgctgacag tgtgaaggat aggttcacca tttcacgcga cgatagcaaa 720
aacacagctt atctgcagat gaataacctg aagaccgagg atacagcagt gtactattgc 780
gtcagacacg gcaatttcgg gaactcttac gtgagttggc ttgcctattg gggacagggg 840
aactgggtca ccgtctcctc aggaggtggc ggatcccagg tgcagctgaa acagagcggc 900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc 960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg 1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc 1080
attaacaaag ataacagcaa aagccaggtg ttttttaaaa tgaacagcct gcaaagccag 1140
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tggggccagg gcaccctggc gaccgtgagc gcggctagca ccaagggcc atcggctctc 1260
cccctggcac cctcctcaa gagcacctct gggggcacag cggccctggg ctgcctggctc 1320
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgcctt gaccagcggc 1380

gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500
agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt cccccaaaa	1620
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg	1680
agccacgaag accctgaggt caagttcaac tggtagctgg acggcgtgga ggtgcataat	1740
gccaagacaa agccgcggga ggagcagtac cagagcacgt accgtgtggt cagcgtcctc	1800
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa	1860
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca	1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc	1980
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag	2040
ccggagaaca actacaagac cagcctccc gtgctggact ccgacggctc cttcttcctc	2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc	2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt	2220
aaa	2223

<210> 178
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 178

Gln	Gly	Gln	Ser	Gly	Gln
1				5	

<210> 179
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 179

Met Met Tyr Cys Gly Gly Asn Glu Val Leu Cys Gly Pro Arg Val Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
35 40 45

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
100 105 110

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
195 200 205

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr

210

215

220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
 245 250 255

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
 260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
 290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
 325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn
 340 345 350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
 355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
 370 375 380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
 385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
 405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
515 520 525

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
530 535 540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
610 615 620

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
625 630 635 640

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

645

650

655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 725 730 735

Leu Ser Pro Gly Lys
 740

<210> 180
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 180
 caaggccagt ctggccag

18

<210> 181
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 181
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 agcgggtggct ctggtggatc cggctctgagc ggccgttccg ataattcatgg cagtagcgggt 120
 acccagatct tgctgaccca gagcccgggtg attctgagcg tgagcccggg cgaacgtgtg 180

agctttagct gccgcgcgag ccagagcatt ggcaccaaca ttcattggta tcagcagcgc 240
 accaacggca gcccgcgcct gctgattaa tatgcgagcg aaagcattag cggcattccg 300
 agccgcttta gcggcagcgg cagcggcacc gattttaccc tgagcattaa cagcgtggaa 360
 agcgaagata ttgcggatta ttattgccag cagaacaaca actggccgac cacctttggc 420
 gcgggcacca aactggaact gaaacgtacg gtggctgcac catctgtctt catcttccc 480
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 540
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 600
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 660
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 720
 ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 765

<210> 182
 <211> 255
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 182

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

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Leu Ser Gly Arg
 20 25 30

Ser Asp Asn His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
 35 40 45

Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
 50 55 60

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
 65 70 75 80

Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile
 85 90 95

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
115 120 125

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
130 135 140

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
165 170 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
180 185 190

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
195 200 205

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
210 215 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225 230 235 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
245 250 255

<210> 183
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 183
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agcgggtggct ctggtggtgg tggaggctcg ggcggtggga gcggcggcgg ttctcagacc 120

gtggtcacac aggagccctc actgacagtg agccctggcg ggaccgtcac actgacttgt	180
cgcagttcaa ctggcgccgt gactaccagc aattacgcta actgggtcca gcagaaacca	240
ggacaggcac cacgaggact gatcggagga actaataaga gagcaccagg aacccttgca	300
aggttctccg gatctctgct ggggggaaaa gccgctctga cactgagcgg cgtgcagcct	360
gaggacgaag ctgagtacta ttgcgcactg tggtactcca acctgtgggt gtttggcggg	420
ggaactaagc tgaccgtcct gggaggagga ggaagcggag gaggaggag cggaggagga	480
ggatccgaag tgcagctggt cgagagcggg ggaggactgg tgcagccagg aggatccctg	540
aagctgtctt gtgcagccag tggtctcacc ttcaacactt acgcaatgaa ctgggtgcgg	600
caggcacctg ggaagggact ggaatgggtc gcccggtatca gatctaaata caataactat	660
gccacctact atgctgacag tgtgaaggat aggttcacca tttcacgcga cgatagcaaa	720
aacacagctt atctgcagat gaataacctg aagaccgagg atacagcagt gtactattgc	780
gtcagacacg gcaatttcgg gaactcttac gtgagttggt ttgcctattg gggacagggg	840
acactgggtca ccgtctcctc aggaggtggt ggatcccagg tgcagctgaa acagagcggc	900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc	960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg	1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc	1080
attaacaaag ataacagcaa aagccagggtg ttttttaaaa tgaacagcct gcaaagccag	1140
gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggt gaccgtgagc gcggctagca ccaagggcc atcggctctt	1260
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc	1320
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500
agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga actcctgggg ggaccgtcag tcttcctctt cccccaaaa	1620
ccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg	1680
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat	1740

gccaagacaa agccgcggga ggagcagtac cagagcacgt accgtgtggt cagcgtcctc 1800
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1860
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1980
tgctgtgtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 2040
ccggagaaca actacaagac cagcctccc gtgctggact ccgacggctc cttcttcctc 2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 2220
aaa 2223

<210> 184
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 184

Met Met Tyr Cys Gly Gly Asn Glu Val Leu Cys Gly Pro Arg Val Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Ser Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu
35 40 45

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala

100

105

110

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
 115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
 180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 195 200 205

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
 210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
 245 250 255

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
 260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
 290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn
340 345 350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
370 375 380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
515 520 525

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

530

535

540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
 580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 610 615 620

