

eolf-seql
SEQUENCE LISTING

<110> Adamed Sp. z o.o.

<120> Anticancer fusion protein

<130> P072 02 PL

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 345

<212> PRT

<213> Artificial Sequence

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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145 150 155 160

Leu Arg Ser Lys Glu Pro Leu Gly Leu Ala Gly Arg Val Val Arg Pro
165 170 175

Leu Gly Leu Ala Gly Arg Val Val Arg Val Ala Ala His Ile Thr Gly
180 185 190

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Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
195 200 205

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

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
225 230 235 240

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
245 250 255

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
260 265 270

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
275 280 285

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
290 295 300

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
305 310 315 320

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
325 330 335

Ser Phe Phe Gly Ala Phe Leu Val Gly
340 345

<210> 2
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<400> 2

Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
1 5 10 15

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

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Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
100 105 110

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
130 135 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
145 150 155 160

Val Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg Pro Leu Gly Leu
165 170 175

Ala Gly Arg Val Val Arg Cys Asp Leu Pro Gln Thr His Ser Leu Gly
180 185 190

Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu
195 200 205

Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu
210 215 220

Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu
225 230 235 240

Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala
245 250 255

Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln
260 265 270

Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr
275 280 285

Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr
290 295 300

Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys
305 310 315 320

Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser
325 330 335

Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 340 345 eolf-seql

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<400> 3

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
 145 150 155 160

Leu Arg Ser Lys Glu Pro Leu Gly Leu Ala Gly Arg Val Val Arg Ala
 165 170 175

Ser Gly Cys Gly Pro Glu Pro Leu Gly Leu Ala Gly Arg Val Val Arg
 180 185 190

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 195 200 205

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

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Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
225 230 235 240

Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
245 250 255

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
260 265 270

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
275 280 285

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
290 295 300

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
305 310 315 320

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
325 330 335

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
340 345 350

<210> 4
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<213> Artificial Sequence

<220>
<223> artificial

<400> 4

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
1 5 10 15

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
20 25 30

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
35 40 45

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
50 55 60

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
65 70 75 80

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
85 90 95

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 Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
 100 105 110
 Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
 115 120 125
 Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
 130 135 140
 Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
 145 150 155 160
 Gly Pro Leu Gly Leu Ala Gly Arg Val Val Arg Ala Ser Gly Cys Gly
 165 170 175
 Pro Glu Pro Leu Gly Leu Ala Gly Arg Val Val Arg Cys Asp Leu Pro
 180 185 190
 Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln
 195 200 205
 Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe
 210 215 220
 Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr
 225 230 235 240
 Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser
 245 250 255
 Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe
 260 265 270
 Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile
 275 280 285
 Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile
 290 295 300
 Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu
 305 310 315 320
 Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met
 325 330 335
 Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys
 340 345 350
 Glu

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<400> 5

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
 1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
 20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
 35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
 65 70 75 80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
 85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
 100 105 110

Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Pro Leu Gly Leu
 115 120 125

Ala Gly Arg Val Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His
 130 135 140

Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser
 145 150 155 160

Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser
 165 170 175

Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu
 180 185 190

Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr
 195 200 205

Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln
 210 215 220

Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu
 225 230 235 240

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Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr
245 250 255

Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn
260 265 270

Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp
275 280 285

His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
290 295 300

<210> 6
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<213> Artificial Sequence

<220>
<223> artificial

<400> 6

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
1 5 10 15

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
20 25 30

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
35 40 45

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
50 55 60

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
65 70 75 80

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
85 90 95

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
100 105 110

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
115 120 125

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
130 135 140

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
145 150 155 160

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Gly Ala Phe Leu Val Gly Gly Gly Ser Pro Leu Gly Leu Ala Gly Arg
165 170 175

