

eolf-seq1
SEQUENCE LISTING

<110> CureVac AG

<120> Method for in vitro transcription using an immobilized restriction enzyme

<130> C 9809-W02/RN

<150> PCT/EP2015/059559

<151> 30.04.2015

<160> 80

<170> PatentIn version 3.5

<210> 1

<211> 277

<212> PRT

<213> Escherichia coli

<400> 1

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu

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180

185

190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys
275

<210> 2
<211> 300
<212> PRT
<213> Haemophilus influenzae

<400> 2

Met Lys Lys Ser Ala Leu Glu Lys Leu Leu Ser Leu Ile Glu Asn Leu
1 5 10 15

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

Tyr Lys Leu Asn Arg Asn Glu Val Ile Glu Leu Val Arg Ser Ile Gly
35 40 45

Ile Leu Pro Glu Ala Ile Lys Pro Ser Ser Thr Gln Glu Lys Leu Phe
50 55 60

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

Leu Asn Ser Lys Pro Leu Glu Gln Arg Gly Asn Ala Gly Asp Val Ile
85 90 95

Ala Leu Ser Lys Glu Phe Asn Tyr Gly Leu Val Ala Asp Ala Lys Ser
100 105 110

Phe Arg Leu Ser Arg Thr Ala Lys Asn Gln Lys Asp Phe Lys Val Lys
115 120 125

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

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Pro Phe Phe Gln Tyr Pro Thr Thr Lys Ser Gln Ile Phe Lys Gln Ser
145 150 155 160

Leu Asp Glu Asn Val Leu Leu Phe Ser Trp Glu His Leu Ala Ile Leu
165 170 175

Leu Gln Leu Asp Leu Glu Glu Thr Asn Ile Phe Ser Phe Glu Gln Leu
180 185 190

Trp Asn Phe Pro Lys Lys Gln Ser Lys Lys Thr Ser Val Ser Asp Ala
195 200 205

Glu Asn Asn Phe Met Arg Asp Phe Asn Lys Tyr Phe Met Asp Leu Phe
210 215 220

Lys Ile Asp Lys Asp Thr Leu Asn Gln Leu Leu Gln Lys Glu Ile Asn
225 230 235 240

Phe Ile Glu Glu Arg Ser Leu Ile Glu Lys Glu Tyr Trp Lys Lys Gln
245 250 255

Ile Asn Ile Ile Lys Asn Phe Thr Arg Glu Glu Ala Ile Glu Ala Leu
260 265 270

Leu Lys Asp Ile Asn Met Ser Ser Lys Ile Glu Thr Ile Asp Ser Phe
275 280 285

Ile Lys Gly Ile Lys Ser Asn Asp Arg Leu Tyr Leu
290 295 300

<210> 3
<211> 358
<212> PRT
<213> Bacillus circulans

<400> 3

Met Asn Phe Phe Ser Leu His Pro Asn Val Tyr Ala Thr Gly Arg Pro
1 5 10 15

Lys Gly Leu Ile Gly Met Leu Glu Asn Val Trp Val Ser Asn His Thr
20 25 30

Pro Gly Glu Gly Thr Leu Tyr Leu Ile Ser Gly Phe Ser Asn Tyr Asn
35 40 45

Gly Gly Val Arg Phe Tyr Glu Thr Phe Thr Glu His Ile Asn Gln Gly
50 55 60

Gly Arg Val Ile Ala Ile Leu Gly Gly Ser Thr Ser Gln Arg Leu Ser
65 70 75 80

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Ser Arg Gln Val Val₈₅ Glu Glu Leu Leu Asn₉₀ Arg Gly Val Glu Val₉₅ His