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 725 730 735

Leu Ser Pro Gly Lys
 740

<210> 185
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 185
tgcattctcac ctcgtggttg tccggacggc ccatacgtca tgtacggctc gagcgggtggc 60
agcgggtggct ctgggtggctc aggtggaggc tcgggcgggtg ggagcggcgg ttctgatatc 120
ttgctgaccc agagcccggg gattctgagc gtgagcccgg gcgaacgtgt gagctttagc 180
tgccgcgcga gccagagcat tggcaccaac attcattggt atcagcagcg caccaacggc 240
agcccgcgcc tgctgattaa atatgcgagc gaaagcatta gcggcattcc gagccgcttt 300
agcggcagcg gcagcggcac cgattttacc ctgagcatta acagcgtgga aagcgaagat 360
attgcggatt attattgcca gcagaacaac aactggccga ccacctttgg cgcgggcacc 420
aaactggaac tgaaacgtac ggtggctgca ccatctgtct tcattcttccc gccatctgat 480
gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga 540
gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 600
gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 660
aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 720
tcgcccgtca caaagagctt caacagggga gagtgt 756

<210> 186
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 186

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

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly
20 25 30

Gly Gly Ser Gly Gly Ser Asp Ile Leu Leu Thr Gln Ser Pro Val Ile
35 40 45

Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser
50 55 60

Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly
65 70 75 80

Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile
85 90 95

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
100 105 110

Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln
115 120 125

Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
130 135 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145 150 155 160

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

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
180 185 190

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
195 200 205

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
210 215 220

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225 230 235 240

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

<210> 187
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 187
 atgatgtatt gcggtgggaa tgaggtgttg tgcgggccgc gggttggctc gagcgggtggc 60
 agcgggtggct ctggtggtat ctcttccgga ctgctgtccg gcagatccga caatcacggc 120
 ggcggttctc agaccgtggt cacacaggag ccctcactga cagttagccc tggcgggacc 180
 gtcacactga cttgtcgcag ttcaactggc gccgtgacta ccagcaatta cgctaactgg 240
 gtccagcaga aaccaggaca ggcaccacga ggactgatcg gaggaactaa taagagagca 300
 ccaggaaccc ctgcaaggtt ctccggatct ctgctggggg gaaaagccgc tctgacactg 360
 agcggcgtgc agcctgagga cgaagctgag tactattgcg cactgtggta ctccaacctg 420
 tgggtgtttg gcgggggaac taagctgacc gtcctgggag gaggaggaag cggaggagga 480
 gggagcggag gaggaggatc cgaagtgcag ctggctgaga gcggaggagg actggtgcag 540
 ccaggaggat ccctgaagct gtcttgtgca gccagtggct tcaccttcaa cacttacgca 600
 atgaactggg tgcggcaggc acctgggaag ggactggaat gggtcgcccg gatcagatct 660
 aaatacaata actatgccac ctactatgct gacagtgtga aggataggtt caccatttca 720
 cgcgacgata gcaaaaacac agcttatctg cagatgaata acctgaagac cgaggataca 780
 gcagtgtact attgcgtcag acacggcaat ttcgggaact cttacgtgag ttggtttgcc 840
 tattggggac aggggacact ggtcaccgtc tcctcaggag gtggtggatc ccaggtgcag 900
 ctgaaacaga gcggcccggg cctggtgcag ccgagccaga gcctgagcat tacctgcacc 960
 gtgagcggct ttagcctgac caactatggc gtgcattggg tgcgccagag cccgggcaaa 1020
 ggccctggaat ggctgggcgt gatttggagc ggcggcaaca ccgattataa caccctgttt 1080
 accagccgcc tgagcattaa caaagataac agcaaaagcc aggtgttttt taaaatgaac 1140
 agcctgcaaa gccaggatac cgcgatttat tattgcgcgc gcgcgctgac ctattatgat 1200
 tatgaatttg cgtattgggg ccagggcacc ctggtgaccg tgagcgcggc tagcaccaag 1260

ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 1320
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc 1380
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 1440
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1500
 gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 1560
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 1620
 ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 1680
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1740
 gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtaccagag cacgtaccgt 1800
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1860
 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg 1920
 cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1980
 caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 2040
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 2100
 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggaac 2160
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 2220
 tccctgtctc cgggtaaa 2238

<210> 188
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 188

Met	Met	Tyr	Cys	Gly	Gly	Asn	Glu	Val	Leu	Cys	Gly	Pro	Arg	Val	Gly
1				5					10					15	

Ser	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ile	Ser	Ser	Gly	Leu	Leu
		20					25						30		

Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Gln Thr Val Val Thr

35

40

45

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
 50 55 60

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
 65 70 75 80

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
 85 90 95

Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
 100 105 110

Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu
 115 120 125

Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly
 130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
 165 170 175

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 180 185 190

Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro
 195 200 205

Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn
 210 215 220

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 225 230 235 240

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys
 245 250 255

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly
260 265 270

Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
275 280 285

Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser
290 295 300

Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr
305 310 315 320

Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln
325 330 335

Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly
340 345 350

Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys
355 360 365

Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser
370 375 380

Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp
385 390 395 400

Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
405 410 415

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
420 425 430

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
435 440 445

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
450 455 460

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

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

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
705 710 715 720

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
725 730 735

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 189
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 189
tgcattctcac ctctgtggttg tccggacggc ccatactgca tgtacggctc gagcgggtggc 60
agcgggtggct ctggtggatc cggtattagc agtgggtctgt taagcggctg tagcgataat 120
catggcagta gcggtaccca gatcttgctg acccagagcc cggtgattct gagcgtgagc 180
ccggggcgaac gtgtgagctt tagctgccgc gcgagccaga gcattggcac caacattcat 240
tggtatcagc agcgcaccaa cggcagcccc gcctgtctga ttaaatatgc gagcgaaagc 300
attagcggca ttccgagccg ctttagcggc agcggcagcg gcaccgattt taccctgagc 360
attaacagcg tggaaagcga agatattgctg gattattatt gccagcagaa caacaactgg 420
ccgaccacct ttggcgcggg caccaaactg gaactgaaac gtacgggtggc tgcaccatct 480
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 540
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgcctc 600
caatcgggta actcccagga gactgtcaca gagcaggaca gcaaggacag cacctacagc 660
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 720
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 780