Val Val Arg Gly Gly Gly Ser Gln Asp Pro Tyr Val Lys Glu Ala Glu
180 185 190

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
195 200 205

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
210 215 220

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
225 230 235 240

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
245 250 255

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
260 265 270

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

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
290 295 300

Pro Ala Ala
305

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<213> Artificial Sequence

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<223> artificial

<400> 7

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

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Phe Phe Asn Ser Asn₈₅ Lys Lys Lys Arg Asp₉₀ Asp Phe Glu Lys Leu₉₅ Thr
 Asn Tyr Ser Val₁₀₀ Thr Asp Leu Asn₁₀₅ Val Gln Arg Lys Ala Ile₁₁₀ His Glu
 Leu Ile Gln₁₁₅ Val Met Ala Glu Leu₁₂₀ Ser Pro Ala Ala Gly₁₂₅ Ser Gly Gly
 Gly Pro₁₃₀ Leu Gly Leu Ala Gly₁₃₅ Arg Val Val Arg Gly₁₄₀ Ser Gly Gly Gly
 Glu₁₄₅ Arg Gly Pro Gln Arg₁₅₀ Val Ala Ala His Ile₁₅₅ Thr Gly Thr Arg Gly₁₆₀
 Arg Ser Asn Thr Leu₁₆₅ Ser Ser Pro Asn Ser₁₇₀ Lys Asn Glu Lys Ala₁₇₅ Leu
 Gly Arg Lys Ile₁₈₀ Asn Ser Trp Glu Ser₁₈₅ Ser Arg Ser Gly His₁₉₀ Ser Phe
 Leu Ser Asn₁₉₅ Leu His Leu Arg Asn₂₀₀ Gly Glu Leu Val Ile₂₀₅ His Glu Lys
 Gly Phe Tyr Tyr Ile Tyr Ser₂₁₅ Gln Thr Tyr Phe Arg₂₂₀ Phe Gln Glu Glu
 Ile₂₂₅ Lys Glu Asn Thr Lys₂₃₀ Asn Asp Lys Gln Met₂₃₅ Val Gln Tyr Ile Tyr₂₄₀
 Lys Tyr Thr Ser Tyr₂₄₅ Pro Asp Pro Ile Leu₂₅₀ Leu Met Lys Ser Ala₂₅₅ Arg
 Asn Ser Cys Trp₂₆₀ Ser Lys Asp Ala Glu₂₆₅ Tyr Gly Leu Tyr Ser₂₇₀ Ile Tyr
 Gln Gly Gly₂₇₅ Ile Phe Glu Leu Lys₂₈₀ Glu Asn Asp Arg Ile₂₈₅ Phe Val Ser
 Val Thr Asn Glu His Leu Ile₂₉₅ Asp Met Asp His Glu₃₀₀ Ala Ser Phe Phe
 Gly Ala Phe Leu Val Gly₃₁₀

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 <213> Artificial Sequence

<220>

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<223> artificial

<400> 8

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
1 5 10 15

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
20 25 30

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
35 40 45

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
50 55 60

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
65 70 75 80

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
85 90 95

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
100 105 110

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
115 120 125

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
130 135 140

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
145 150 155 160

Gly Ala Phe Leu Val Gly Gly Ser Gly Gly Gly Pro Leu Gly Leu Ala
165 170 175

Gly Arg Val Val Arg Gly Ser Gly Gly Gly Gln Asp Pro Tyr Val Lys
180 185 190

Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val
195 200 205

Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu
210 215 220

Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe
225 230 235 240

Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
245 250 255

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Glu Thr Ile Lys₂₆₀ Glu Asp Met Asn Val₂₆₅ Lys Phe Phe Asn Ser₂₇₀ Asn Lys

Lys Lys Arg₂₇₅ Asp Asp Phe Glu Lys₂₈₀ Leu Thr Asn Tyr Ser₂₈₅ Val Thr Asp

Leu Asn₂₉₀ Val Gln Arg Lys Ala₂₉₅ Ile His Glu Leu Ile₃₀₀ Gln Val Met Ala

Glu Leu Ser Pro Ala Ala₃₁₀

<210> 9
 <211> 317
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<220>
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<400> 9