Ile Ile Asn₁₀₀ Arg Lys Arg Ile Leu His₁₀₅ Ala Lys Leu Tyr Gly₁₁₀ Thr Ser

Asn Asn₁₁₅ Leu Gly Glu Ser Leu Val₁₂₀ Val Ser Ser Gly Asn₁₂₅ Phe Thr Gly

Pro Gly₁₃₀ Met Ser Gln Asn Ile₁₃₅ Glu Ala Ser Leu Leu₁₄₀ Leu Asp Asn Asn

Thr₁₄₅ Thr Gln Ser Met Gly₁₅₀ Phe Ser Trp Asn₁₅₅ Asp Met Ile Ser Glu Met₁₆₀

Leu Asn Gln Asn Trp₁₆₅ His Ile His Asn₁₇₀ Met Thr Asn Ala Thr Asp₁₇₅ Ala

Ser Pro Gly₁₈₀ Trp Asn Leu Leu Tyr Asp₁₈₅ Glu Arg Thr Thr Asn₁₉₀ Leu Thr

Leu Asp Glu₁₉₅ Thr Glu Arg Val Thr₂₀₀ Leu Ile Val Thr Leu₂₀₅ Gly His Ala

Asp Thr₂₁₀ Ala Arg Ile Gln Ala₂₁₅ Ala Pro Gly Thr Thr₂₂₀ Ala Gly Gln Gly

Thr₂₂₅ Gln Tyr Phe Trp Leu₂₃₀ Ser Lys Asp Ser Tyr₂₃₅ Asp Phe Phe Pro Pro₂₄₀

Leu Thr Ile Arg Asn₂₄₅ Arg Arg Gly Thr Lys₂₅₀ Ala Thr Tyr Ser Ser₂₅₅ Leu

Ile Asn Met Asn₂₆₀ Tyr Ile Asp Ile Asn₂₆₅ Tyr Thr Asp Thr Gln₂₇₀ Cys Arg

Val Thr Phe₂₇₅ Glu Ala Glu Asn Asn₂₈₀ Phe Asp Phe Arg Leu₂₈₅ Gly Thr Gly

Lys Leu₂₉₀ Arg Tyr Thr Gly Val₂₉₅ Ala Lys Ser Asn Asp₃₀₀ Ile Ala Ala Ile

Thr₃₀₅ Arg Val Gly Asp Ser₃₁₀ Asp Tyr Glu Leu Arg₃₁₅ Ile Ile Lys Gln Gly₃₂₀

Thr Pro Glu His Ser₃₂₅ Gln Leu Asp Pro Tyr₃₃₀ Ala Val Ser Phe Ile₃₃₅ Gly

Asn Arg Gly Lys₃₄₀ Arg Phe Gly Tyr Ile₃₄₅ Ser Asn Glu Glu Phe₃₅₀ Gly Arg

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Ile Ile Gly Val Thr Phe
355

<210> 4
<211> 277
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI K277C

<400> 4

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
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210

215

220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Cys
275

<210> 5
<211> 277
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI K277C, C218A

<400> 5

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ala Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Cys
275

<210> 6
<211> 277
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI K277C, C218S

<400> 6

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
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100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Cys
275

<210> 7
<211> 290
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI 278(12xG)C

<400> 7

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

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Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
 50 55 60
 Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
 65 70 75 80
 Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
 85 90 95
 Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
 100 105 110
 Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
 115 120 125
 Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
 130 135 140
 Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
 145 150 155 160
 Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr
 165 170 175
 Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
 180 185 190
 Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
 195 200 205
 Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
 210 215 220
 His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
 225 230 235 240
 Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
 245 250 255
 Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
 260 265 270
 Gln Leu Thr Ser Lys Gly Gly Gly Gly Gly Gly Gly Gly Gly
 275 280 285
 Gly Cys
 290

<210> 8
 <211> 290
 <212> PRT

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<213> Artificial sequence

<220>

<223> EcoRI 278(12xG)C, C218A

<400> 8

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ala Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
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250

245

255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
275 280 285

Gly Cys
290

<210> 9
<211> 290
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI 278(12xG)C, C218S

<400> 9

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

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Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
275 280 285