<210> 190

<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 190

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

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

Leu Leu Ser Gly Arg Ser Asp Asn His Gly Ser Ser Gly Thr Gln Ile
35 40 45

Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg
50 55 60

Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
65 70 75 80

Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr
85 90 95

Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly
100 105 110

Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp
115 120 125

Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe
130 135 140

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

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

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val

180

185

190

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
 195 200 205

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
 210 215 220

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
 225 230 235 240

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 245 250 255

Arg Gly Glu Cys
 260

<210> 191
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 191
 caaggccagt ctggatcc

18

<210> 192
 <211> 2226
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 192
 gggttatctgt ggggttgca gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
 agcgggtggct ctggtggtct gagcggccgt tccgataatc atggcggcgg ttctcaaact 120
 gtagtaactc aagaaccaag cttctccgtc tcccctgggg gaacagtcac acttacctgc 180
 cgaagtagta caggtgctgt tacgaccagt aactatgcca attgggtaca acaaacgcct 240
 ggtcaggctc cgcgcggatt gataggaggc acgaataaac gggcaccggg tgtcccggac 300

agattcagcg gaagcatact cggtataaag gcagctctta ctatcactgg ggcccaagct	360
gatgatgaaa gtgattatta ttgtgcgctc tggtagagca acctctgggt gtttgggggt	420
ggcacgaaac ttactgtctt gggcggcggc ggatcagggg gaggtggctc tggaggagga	480
ggctcagaag tccaactggt cgaatccggg ggagggctcg tacagccggg tgggtccctc	540
aaactctctt gtgcggcctc agggtttacc ttcagtacat acgcgatgaa ttgggtccgg	600
caggccagtg ggaaagggt cgaatgggta ggacgaatcc gatcaaaata caacaactac	660
gctacttatt acgctgattc cgtgaaggac agattcacia tatcccgcga cgatagcaag	720
aatacggcat atcttcagat gaattctctt aaaactgagg ataccgctgt gtattactgc	780
acaagacatg gtaatttttg aaactcatat gtctcttggt tcgcttattg gggacagggc	840
acgttggtta ccgtgtctag cggaggtggt ggatcccagg tgcagctgaa acagagcggc	900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc	960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg	1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc	1080
attaacaaag ataacagcaa aagccaggtg ttttttaaaa tgaacagcct gcaaagccag	1140
gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggt gaccgtgagc gcggctagca ccaaggggcc atcggctctc	1260
cccctggcac cctcctcaa gagcacctct gggggcacag cggccctggg ctgcctggctc	1320
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500
agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga atttgaaggg ggaccgtcag tcttcctctt cccccaaaa	1620
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agccacgaag acctgaggt caagttcaac tggtagctgg acggcgtgga ggtgcataat	1740
gccaagacaa agccgcggga ggagcagtag aatagcacgt accgtgtggt cagcgtcctc	1800
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa	1860
gccctcccag cctcaatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca	1920

caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc	1980
tgccttgtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag	2040
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc	2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc	2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt	2220
aaatga	2226

<210> 193
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 193

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe
35 40 45

Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala
100 105 110

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu
195 200 205

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
245 250 255

Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn

340

345

350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
 355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
 370 375 380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
 385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
 405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe
 515 520 525

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 530 535 540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
610 615 620

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
725 730 735

Leu Ser Pro Gly Lys
740

<210> 194
<211> 2226
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 194

ggttatctgt ggggttgcca gtggaattgc ggagggatca ctacaggctc gagcgggtggc	60
agcgggtggct ctgggtgtct gagcggccgt tccgataatc atggcggcgg ttctcaaact	120
gtagtaactc aagaaccaag cttctccgtc tcccctgggg gaacagtcac acttacctgc	180
cgaagtagta caggtgctgt tacgaccagt aactatgcca attgggtaca acaaacgcct	240
ggtcaggctc cgcgcggatt gataggaggc acgaataaac gggcacccgg tgtcccggac	300
agattcagcg gaagcatact cggtataaag gcagctctta ctatcactgg ggcccaagct	360
gatgatgaaa gtgattatta ttgtgcgctc tggtagagca acctctgggt gtttgggggt	420
ggcacgaaac ttactgtctt gggcggcggc ggatcagggg gaggtggctc tggaggagga	480
ggctcagaag tccaactggt cgaatccggg ggagggtcgt tacagccggg tgggtccctc	540
aaactctctt gtgcggcctc agggtttacc ttcagtacat acgcgatgaa ttgggtccgg	600
caggccagtg ggaaagggt cgaatgggta ggacgaatcc gatcaaaata caacaactac	660
gctacttatt acgctgattc cgtgaaggac agattcacia tatcccgcga cgatagcaag	720
aatacggcat atcttcagat gaattctctt aaaactgagg ataccgctgt gtattactgc	780
acaagacatg gtaatttttg aaactcatat gtctcttgggt tcgcttattg gggacagggc	840
acgttggtta ccgtgtctag cggaggtgggt ggatcccagg tgcagctgaa acagagcggc	900
ccgggcctgg tgagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc	960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg	1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc	1080
attaacaaag ataacagcaa aagccaggtg ttttttaaaa tgaacagcct gcaaagccag	1140
gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggt gaccgtgagc gcggctagca ccaagggcc atcggctcttc	1260
cccctggcac cctcctcaa gagcacctct gggggcacag cggccctggg ctgcctggctc	1320
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgcctt gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtgggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500

agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga atttgaaggg ggaccgtcag tcttcctctt cccccaaaa	1620
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg	1680
agccacgaag accctgaggt caagttcaac tggtagctgg acggcgtgga ggtgcataat	1740
gccaagacaa agccgcggga ggagcagtac cagagcacgt accgtgtggt cagcgtcctc	1800
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa	1860
gccctcccag cctcaatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca	1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc	1980
tgcttggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag	2040
ccggagaaca actacaagac cagcctccc gtgctggact ccgacggctc cttcttcctc	2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc	2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt	2220
aaatga	2226