Gln Asp Pro Tyr Val₅ Lys Glu Ala Glu Asn₁₀ Leu Lys Lys Tyr Phe Asn₁₅

Ala Gly His Ser₂₀ Asp Val Ala Asp Asn₂₅ Gly Thr Leu Phe Leu₃₀ Gly Ile

Leu Lys Asn₃₅ Trp Lys Glu Glu Ser₄₀ Asp Arg Lys Ile Met₄₅ Gln Ser Gln

Ile Val₅₀ Ser Phe Tyr Phe Lys₅₅ Leu Phe Lys Asn Phe₆₀ Lys Asp Asp Gln

Ser Ile Gln Lys Ser Val₇₀ Glu Thr Ile Lys Glu₇₅ Asp Met Asn Val Lys₈₀

Phe Phe Asn Ser Asn₈₅ Lys Lys Lys Arg Asp₉₀ Asp Phe Glu Lys Leu₉₅ Thr

Asn Tyr Ser Val₁₀₀ Thr Asp Leu Asn Val₁₀₅ Gln Arg Lys Ala Ile₁₁₀ His Glu

Leu Ile Gln Val Met Ala Glu Leu₁₂₀ Ser Pro Ala Ala Gly₁₂₅ Ser Gly Gly

Gly Pro₁₃₀ Leu Gly Leu Ala Gly₁₃₅ Ala Ser Gly Cys Gly₁₄₀ Pro Glu Arg Val

Val Arg Gly Ser Gly Gly₁₅₀ Glu Arg Gly Pro₁₅₅ Gln Arg Val Ala Ala₁₆₀

His Ile Thr Gly Thr₁₆₅ Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn₁₇₅

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Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
180 185 190

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
195 200 205

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
210 215 220

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
225 230 235 240

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
245 250 255

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
260 265 270

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
275 280 285

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
290 295 300

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
305 310 315

<210> 10
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<223> artificial

<400> 10

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

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Phe Phe Asn Ser Asn₈₅ Lys Lys Lys Arg Asp₉₀ Asp Phe Glu Lys Leu₉₅ Thr

Asn Tyr Ser Val₁₀₀ Thr Asp Leu Asn Val₁₀₅ Gln Arg Lys Ala Ile₁₁₀ His Glu

Leu Ile Gln₁₁₅ Val Met Ala Glu Leu₁₂₀ Ser Pro Ala Ala Gly₁₂₅ Ser Gly Gly

Gly Pro₁₃₀ Leu Gly Leu Ala Gly₁₃₅ Arg Val Val Arg Ala₁₄₀ Ser Gly Cys Gly

Pro Glu Gly Ser Gly Gly₁₅₀ Gly Thr Ser Glu Glu₁₅₅ Thr Ile Ser Thr Val₁₆₀

Gln Glu Lys Gln Gln₁₆₅ Asn Ile Ser Pro Leu₁₇₀ Val Arg Glu Arg Gly₁₇₅ Pro

Gln Arg Val Ala₁₈₀ Ala His Ile Thr Gly₁₈₅ Thr Arg Gly Arg Ser₁₉₀ Asn Thr

Leu Ser Ser₁₉₅ Pro Asn Ser Lys Asn₂₀₀ Glu Lys Ala Leu Gly₂₀₅ Arg Lys Ile

Asn Ser₂₁₀ Trp Glu Ser Ser Arg₂₁₅ Ser Gly His Ser Phe₂₂₀ Leu Ser Asn Leu

His₂₂₅ Leu Arg Asn Gly Glu₂₃₀ Leu Val Ile His Glu₂₃₅ Lys Gly Phe Tyr Tyr₂₄₀

Ile Tyr Ser Gln Thr₂₄₅ Tyr Phe Arg Phe Gln₂₅₀ Glu Glu Ile Lys Glu₂₅₅ Asn

Thr Lys Asn Asp₂₆₀ Lys Gln Met Val Gln₂₆₅ Tyr Ile Tyr Lys Tyr₂₇₀ Thr Ser

Tyr Pro Asp₂₇₅ Pro Ile Leu Leu Met₂₈₀ Lys Ser Ala Arg Asn₂₈₅ Ser Cys Trp

Ser Lys₂₉₀ Asp Ala Glu Tyr Gly₂₉₅ Leu Tyr Ser Ile Tyr₃₀₀ Gln Gly Gly Ile

Phe Glu Leu Lys Glu Asn₃₁₀ Asp Arg Ile Phe Val₃₁₅ Ser Val Thr Asn Glu₃₂₀

His Leu Ile Asp Met₃₂₅ Asp His Glu Ala Ser₃₃₀ Phe Phe Gly Ala Phe₃₃₅ Leu

Val Gly

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<210> 11
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> artificial

<400> 11

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
 1 5 10 15

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
 20 25 30

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
 35 40 45

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
 50 55 60

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
 65 70 75 80

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
 85 90 95

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
 100 105 110

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
 115 120 125

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
 130 135 140

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
 145 150 155 160

Gly Ala Phe Leu Val Gly Gly Ser Gly Gly Gly Ala Ser Gly Cys Gly
 165 170 175

Pro Glu Pro Leu Gly Leu Ala Gly Arg Val Val Arg Gly Ser Gly Gly
 180 185 190

Gly Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
 195 200 205

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
 210 215 220

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
 225 230 235 240

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Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
245 250 255