Gly Cys
290

<210> 10
<211> 300
<212> PRT
<213> Artificial sequence

<220>
<223> HindIII L300C

<400> 10

Met Lys Lys Ser Ala Leu Glu Lys Leu Leu Ser Leu Ile Glu Asn Leu
1 5 10 15

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

Tyr Lys Leu Asn Arg Asn Glu Val Ile Glu Leu Val Arg Ser Ile Gly
35 40 45

Ile Leu Pro Glu Ala Ile Lys Pro Ser Ser Thr Gln Glu Lys Leu Phe
50 55 60

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

Leu Asn Ser Lys Pro Leu Glu Gln Arg Gly Asn Ala Gly Asp Val Ile
85 90 95

Ala Leu Ser Lys Glu Phe Asn Tyr Gly Leu Val Ala Asp Ala Lys Ser

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100 105 110

Phe Arg Leu Ser Arg Thr Ala Lys Asn Gln Lys Asp Phe Lys Val Lys
115 120 125

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

Pro Phe Phe Gln Tyr Pro Thr Thr Lys Ser Gln Ile Phe Lys Gln Ser
145 150 155 160

Leu Asp Glu Asn Val Leu Leu Phe Ser Trp Glu His Leu Ala Ile Leu
165 170 175

Leu Gln Leu Asp Leu Glu Glu Thr Asn Ile Phe Ser Phe Glu Gln Leu
180 185 190

Trp Asn Phe Pro Lys Lys Gln Ser Lys Lys Thr Ser Val Ser Asp Ala
195 200 205

Glu Asn Asn Phe Met Arg Asp Phe Asn Lys Tyr Phe Met Asp Leu Phe
210 215 220

Lys Ile Asp Lys Asp Thr Leu Asn Gln Leu Leu Gln Lys Glu Ile Asn
225 230 235 240

Phe Ile Glu Glu Arg Ser Leu Ile Glu Lys Glu Tyr Trp Lys Lys Gln
245 250 255

Ile Asn Ile Ile Lys Asn Phe Thr Arg Glu Glu Ala Ile Glu Ala Leu
260 265 270

Leu Lys Asp Ile Asn Met Ser Ser Lys Ile Glu Thr Ile Asp Ser Phe
275 280 285

Ile Lys Gly Ile Lys Ser Asn Asp Arg Leu Tyr Cys
290 295 300

<210> 11
<211> 301
<212> PRT
<213> Artificial sequence

<220>
<223> HindIII 301C

<400> 11

Met Lys Lys Ser Ala Leu Glu Lys Leu Leu Ser Leu Ile Glu Asn Leu
1 5 10 15

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

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Tyr Lys Leu Asn Arg Asn Glu Val Ile Glu Leu Val Arg Ser Ile Gly
 35 40 45
 Ile Leu Pro Glu Ala Ile Lys Pro Ser Ser Thr Gln Glu Lys Leu Phe
 50 55 60
 Ser Lys Ala Gly Asp Ile Val Leu Ala Lys Ala Phe Gln Leu Leu Asn
 65 70 75 80
 Leu Asn Ser Lys Pro Leu Glu Gln Arg Gly Asn Ala Gly Asp Val Ile
 85 90 95
 Ala Leu Ser Lys Glu Phe Asn Tyr Gly Leu Val Ala Asp Ala Lys Ser
 100 105 110
 Phe Arg Leu Ser Arg Thr Ala Lys Asn Gln Lys Asp Phe Lys Val Lys
 115 120 125
 Ala Leu Ser Glu Trp Arg Glu Asp Lys Asp Tyr Ala Val Leu Thr Ala
 130 135 140
 Pro Phe Phe Gln Tyr Pro Thr Thr Lys Ser Gln Ile Phe Lys Gln Ser
 145 150 155 160
 Leu Asp Glu Asn Val Leu Leu Phe Ser Trp Glu His Leu Ala Ile Leu
 165 170 175
 Leu Gln Leu Asp Leu Glu Glu Thr Asn Ile Phe Ser Phe Glu Gln Leu
 180 185 190
 Trp Asn Phe Pro Lys Lys Gln Ser Lys Lys Thr Ser Val Ser Asp Ala
 195 200 205
 Glu Asn Asn Phe Met Arg Asp Phe Asn Lys Tyr Phe Met Asp Leu Phe
 210 215 220
 Lys Ile Asp Lys Asp Thr Leu Asn Gln Leu Leu Gln Lys Glu Ile Asn
 225 230 235 240
 Phe Ile Glu Glu Arg Ser Leu Ile Glu Lys Glu Tyr Trp Lys Lys Gln
 245 250 255
 Ile Asn Ile Ile Lys Asn Phe Thr Arg Glu Glu Ala Ile Glu Ala Leu
 260 265 270
 Leu Lys Asp Ile Asn Met Ser Ser Lys Ile Glu Thr Ile Asp Ser Phe
 275 280 285
 Ile Lys Gly Ile Lys Ser Asn Asp Arg Leu Tyr Leu Cys
 290 295 300

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<210> 12
<211> 359
<212> PRT
<213> Artificial sequence