<210> 195
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 195

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asn His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe
35 40 45

Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro

65

70

75

80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala
100 105 110

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu
195 200 205

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
245 250 255

Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn
340 345 350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
370 375 380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys

500

505

510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe
 515 520 525

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 530 535 540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
 580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 610 615 620

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
725 730 735

Leu Ser Pro Gly Lys
740

<210> 196
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 196
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agcgggtggct ctgggtgtct gagcggccgt tccgatgata atggcggcgg ttctcaaact 120
gtagtaactc aagaaccaag cttctccgtc tcccctgggg gaacagtcac acttacctgc 180
cgaagtagta caggtgctgt tacgaccagt aactatgcca attgggtaca acaaacgcct 240
ggtcaggctc cgcgcggtatt gataggaggc acgaataaac gggcacccgg tgtcccggac 300
agattcagcg gaagcatact cggttaataag gcagctctta ctatcactgg ggcccaagct 360
gatgatgaaa gtgattatta ttgtgcgctc tggtagagca acctctgggt gtttgggggt 420
ggcacgaaac ttactgtctt gggcggcggc ggatcagggg gaggtggctc tggaggagga 480
ggctcagaag tccaactggt cgaatccggg ggagggctcg tacagccggg tgggtccctc 540
aaactctctt gtgcggcctc agggtttacc ttcagtacat acgcgatgaa ttgggtccgg 600
caggccagtg ggaaagggtc cgaatgggta ggacgaatcc gatcaaaata caacaactac 660
gctacttatt acgctgattc cgtgaaggac agattcaca tatcccgcga cgatagcaag 720
aatacggcat atcttcagat gaattctctt aaaactgagg ataccgctgt gtattactgc 780
acaagacatg gtaatttttg aaactcatat gtctcttgggt tcgcttattg gggacagggc 840
acgttgggta ccgtgtctag cggaggtggg ggatcccagg tgcagctgaa acagagcggc 900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc 960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg 1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc 1080

attaacaaaag ataacagcaa aagccaggtg ttttttaaaa tgaacagcct gcaaagccag	1140
gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggt gaccgtgagc gcggctagca ccaagggcc atcggctctt	1260
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc	1320
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500
agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga atttgaaggg ggaccgtcag tcttcctctt cccccaaaa	1620
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg	1680
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat	1740
gccaagacaa agccgcggga ggagcagtac cagagcacgt accgtgtggt cagcgtcctc	1800
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa	1860
gccctcccag cctcaatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca	1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc	1980
tgcttggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag	2040
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc	2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc	2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt	2220
aaa	2223

<210> 197
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 197

Gly	Tyr	Leu	Trp	Gly	Cys	Glu	Trp	Asn	Cys	Gly	Gly	Ile	Thr	Thr	Gly
1				5				10						15	

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asp His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe
35 40 45

Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala
100 105 110

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu
195 200 205

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys

225		230		235		240
Asn Thr Ala Tyr	Leu Gln Met Asn Ser	Leu Lys Thr Glu Asp Thr Ala				
	245	250				255
Val Tyr Tyr Cys Thr Arg His Gly	Asn Phe Gly Asn Ser Tyr Val Ser					
	260	265				270
Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly						
	275	280				285
Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val						
	290	295				300
Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser						
	305	310			315	320
Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly						
	325	330				335
Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn						
	340	345				350
Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser						
	355	360				365
Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile						
	370	375				380
Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr						
	385	390			395	400
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly						
	405	410				415
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly						
	420	425				430
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val						
	435	440				445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe
515 520 525

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
530 535 540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
610 615 620

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

660

665

670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 725 730 735

Leu Ser Pro Gly Lys
 740

<210> 198
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 198
 caaggtctta gttgtgaagg ttgggcgatg aatagagaac aatgtcgagc cggaggtggc 60
 tcgagcggcg gctctatctc ttccggactg ctgtccggca gatccgacca gcacggcgga 120
 ggatcccaaa tcctgctgac acagtctcct gtcatactga gtgtctcccc cggcgagaga 180
 gtctcttttct catgtcgggc cagtcagtct attgggacta acatacactg gtaccagcaa 240
 cgcaccaacg gaagcccgcg cctgctgatt aaatatgcga gcgaaagcat tagcggcatt 300
 ccgagccgct ttagcggcag cggcagcggc accgatttta ccctgagcat taacagcgtg 360
 gaaagcgaag atattgcgga ttattattgc cagcagaaca acaactggcc gaccaccttt 420
 ggcgcggggca ccaaactgga actgaaacgt acggtggctg caccatctgt cttcatcttc 480
 ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 540
 ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 600
 tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 660

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 720

cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt 768

<210> 199

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 199

Leu Ser Cys Glu Gly Trp Ala Met Asn Arg Glu Gln Cys Arg Ala Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Gln His Gly Gly Gly Ser Gln Ile Leu Leu Thr Gln Ser Pro
35 40 45

Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg
50 55 60

Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr
65 70 75 80

Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser
85 90 95

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
100 105 110

Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys
115 120 125

Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu
130 135 140

Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
145 150 155 160

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

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
180 185 190

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
195 200 205

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
210 215 220

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
225 230 235 240

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
245 250

<210> 200
<211> 2238
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 200
ggttatctgt ggggttgca gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
agcgggtggct ctggtggtat atcgagtgga ttgctgtctg gcagatctga cgatcacggc 120
ggcggttctc aaactgtagt aactcaagaa ccaagcttct ccgtctcccc tgggggaaca 180
gtcacactta cctgccgaag tagtacaggt gctgttacga ccagtaacta tgccaattgg 240
gtacaacaaa cgcctggtca ggctccgcgc ggattgatag gaggcacgaa taaacgggca 300
cccggtgtcc cggacagatt cagcgggaagc atactcggtataaaggcagc tcttactatc 360
actggggccc aagctgatga tgaaagtgat tattattgtg cgctctggta cagcaacctc 420
tgggtgtttg ggggtggcac gaaacttact gtcttgggcg gcggcggatc agggggaggt 480
ggctctggag gaggaggctc agaagtccaa ctggtcgaat ccgggggagg gctcgtacag 540
ccgggtgggt ccctcaaact ctcttgtgcg gcctcagggt ttaccttcag tacatacgcg 600

atgaattggg tccggcaggc cagtgggaaa gggctcgaat gggtaggacg aatccgatca	660
aaatacaaca actacgctac ttattacgct gattccgtga aggacagatt cacaatatcc	720
cgcgacgata gcaagaatac ggcatatctt cagatgaatt ctcttaaaac tgaggatacc	780
gctgtgtatt actgcacaag acatggtaat tttggaaact catatgtctc ttggttcgct	840
tattggggac agggcacgtt ggttaccgtg tctagcggag gtggtggatc ccaggtgcag	900
ctgaaacaga gcggcccggg cctggtgcag ccgagccaga gcctgagcat tacctgcacc	960
gtgagcggct ttagcctgac caactatggc gtgcattggg tgcgccagag cccgggcaaa	1020
ggcctggaat ggctgggcgt gatttggagc ggcggaaca ccgattataa cccccgttt	1080
accagccgcc tgagcattaa caaagataac agcaaaagcc aggtgttttt taaaatgaac	1140
agcctgcaaa gccaggatac cgcgatttat tattgcgcgc gcgcgctgac ctattatgat	1200
tatgaatttg cgtattgggg ccagggcacc ctggtgaccg tgagcgcggc tagcaccaag	1260
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	1320
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	1380
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	1440
ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagacctt catctgcaac	1500
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagcccaa atcttgtgac	1560
aaaactcaca catgcccacc gtgcccagca cctgaatttg aaggggggacc gtcagtcttc	1620
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	1680
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	1740
gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtaccagag cacgtaccgt	1800
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	1860
aaggcttcca acaaagccct ccagcctca atcgagaaaa ccatctcaa agccaaaggg	1920
cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac	1980
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg	2040
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	2100
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggaac	2160
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	2220

tccctgtctc cgggtaaa

2238

<210> 201
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 201

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu Leu
20 25 30

Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val Thr
35 40 45

Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr
50 55 60

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
65 70 75 80

Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
85 90 95

Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu
100 105 110

Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu
115 120 125

Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly
130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

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

165

170

175

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
 180 185 190

Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser
 195 200 205

Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn
 210 215 220

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
 225 230 235 240

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
 245 250 255

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly
 260 265 270

Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 275 280 285

Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser
 290 295 300

Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr
 305 310 315 320

Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln
 325 330 335

Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly
 340 345 350

Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys
 355 360 365

Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser
 370 375 380

Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp
385 390 395 400

Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
405 410 415

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
420 425 430

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
435 440 445

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
450 455 460

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
465 470 475 480

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
485 490 495

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
500 505 510

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
515 520 525

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
530 535 540

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
545 550 555 560

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
565 570 575

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
580 585 590

Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

595

600

605

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 610 615 620

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 625 630 635 640

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 645 650 655

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 660 665 670

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 675 680 685

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 705 710 715 720

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 725 730 735

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 740 745

<210> 202
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 202
 tgcacatctcac ctcgtggttg tccggacggc ccatacgtca tgtacggctc gagcgggtggc 60
 agcgggtggct ctggtggatc cggctctgagc ggccgttccg atgatcatgg cagtagcgggt 120
 acccagatct tgctgaccca gagcccgggtg attctgagcg tgagcccggg cgaacgtgtg 180

agctttagct gccgcgcgag ccagagcatt ggcaccaaca ttcattggta tcagcagcgc 240
 accaacggca gcccgcgcct gctgattaa tatgcgagcg aaagcattag cggcattccg 300
 agccgcttta gcggcagcgg cagcggcacc gattttaccc tgagcattaa cagcgtggaa 360
 agcgaagata ttgcggatta ttattgccag cagaacaaca actggccgac cacctttggc 420
 gcgggcacca aactggaact gaaacgtacg gtggctgcac catctgtctt catcttcccg 480
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 540
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 600
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 660
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 720
 ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 765

<210> 203
 <211> 255
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 203

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

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Leu Ser Gly Arg
 20 25 30

Ser Asp Asp His Gly Ser Ser Gly Thr Gln Ile Leu Leu Thr Gln Ser
 35 40 45

Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys
 50 55 60

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg
 65 70 75 80

Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile
 85 90 95

Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr
115 120 125

Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys
130 135 140

Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
165 170 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
180 185 190

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
195 200 205

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
210 215 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225 230 235 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
245 250 255

<210> 204
<211> 2226
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 204
ggttatctgt ggggttcga gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
agcgggtggct ctggtgttct gagcggccgt tccgatgatc atggcggcgg ttctcaaact 120

gtagtaactc aagaaccaag cttctccgtc tcccctgggg gaacagtcac acttacctgc	180
cgaagtagta caggtgctgt tacgaccagt aactatgcc aattgggtaca acaaacgcct	240
ggtcaggctc cgcgcggatt gataggaggc acgaataaac gggcaccggt tgtcccggac	300
agattcagcg gaagcatact cggtaataag gcagctctta ctatcactgg ggcccaagct	360
gatgatgaaa gtgattatta ttgtgcgctc tggtagagca acctctgggt gtttgggggt	420
ggcacgaaac ttactgtctt gggcggcggc ggatcagggg gaggtggctc tggaggagga	480
ggctcagaag tccaactgggt cgaatccggg ggagggtctg tacagccggg tgggtccctc	540
aaactctctt gtgcggcctc agggtttacc ttcagtacat acgcgatgaa ttgggtccgg	600
caggccagtg ggaaagggtc cgaatgggta ggacgaatcc gatcaaaata caacaactac	660
gctacttatt acgctgattc cgtgaaggac agattcaca tatcccgcga cgatagcaag	720
aatacggcat atcttcagat gaattctctt aaaactgagg ataccgctgt gtattactgc	780
acaagacatg gtaattttgg aaactcatat gtctcttgggt tcgcttattg gggacagggc	840
acgttggtta ccgtgtctag cggagggtgg ggatcccaag tgaccctgag agagtctggc	900
cctgccctcg tgaagcctac ccagaccctg acactgacct gcaccttcag cggcttcagc	960
ctgagcacca gcggcatgtc tgtgggctgg atcagacagc ctcttgga ggccctggaa	1020
tggctggccg acatttggtg ggacgacaag aaggactaca accccagcct gaagtcccgg	1080
ctgaccatca gcaaggacac cagcaagaac caggtggtgc tgaaagtgac caacatggac	1140
cccgccgaca ccgccaccta ctactgcgcc agatccatga tcaccaactg gtacttcgac	1200
gtgtggggag ccggcaccac cgtgacagtg tcatctgcta gcaccaaggg cccatcggtc	1260
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg	1320
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc	1380
ggcgtgcaca cttcccggc tgtcctacag tcctcaggac tctactccct cagcagcgtg	1440
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag	1500
cccagcaaca ccaagggtga caagaaagt gagcccaaat cttgtgacaa aactcacaca	1560
tgcccaccgt gccagcacc tgaatttgaa gggggaccgt cagtcttcct cttccccca	1620
aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac	1680
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat	1740