<220>
<223> BciVI 359C

<400> 12

Met Asn Phe Phe Ser Leu His Pro Asn Val Tyr Ala Thr Gly Arg Pro
1 5 10 15

Lys Gly Leu Ile Gly Met Leu Glu Asn Val Trp Val Ser Asn His Thr
20 25 30

Pro Gly Glu Gly Thr Leu Tyr Leu Ile Ser Gly Phe Ser Asn Tyr Asn
35 40 45

Gly Gly Val Arg Phe Tyr Glu Thr Phe Thr Glu His Ile Asn Gln Gly
50 55 60

Gly Arg Val Ile Ala Ile Leu Gly Gly Ser Thr Ser Gln Arg Leu Ser
65 70 75 80

Ser Arg Gln Val Val Glu Glu Leu Leu Asn Arg Gly Val Glu Val His
85 90 95

Ile Ile Asn Arg Lys Arg Ile Leu His Ala Lys Leu Tyr Gly Thr Ser
100 105 110

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

Pro Gly Met Ser Gln Asn Ile Glu Ala Ser Leu Leu Leu Asp Asn Asn
130 135 140

Thr Thr Gln Ser Met Gly Phe Ser Trp Asn Asp Met Ile Ser Glu Met
145 150 155 160

Leu Asn Gln Asn Trp His Ile His Asn Met Thr Asn Ala Thr Asp Ala
165 170 175

Ser Pro Gly Trp Asn Leu Leu Tyr Asp Glu Arg Thr Thr Asn Leu Thr
180 185 190

Leu Asp Glu Thr Glu Arg Val Thr Leu Ile Val Thr Leu Gly His Ala
195 200 205

Asp Thr Ala Arg Ile Gln Ala Ala Pro Gly Thr Thr Ala Gly Gln Gly
210 215 220

Thr Gln Tyr Phe Trp Leu Ser Lys Asp Ser Tyr Asp Phe Phe Pro Pro

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Ile Ile Asn Arg Lys Arg Ile Leu His Ala Lys Leu Tyr Gly Thr Ser
100 105 110

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

Pro Gly Met Ser Gln Asn Ile Glu Ala Ser Leu Leu Leu Asp Asn Asn
130 135 140

Thr Thr Gln Ser Met Gly Phe Ser Trp Asn Asp Met Ile Ser Glu Met
145 150 155 160

Leu Asn Gln Asn Trp His Ile His Asn Met Thr Asn Ala Thr Asp Ala
165 170 175

Ser Pro Gly Trp Asn Leu Leu Tyr Asp Glu Arg Thr Thr Asn Leu Thr
180 185 190

Leu Asp Glu Thr Glu Arg Val Thr Leu Ile Val Thr Leu Gly His Ala
195 200 205

Asp Thr Ala Arg Ile Gln Ala Ala Pro Gly Thr Thr Ala Gly Gln Gly
210 215 220

Thr Gln Tyr Phe Trp Leu Ser Lys Asp Ser Tyr Asp Phe Phe Pro Pro
225 230 235 240

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

Ile Asn Met Asn Tyr Ile Asp Ile Asn Tyr Thr Asp Thr Gln Ala Arg
260 265 270

Val Thr Phe Glu Ala Glu Asn Asn Phe Asp Phe Arg Leu Gly Thr Gly
275 280 285

Lys Leu Arg Tyr Thr Gly Val Ala Lys Ser Asn Asp Ile Ala Ala Ile
290 295 300

Thr Arg Val Gly Asp Ser Asp Tyr Glu Leu Arg Ile Ile Lys Gln Gly
305 310 315 320

Thr Pro Glu His Ser Gln Leu Asp Pro Tyr Ala Val Ser Phe Ile Gly
325 330 335

Asn Arg Gly Lys Arg Phe Gly Tyr Ile Ser Asn Glu Glu Phe Gly Arg
340 345 350

Ile Ile Gly Val Thr Phe Cys
355

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<210> 14
<211> 359
<212> PRT
<213> Artificial sequence