aatgccaaga caaagccgcg ggaggagcag taccagagca cgtaccgtgt ggtcagcgtc 1800
 ctaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1860
 aaagccctcc cagcctcaat cgagaaaacc atctccaaag ccaaaggga gccccgagaa 1920
 ccacaggtgt acaccctgcc cccatcccgg gaggagatga ccaagaacca ggtcagcctg 1980
 acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 2040
 cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 2100
 ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 2160
 tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 2220
 ggtaaa 2226

<210> 205
 <211> 742
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 205

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
 1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
 20 25 30

Asp His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe
 35 40 45

Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
 50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro
 65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
 85 90 95

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala

100

105

110

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
 115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu
 195 200 205

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
 210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
 245 250 255

Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
 260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 275 280 285

Gly Gly Gly Ser Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val
 290 295 300

Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
 305 310 315 320

Leu Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly
325 330 335

Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
340 345 350

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
355 360 365

Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr
370 375 380

Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp
385 390 395 400

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
405 410 415

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
420 425 430

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
435 440 445

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
450 455 460

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
465 470 475 480

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
485 490 495

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
500 505 510

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
515 520 525

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

530

535

540

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 545 550 555 560

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 565 570 575

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln
 580 585 590

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 595 600 605

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 610 615 620

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 625 630 635 640

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 645 650 655

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 660 665 670

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 675 680 685

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 690 695 700

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 705 710 715 720

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 725 730 735

Ser Leu Ser Pro Gly Lys
 740

<210> 206
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 206
ggttatctgt ggggttgcca gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
agcgggtggct ctgggtggtat atcgagtgga ttgctgtctg gcagatctga cgatcacggc 120
ggcggttctc aaactgtagt aactcaagaa ccaagcttct ccgtctcccc tgggggaaca 180
gtcacactta cctgccgaag tagtacaggt gctgttacga ccagtaacta tgccaattgg 240
gtacaacaaa cgcctggcca ggctccgcgc ggattgatag gaggcacgaa taaacgggca 300
cccgggtgtcc cggacagatt cagcgggaagc atactcggta ataaggcagc tcttactatc 360
actggggccc aagctgatga tgaaagtgat tattattgtg cgctctggta cagcaacctc 420
tgggtgtttg ggggtggcac gaaacttact gtcttgggcg gcggcggatc agggggaggt 480
ggctctggag gaggaggctc agaagtccaa ctggtcgaat ccgggggagg gctcgtacag 540
ccgggtgggt ccctcaaact ctcttgtgcg gcctcagggt ttaccttcag tacatacgcg 600
atgaattggg tccggcaggc cagtgggaaa gggctcgaat gggtaggacg aatccgatca 660
aaatacaaca actacgctac ttattacgct gattccgtga aggacagatt cacaatatcc 720
cgcgacgata gcaagaatac ggcatatctt cagatgaatt ctcttaaaac tgaggatacc 780
gctgtgtatt actgcacaag acatggtaat tttggaaact catatgtctc ttggttcgct 840
tattggggac agggcacgtt ggttaccgtg tctagcggag gtggtggatc ccaagtgacc 900
ctgagagagt ctggccctgc cctcgtgaag cctaccaga ccctgacact gacctgcacc 960
ttcagcggct tcagcctgag caccagcggc atgtctgtgg gctggatcag acagcctcct 1020
ggcaaggccc tggaatggct ggccgacatt tgggtgggacg acaagaagga ctacaacccc 1080
agcctgaagt cccggctgac catcagcaag gacaccagca agaaccaggt ggtgctgaaa 1140
gtgaccaaca tggacccgc cgacaccgcc acctactact gcgccagatc catgatcacc 1200
aactggtact tcgacgtgtg gggagccggc accaccgtga cagtgtcatc tgctagcacc 1260
aagggcccat cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 1320

gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 1380
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1440
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1500
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 1560
 gacaaaactc acacatgccc accgtgcccga gcacctgaat ttgaaggggg accgtcagtc 1620
 ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 1680
 tgcgtgggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1740
 ggctgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtagca gagcacgtac 1800
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1860
 tgcaaggtct ccaacaaagc cctcccagcc tcaatcgaga aaaccatctc caaagccaaa 1920
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 1980
 aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 2040
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 2100
 gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 2160
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 2220
 ctctccctgt ctccgggtaa a 2241

<210> 207
 <211> 747
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 207

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
 1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu Leu
 20 25 30

Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Gln Thr Val Val Thr
 35 40 45

Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr
50 55 60

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
65 70 75 80

Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
85 90 95

Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu
100 105 110

Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu
115 120 125

Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly
130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
165 170 175