<220>
<223> BciVI 359C, C271S

<400> 14

Met Asn Phe Phe Ser Leu His Pro Asn Val Tyr Ala Thr Gly Arg Pro
1 5 10 15

Lys Gly Leu Ile Gly Met Leu Glu Asn Val Trp Val Ser Asn His Thr
20 25 30

Pro Gly Glu Gly Thr Leu Tyr Leu Ile Ser Gly Phe Ser Asn Tyr Asn
35 40 45

Gly Gly Val Arg Phe Tyr Glu Thr Phe Thr Glu His Ile Asn Gln Gly
50 55 60

Gly Arg Val Ile Ala Ile Leu Gly Gly Ser Thr Ser Gln Arg Leu Ser
65 70 75 80

Ser Arg Gln Val Val Glu Glu Leu Leu Asn Arg Gly Val Glu Val His
85 90 95

Ile Ile Asn Arg Lys Arg Ile Leu His Ala Lys Leu Tyr Gly Thr Ser
100 105 110

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

Pro Gly Met Ser Gln Asn Ile Glu Ala Ser Leu Leu Leu Asp Asn Asn
130 135 140

Thr Thr Gln Ser Met Gly Phe Ser Trp Asn Asp Met Ile Ser Glu Met
145 150 155 160

Leu Asn Gln Asn Trp His Ile His Asn Met Thr Asn Ala Thr Asp Ala
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Ser Pro Gly Trp Asn Leu Leu Tyr Asp Glu Arg Thr Thr Asn Leu Thr
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Leu Asp Glu Thr Glu Arg Val Thr Leu Ile Val Thr Leu Gly His Ala
195 200 205

Asp Thr Ala Arg Ile Gln Ala Ala Pro Gly Thr Thr Ala Gly Gln Gly
210 215 220

Thr Gln Tyr Phe Trp Leu Ser Lys Asp Ser Tyr Asp Phe Phe Pro Pro
Page 18

eof-seq1

225 230 235 240

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

Ile Asn Met Asn Tyr Ile Asp Ile Asn Tyr Thr Asp Thr Gln Ser Arg
 260 265 270

Val Thr Phe Glu Ala Glu Asn Asn Phe Asp Phe Arg Leu Gly Thr Gly
 275 280 285

Lys Leu Arg Tyr Thr Gly Val Ala Lys Ser Asn Asp Ile Ala Ala Ile
 290 295 300

Thr Arg Val Gly Asp Ser Asp Tyr Glu Leu Arg Ile Ile Lys Gln Gly
305 310 315 320

Thr Pro Glu His Ser Gln Leu Asp Pro Tyr Ala Val Ser Phe Ile Gly
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Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
 35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
 85 90 95

eof-seq1

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
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Gln Leu Thr Ser Lys Cys
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20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
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eo1f-seq1

35

40

45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
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Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80
Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95
Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
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Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125
Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140
Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
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Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr
165 170 175
Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190
Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205
Tyr Gly Met Pro Ile Asn Ser Asn Leu Ala Ile Asn Lys Phe Val Asn
210 215 220
His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240
Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255
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Gln Leu Thr Ser Lys Cys
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eof-seq1

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<223> EcoRI 278C, C218S

<400> 17

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Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35      40      45
Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50      55      60
Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65      70      75      80
Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85      90      95
Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100     105     110
Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115     120     125
Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130     135     140
Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145     150     155     160
Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr
165     170     175
Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180     185     190
Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195     200     205
Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210     215     220
His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225     230     235     240
Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
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eof-seq1

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
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Gln Leu Thr Ser Lys Cys
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eof-seq1

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Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
 35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
 50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
 65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
 85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
 100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
 115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
 130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu

eo1f-seq1

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Val Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Gly Gly Gly Gly Gly
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Gly Cys
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<212> PRT
<213> Artificial sequence

<220>
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<400> 22

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Page 28

co1f-seq1

20

25

30

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 Glu Ile Asn Glu Ala Leu₇₀ Lys Lys Ile Asp Pro₇₅ Asp Leu Gly Gly Thr₈₀
 Leu Phe Val Ser Asn₈₅ Ser Ser Ile Lys Pro₉₀ Asp Gly Gly Ile Val₉₅ Glu
 Val Lys Asp Asp₁₀₀ Tyr Gly Glu Trp Arg₁₀₅ Val Val Leu Val Ala₁₁₀ Glu Ala
 Lys His Gln₁₁₅ Gly Lys Asp Ile Ile₁₂₀ Asn Ile Arg Asn Gly₁₂₅ Leu Leu Val
 Gly Lys₁₃₀ Arg Gly Asp Gln Asp₁₃₅ Leu Met Ala Ala Gly₁₄₀ Asn Ala Ile Glu
 Arg Ser His Lys Asn Ile₁₅₀ Ser Glu Ile Ala Asn₁₅₅ Phe Met Leu Ser Glu₁₆₀
 Ser His Phe Pro Tyr₁₆₅ Val Leu Phe Leu Glu₁₇₀ Gly Ser Asn Phe Leu₁₇₅ Thr
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 Tyr Gly₂₁₀ Met Pro Ile Asn Ser₂₁₅ Asn Leu Val Ile Asn₂₂₀ Lys Phe Val Asn
 His Lys Asp Lys Ser Ile₂₃₀ Met Leu Gln Ala Ala₂₃₅ Ser Ile Tyr Thr Gln₂₄₀
 Gly Asp Gly Arg Glu₂₄₅ Trp Asp Ser Lys Ile₂₅₀ Met Phe Glu Ile Met₂₅₅ Phe
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<210> 23