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
180 185 190

Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser
195 200 205

Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn
210 215 220

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
225 230 235 240

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
245 250 255

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly

260

265

270

Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 275 280 285

Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Arg Glu Ser
 290 295 300

Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr
 305 310 315 320

Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp Ile
 325 330 335

Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp
 340 345 350

Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile
 355 360 365

Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn Met
 370 375 380

Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr
 385 390 395 400

Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser
 405 410 415

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
 420 425 430

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 435 440 445

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 450 455 460

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 465 470 475 480

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
485 490 495

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
500 505 510

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
515 520 525

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
530 535 540

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
545 550 555 560

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
565 570 575

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
580 585 590

Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
595 600 605

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
610 615 620

Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
625 630 635 640

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
645 650 655

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
660 665 670

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
675 680 685

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

690

695

700

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 705 710 715 720

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 725 730 735

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 740 745

<210> 208
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 208
 caaggccagt ctggttct

18

<210> 209
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 209
 gggttatctgt ggggttgcca gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
 agcgggtggct ctggtggtct gagcggccgt tccgatgata atggcggcgg atcccagacg 120
 gtagtgactc aggagccatc attttctgtc tctcctggag gtactgtgac actcacatgt 180
 agaagctcaa ctggtgcagt caccacttca aattacgcga attgggtcca gcagaccctt 240
 gggcaggctc cgagagggtt gattggaggt actaacaac gggcaccggg agtgcctgat 300
 aggtttttccg gttctattct cggaacaag gcggctctca cgatcacggg tgcgcaggcc 360
 gacgatgaat cagactatta ctgcgctttg tgggtactcaa acctgtgggt attcggaggg 420
 ggcaccaagc tgacggtggt ggggtggggg ggctctgggg gagggggaag cggaggtggg 480
 ggcagcgagg ttcagcttgt tgaaagtggg ggcggactcg tacaaccggg tggaagtctt 540

agactctcat gtgcagcatc tggatttact ttttctactt atgctatgaa ctgggtaaga	600
caggcaccgg ggaaagggtc ggaatgggtt gcacgcattc gatctaaata caataactat	660
gctacatact acgccgatag tgtaaggat cgattcacta tatctcggga cgacagtaag	720
aactcacttt acctgcagat gaattccttg aaaactgagg acacggccgt ttattattgt	780
gtacggcacg ggaatttcgg caattcttac gtttcctggt tcgcctattg ggggcaaggt	840
acgctggtca cgggtgtctag cggaggtggt ggatcccagg tgcagctgaa acagagcggc	900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc	960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg	1020
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gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggt gaccgtgagc gcggctagca ccaagggcc atcggctctt	1260
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aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1440
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agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
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accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa	1860
gccctcccag cctcaatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca	1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc	1980
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag	2040
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc	2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc	2160

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 2220

aaa 2223

<210> 210
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 210

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

Asp His Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe
35 40 45

Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala
100 105 110

Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys
115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
165 170 175

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
195 200 205

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
225 230 235 240

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
245 250 255

Val Tyr Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn
340 345 350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile

370

375

380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
 385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
 405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe
 515 520 525

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 530 535 540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
 580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
610 615 620

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
725 730 735

Leu Ser Pro Gly Lys
740

<210> 211
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 211
ggttatctgt ggggttcga gtggaattgc ggagggatca ctacaggctc gagcgggtggc 60
agcgggtggct ctggtggtct gagcggccgt tccgatgata atggcggcgg ttctcaggcc 120

gttgttacac aagagccttc acttactgtg tctccaggag gcactgtgac acttacgtgc	180
cgatcctcta cgggtgccgt gaccacaagc aactatgcc aactgggtcca gcagaagcca	240
ggtcaagcgc ctcgaggctt gatcgggggc acgaataaac gagctcctgg aactccggcc	300
agattttctg ggagtcttat tgggtggcaag gcggcggtga ccctgagtgg agcccaaccg	360
gaagacgagg ccgagtacta ctgcgccttg tggatttcca atttgtgggt cttcggaggc	420
ggaacaaagc tcacagtact gggaggtgga ggtagcgggg gcggaggctc cgggggaggt	480
ggttccgaag tccagcttgt tgaatcaggt gggggccttg tacaaccagg tggttcactg	540
aagttgtcct gtgcagcgtc cggatttaca tttagtacgt atgctatgaa ctgggtcagg	600
caggccagtg gtaaaggctt cgaatgggtt ggccggataa ggtcaaagta caataattac	660
gcaacctact acgcggattc cgtgaaagac aggttcacta tttcacgaga tgatagcaaa	720
aatactgcgt atctccaaat gaatagtctt aaaactgaag acactgccgt atattattgc	780
actaggcacg gcaactttgg taactcttat gtttcttggt tcgcatactg gggacaagga	840
actttgggtca ctgtctcatc tggaggtggg ggatcccagg tgcagctgaa acagagcggc	900
ccgggcctgg tgcagccgag ccagagcctg agcattacct gcaccgtgag cggctttagc	960
ctgaccaact atggcgtgca ttgggtgctc cagagcccgg gcaaaggcct ggaatggctg	1020
ggcgtgattt ggagcggcgg caacaccgat tataacaccc cgtttaccag ccgcctgagc	1080
attaacaaag ataacagcaa aagccagggtg ttttttaaaa tgaacagcct gcaaagccag	1140
gataccgcga tttattattg cgcgcgcgcg ctgacctatt atgattatga atttgcgtat	1200
tggggccagg gcaccctggg gaccgtgagc gcggctagca ccaagggcc atcggctctt	1260
cccctggcac cctcctcaa gagcacctct gggggcacag cggccctggg ctgcctggtc	1320
aaggactact tccccgaacc ggtgacgggt tcgtggaact caggcgccct gaccagcggc	1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtgggtg	1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1500
agcaacacca aggtggacaa gaaagttgag cccaaatctt gtgacaaaac tcacacatgc	1560
ccaccgtgcc cagcacctga atttgaaggg ggaccgtcag tcttcctctt cccccaaaa	1620
ccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggg ggtggacgtg	1680
agccacgaag accctgaggt caagttcaac tggtagctgg acggcgtgga ggtgcataat	1740