eof-seq1

<211> 284
 <212> PRT
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Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50    55    60
Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65    70    75
Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85    90    95
Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100   105  110
Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115   120  125
Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130   135  140
Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145   150  155
Ser His Phe Pro Tyr Val Leu Phe Leu Glu Gly Ser Asn Phe Leu Thr
165   170  175
Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180   185  190
Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195   200  205
Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
210   215  220
His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225   230  235  240
  
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co1f-seq1

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Gln Leu Thr Ser Lys His His His His His His Cys
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<223> EcoRI 278HisTag-C, C218A

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Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu

eo1f-seq1

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys His His His His His Cys
275 280

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<220>
<223> EcoRI 278HisTag-C, C218V

<400> 26

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr

co1f-seq1

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
275 280 285

eolf-seq1

<210> 28

<211> 288

<212> PRT

<213> Artificial sequence

<220>

<223> EcoRI 278FlexLinker-C, C218A

<400> 28

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ala Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln

eolf-seq1																
225	230										235	240				
Gly	Asp	Gly	Arg	Glu	Trp	Asp	Ser	Lys	Ile	Met	Phe	Glu	Ile	Met	Phe	
				245					250					255		
Asp	Ile	Ser	Thr	Thr	Ser	Leu	Arg	Val	Leu	Gly	Arg	Asp	Leu	Phe	Glu	
			260					265					270			
Gln	Leu	Thr	Ser	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Cys	
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Ser	Gln	Gly	Val	Ile	Gly	Ile	Phe	Gly	Asp	Tyr	Ala	Lys	Ala	His	Asp	
			20					25					30			
Leu	Ala	Val	Gly	Glu	Val	Ser	Lys	Leu	Val	Lys	Lys	Ala	Leu	Ser	Asn	
		35					40					45				
Glu	Tyr	Pro	Gln	Leu	Ser	Phe	Arg	Tyr	Arg	Asp	Ser	Ile	Lys	Lys	Thr	
	50					55					60					
Glu	Ile	Asn	Glu	Ala	Leu	Lys	Lys	Ile	Asp	Pro	Asp	Leu	Gly	Gly	Thr	
65					70					75					80	
Leu	Phe	Val	Ser	Asn	Ser	Ser	Ile	Lys	Pro	Asp	Gly	Gly	Ile	Val	Glu	
				85					90					95		
Val	Lys	Asp	Asp	Tyr	Gly	Glu	Trp	Arg	Val	Val	Leu	Val	Ala	Glu	Ala	
			100					105					110			
Lys	His	Gln	Gly	Lys	Asp	Ile	Ile	Asn	Ile	Arg	Asn	Gly	Leu	Leu	Val	
		115					120					125				
Gly	Lys	Arg	Gly	Asp	Gln	Asp	Leu	Met	Ala	Ala	Gly	Asn	Ala	Ile	Glu	
	130					135					140					
Arg	Ser	His	Lys	Asn	Ile	Ser	Glu	Ile	Ala	Asn	Phe	Met	Leu	Ser	Glu	
145					150					155					160	
Ser	His	Phe	Pro	Tyr	Val	Leu	Phe	Leu	Glu	Gly	Ser	Asn	Phe	Leu	Thr	
				165					170					175		

eof-seq1

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
275 280 285

<210> 30

<211> 288

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<213> Artificial sequence

<220>

<223> EcoRI 278FlexLinker-C, C218V

<400> 30

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val

eo1f-seq1

115

120

125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Val Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
275 280 285

<210> 31
<211> 294
<212> PRT
<213> Artificial sequence

<220>
<223> EcoRI 278-FlexLinker-HisTag-C

<400> 31

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

eolff-seql

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Cys Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His
275 280 285

His His His His His Cys
290

<210> 32

<211> 294

<212> PRT

<213> Artificial sequence

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<223> EcoRI 278-FlexLinker-HisTag-C, C218A

eo1f-seq1

<400> 32

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ala Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu

eolf-seq1															
260				265				270							
Gln	Leu	Thr	Ser	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	His
		275					280					285			
His	His	His	His	His	Cys										
290															
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1				5					10					15	
Ser	Gln	Gly	Val	Ile	Gly	Ile	Phe	Gly	Asp	Tyr	Ala	Lys	Ala	His	Asp
			20					25					30		
Leu	Ala	Val	Gly	Glu	Val	Ser	Lys	Leu	Val	Lys	Lys	Ala	Leu	Ser	Asn
		35					40					45			
Glu	Tyr	Pro	Gln	Leu	Ser	Phe	Arg	Tyr	Arg	Asp	Ser	Ile	Lys	Lys	Thr
	50					55					60				
Glu	Ile	Asn	Glu	Ala	Leu	Lys	Lys	Ile	Asp	Pro	Asp	Leu	Gly	Gly	Thr
65					70					75					80
Leu	Phe	Val	Ser	Asn	Ser	Ser	Ile	Lys	Pro	Asp	Gly	Gly	Ile	Val	Glu
				85					90					95	
Val	Lys	Asp	Asp	Tyr	Gly	Glu	Trp	Arg	Val	Val	Leu	Val	Ala	Glu	Ala
			100					105					110		
Lys	His	Gln	Gly	Lys	Asp	Ile	Ile	Asn	Ile	Arg	Asn	Gly	Leu	Leu	Val
		115					120					125			
Gly	Lys	Arg	Gly	Asp	Gln	Asp	Leu	Met	Ala	Ala	Gly	Asn	Ala	Ile	Glu
	130					135					140				
Arg	Ser	His	Lys	Asn	Ile	Ser	Glu	Ile	Ala	Asn	Phe	Met	Leu	Ser	Glu
145					150					155					160
Ser	His	Phe	Pro	Tyr	Val	Leu	Phe	Leu	Glu	Gly	Ser	Asn	Phe	Leu	Thr
				165					170					175	
Glu	Asn	Ile	Ser	Ile	Thr	Arg	Pro	Asp	Gly	Arg	Val	Val	Asn	Leu	Glu
			180					185					190		

eof-seq1

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Ser Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His
275 280 285

His His His His His Cys
290

<210> 34
<211> 294
<212> PRT
<213> Artificial sequence

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<223> EcoRI 278-FlexLinker-HisTag-C, C218V

<400> 34

Met Ser Asn Lys Lys Gln Ser Asn Arg Leu Thr Glu Gln His Lys Leu
1 5 10 15

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val Lys Asp Asp Tyr Gly Glu Trp Arg Val Val Leu Val Ala Glu Ala
100 105 110

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
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eo1f-seq1

115

120

125

Gly Lys Arg Gly Asp Gln Asn Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg Ser His Lys Asn Ile Ser Glu Ile Ala Asn Phe Met Leu Ser Glu
145 150 155 160

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

Glu Asn Ile Ser Ile Thr Arg Pro Asp Gly Arg Val Val Asn Leu Glu
180 185 190

Tyr Asn Ser Gly Ile Leu Asn Arg Leu Asp Arg Leu Thr Ala Ala Asn
195 200 205

Tyr Gly Met Pro Ile Asn Ser Asn Leu Val Ile Asn Lys Phe Val Asn
210 215 220

His Lys Asp Lys Ser Ile Met Leu Gln Ala Ala Ser Ile Tyr Thr Gln
225 230 235 240

Gly Asp Gly Arg Glu Trp Asp Ser Lys Ile Met Phe Glu Ile Met Phe
245 250 255

Asp Ile Ser Thr Thr Ser Leu Arg Val Leu Gly Arg Asp Leu Phe Glu
260 265 270

Gln Leu Thr Ser Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His
275 280 285

His His His His His Cys
290

<210> 35
<211> 26
<212> PRT
<213> Artificial sequence

<220>
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<400> 35

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

Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
20 25

<210> 36
<211> 12
<212> PRT

eo1f-seq1

<213> Artificial sequence

<220>

<223> Rigid-linker_AEAAAKEAAAKA

<400> 36

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
1 5 10

<210> 37

<211> 46

<212> PRT

<213> Artificial sequence

<220>

<223> Rigid-linker

<400> 37

Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 38

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Rigid-linker (EAAAK)1

<400> 38

Glu Ala Ala Ala Lys
1 5

<210> 39

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Rigid-linker (EAAAK)2

<400> 39

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10

<210> 40

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Rigid-linker (EAAAK)3

eol-f-seq1

<400> 40

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

<210> 41

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Linker-GGG(GC)