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gccctcccag cctcaatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1920
caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1980
tgctgtgtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 2040
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 2100
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcattgctcc 2160
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 2220
aaa 2223

<210> 212
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 212

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Leu Ser Gly Arg Ser Asp
20 25 30

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

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr
50 55 60

Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro
65 70 75 80

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro
85 90 95

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Ile Gly Gly Lys Ala Ala

100

105

110

Leu Thr Leu Ser Gly Ala Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
 115 120 125

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

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 145 150 155 160

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 165 170 175

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 180 185 190

Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu
 195 200 205

Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
 210 215 220

Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
 225 230 235 240

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala
 245 250 255

Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser
 260 265 270

Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 275 280 285

Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val
 290 295 300

Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser
 305 310 315 320

Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly
325 330 335

Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn
340 345 350

Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser
355 360 365

Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile
370 375 380

Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
385 390 395 400

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly
405 410 415

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
420 425 430

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
435 440 445

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
450 455 460

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
465 470 475 480

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
485 490 495

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
500 505 510

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe
515 520 525

Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

530

535

540

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 545 550 555 560

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 565 570 575

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser
 580 585 590

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 595 600 605

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 610 615 620

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 625 630 635 640

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 645 650 655

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 660 665 670

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 675 680 685

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 690 695 700

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 705 710 715 720

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 725 730 735

Leu Ser Pro Gly Lys
 740

<210> 213
<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 213
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acaggctcga gcggtggcag cgggtggctct ggtggtatat cgagtggatt gctgtctggc 120
agatctgacc aacacggcgg cggttctcaa actgtagtaa ctcaagaacc aagcttctcc 180
gtctcccctg ggggaacagt cacacttacc tgccgaagta gtacagggtgc tgttacgacc 240
agtaactatg ccaattgggt acaacaaacg cctggtcagg ctccgcgcgg attgatagga 300
ggcacgaata aacgggcacc cgggtgtccg gacagattca gcggaagcat actcggtaat 360
aaggcagctc ttactatcac tggggcccaa gctgatgatg aaagtgatta ttattgtgcg 420
ctctggtaca gcaacctctg ggtgtttggg ggtggcacga aacttactgt cttgggcggc 480
ggcggatcag ggggaggtgg ctctggagga ggaggctcag aagtccaact ggtcgaatcc 540
gggggagggc tcgtacagcc ggggtgggtcc ctcaaactct cttgtgcggc ctcagggttt 600
accttcagta catacgcgat gaattgggtc cggcaggcca gtgggaaagg gctcgaatgg 660
gtaggacgaa tccgatcaaa atacaacaac tacgctactt attacgtga ttccgtgaag 720
gacagattca caatatcccg cgacgatagc aagaatacgg catatcttca gatgaattct 780
cttaaaaactg aggataccgc tgtgtattac tgcacaagac atggtaattt tggaaactca 840
tatgtctctt ggttcgctta ttggggacag ggcacgttgg ttaccgtgtc tagcggaggt 900
ggtggatccc aggtgcagct gaaacagagc ggcccgggcc tgggtgcagcc gagccagagc 960
ctgagcatta cctgcaccgt gagcggcttt agcctgacca actatggcgt gcattgggtg 1020
cgccagagcc cgggcaaagg cctggaatgg ctgggcgtga tttggagcgg cggcaacacc 1080
gattataaca ccccgtttac cagccgcctg agcattaaca aagataacag caaaagccag 1140
gtgtttttta aaatgaacag cctgcaaagc caggataccg cgatttatta ttgcgcgcgc 1200
gcgctgacct attatgatta tgaatttgcg tattggggcc agggcacct ggtgaccgtg 1260
agcgcggcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 1320

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	1380
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	1440
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	1500
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt	1560
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaatttgaa	1620
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg	1680
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1740
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	1800
taccagagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1860
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcctcaat cgagaaaacc	1920
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	1980
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	2040
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	2100
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	2160
aggtaggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	2220
tacacgcaga agagcctctc cctgtctccg ggtaaa	2256

<210> 214
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 214

Gly Tyr Leu Trp Gly Cys Glu Trp Asn Cys Gly Gly Ile Thr Thr Gly
1 5 10 15

Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu Leu
20 25 30

Ser Gly Arg Ser Asp Gln His Gly Gly Gly Ser Gln Thr Val Val Thr
35 40 45

Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly Thr Val Thr Leu Thr
50 55 60

Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp
65 70 75 80

Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr
85 90 95

Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Ile Leu
100 105 110

Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp Asp Glu
115 120 125

Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn Leu Trp Val Phe Gly
130 135 140

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
165 170 175

Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
180 185 190

Gly Phe Thr Phe Ser Thr Tyr Ala Met Asn Trp Val Arg Gln Ala Ser
195 200 205

Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Arg Ser Lys Tyr Asn Asn
210 215 220

Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser
225 230 235 240

Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Lys
245 250 255

Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg His Gly Asn Phe Gly

260

265

270

Asn Ser Tyr Val Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 275 280 285

Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser
 290 295 300

Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr
 305 310 315 320

Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln
 325 330 335

Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly
 340 345 350

Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys
 355 360 365

Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser
 370 375 380

Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp
 385 390 395 400

Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
 405 410 415

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 420 425 430

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 435 440 445

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 450 455 460

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 465 470 475 480

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
485 490 495

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
500 505 510

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
515 520 525

Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
530 535 540

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
545 550 555 560

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
565 570 575

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
580 585 590

Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
595 600 605

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
610 615 620

Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
625 630 635 640

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
645 650 655

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
660 665 670

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
675 680 685

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

690

695

700

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
705 710 715 720

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
725 730 735

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 215
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 215
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<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 216

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Leu Leu Ser Gly Arg Ser Asp Gln His Gly Ser Ser Gly Thr Gln Ile
35 40 45

Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly Glu Arg
50 55 60

Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
65 70 75 80

Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr
85 90 95

Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly
100 105 110

Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser Glu Asp
115 120 125

Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr Thr Phe
130 135 140

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

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

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
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Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
195 200 205

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
210 215 220

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
225 230 235 240

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
245 250 255

Arg Gly Glu Cys
260