<400> 41

Gly Gly Gly Gly
1

<210> 42

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Linker-GGGGG(GC)

<400> 42

Gly Gly Gly Gly Gly
1 5

<210> 43

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Gly-linker (G)6

<400> 43

Gly Gly Gly Gly Gly Gly
1 5

<210> 44

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Gly-linker (G)8

<400> 44

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 45

<211> 5

<212> PRT

<213> Artificial sequence

eof-seq1

<220>
<223> Linker GGS

<400> 45

Gly Gly Gly Gly Ser
1 5

<210> 46
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Linker-G4SG

<400> 46

Gly Gly Gly Gly Ser Gly
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Linker-G4SG4(GC)

<400> 47

Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 48
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Linker-(G4S)2

<400> 48

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

<210> 49
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Linker (GGGS)2

<400> 49

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

<210> 50
<211> 15
<212> PRT

eo1f-seq1

<213> Artificial sequence

<220>

<223> Linker-(GGGGS)3

<400> 50

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

<210> 51

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> Linker (GGGGS)4

<400> 51

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

Gly Gly Gly Ser
20

<210> 52

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Linker-GGGSGGGSGGGSGG(GC)

<400> 52

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

<210> 53

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Linker-GGSGGGSGGGSGG

<400> 53

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

<210> 54

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Linker-GSG

<400> 54

Gly Ser Gly Ser

eo1f-seq1

1

<210> 55
 <211> 21
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker(GC)

<400> 55

Gly Ser Gly Gly Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 1 5 10 15

Gly Gly Gly Gly ser
 20

<210> 56
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Rigid-linker

<400> 56

Pro Ala Pro Ala Pro
 1 5

<210> 57
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker-PPGSRHDKIH(GC)

<400> 57

Pro Pro Pro Gly Ser Arg His Asp Lys Ile His
 1 5 10

<210> 58
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker-SGG(GC)

<400> 58

ser Gly Gly Gly
 1

<210> 59
 <211> 4
 <212> PRT
 <213> Artificial sequence

eo1f-seq1

<220>
<223> Linker-SGS

<400> 59

Gly Ser Gly Ser
1

<210> 60
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> 19-A

<400> 60

Glu Trp Leu Lys Ala Phe Tyr Glu Lys Val Leu Glu Lys Leu Lys Glu
1 5 10 15

Leu

<210> 61
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Avi-Tag

<400> 61

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
1 5 10 15

<210> 62
<211> 26
<212> PRT
<213> Artificial sequence

<220>
<223> Calmodulin Tag

<400> 62

Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg
1 5 10 15

Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu
20 25

<210> 63
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> E-tag

<400> 63

eolf-seq1

Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg
1 5 10

<210> 64
<211> 16
<212> PRT
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Leu Glu Leu Glu Leu Lys Leu Lys Leu Glu Leu Glu Leu Lys Leu Lys
1 5 10 15

<210> 65
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<400> 65

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

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Glu Glu Glu Glu Glu Glu
1 5

<210> 67
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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 68
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eof-seq1

<400> 68

His His His His His His
1 5

<210> 69

<211> 16

<212> PRT

<213> Artificial sequence

<220>

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<400> 69

Thr Asp Lys Asp Met Thr Ile Thr Phe Thr Asn Lys Lys Asp Ala Glu
1 5 10 15

<210> 70

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<220>

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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
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<210> 72

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Met Asp Glu Lys Thr Thr Gly Trp Arg Gly Gly His Val Val Glu Gly
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Leu Ala Gly Glu Leu Glu Gln Leu Arg Ala Arg Leu Glu His His Pro
20 25 30

Gln Gly Gln Arg Glu Pro

35

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Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys
 1 5 10

<210> 74
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<400> 74

Ser Leu Ala Glu Leu Leu Asn Ala Gly Leu Gly Gly Ser
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Thr Gln Asp Pro Ser Arg Val Gly
 1 5

<210> 76
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Trp Ser His Pro Gln Phe Glu Lys
 1 5

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<400> 77

eo1f-seq1

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly
1 5 10

<210> 78
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<400> 78

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
1 5 10

<210> 79
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Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
1 5 10

<210> 80
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<400> 80

Asp Leu Tyr Asp Asp Asp Asp Lys
1 5