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
260 265 270

Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu
275 280 285

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

Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala
305 310 315

<210> 12
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<220>
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<400> 12

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile Asp Glu
100 105 110

Leu Ile Gln Val Met Ala Glu Phe Ser Thr Glu Glu Gln Gln Glu Gly
115 120 125

Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly
130 135 140

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His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys
145 150 155 160

Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val
165 170 175

Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile
180 185 190

Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe
195 200 205

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

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

Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys
245 250 255

Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Pro Leu Gly Leu
260 265 270

Ala Gly Arg Val Val Arg Gly Ser Gly Gly Gly Glu Arg Gly Pro Gln
275 280 285

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
290 295 300

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
305 310 315 320

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
325 330 335

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
340 345 350

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
355 360 365

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
370 375 380

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
385 390 395 400

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
405 410 415

self-seq1

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
420 425 430

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
435 440 445

Gly

<210> 13
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial

<400> 13

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
1 5 10 15

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
20 25 30

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
35 40 45

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
50 55 60

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
65 70 75 80

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
85 90 95

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
100 105 110

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
115 120 125

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
130 135 140

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
145 150 155 160

Gly Ala Phe Leu Val Gly Gly Ser Gly Gly Gly Pro Leu Gly Leu Ala
165 170 175

Gly Arg Val Val Arg Gly Ser Gly Gly Gly Gln Asp Pro Tyr Val Lys
180 185 190

eolf-seql

Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val
195 200 205

Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu
210 215 220

Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe
225 230 235 240

Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
245 250 255

Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys
260 265 270

Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp
275 280 285

Leu Asn Val Gln Arg Lys Ala Ile Asp Glu Leu Ile Gln Val Met Ala
290 295 300

Glu Phe Ser Thr Glu Glu Gln Gln Glu Gly Pro Tyr Val Lys Glu Ala
305 310 315 320

Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp
325 330 335

Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser
340 345 350

Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu
355 360 365

Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr
370 375 380

Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
385 390 395 400

Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn
405 410 415

Val Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu
420 425 430

Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe
435 440 445

Arg

eolf-seql

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 <211> 456
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 14

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Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
 20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
 35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
 65 70 75 80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
 85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile Asp Glu
 100 105 110

Leu Ile Gln Val Met Ala Glu Phe Ser Thr Glu Glu Gln Gln Glu Gly
 115 120 125

Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly
 130 135 140

His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys
 145 150 155 160

Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val
 165 170 175

Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile
 180 185 190

Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe
 195 200 205

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

eolf-seql

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

Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys
245 250 255

Arg Ser Gln Met Leu Phe Arg Gly Ser Gly Gly Gly Pro Leu Gly Leu
260 265 270

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

Gly Gly Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
290 295 300

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
305 310 315 320

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
325 330 335

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
340 345 350

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
355 360 365

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
370 375 380

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
385 390 395 400

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
405 410 415

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
420 425 430

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
435 440 445

Phe Phe Gly Ala Phe Leu Val Gly
450 455

<210> 15
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial

eolf-seql

<400> 15

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
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Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
20 25 30

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
35 40 45

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
50 55 60

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
65 70 75 80

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
85 90 95

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
100 105 110

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
115 120 125

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
130 135 140

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
145 150 155 160

Gly Ala Phe Leu Val Gly Gly Ser Gly Gly Gly Pro Leu Gly Leu Ala
165 170 175

Gly Ala Ser Gly Cys Gly Pro Glu Arg Val Val Arg Gly Ser Gly Gly
180 185 190

Gly Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe
195 200 205

Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly
210 215 220

Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser
225 230 235 240

Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp
245 250 255

Gln Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val
260 265 270

eolf-seql

Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu
275 280 285

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

Glu Leu Ile Gln Val Met Ala Glu Phe Ser Thr Glu Glu Gln Gln Glu
305 310 315 320

Gly Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala
325 330 335

Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu
340 345 350

Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile
355 360 365

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

Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe
385 390 395 400

Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr Asn
405 410 415

Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu Leu
420 425 430

Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg
435 440 445

Lys Arg Ser Gln Met Leu Phe Arg
450 455

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<213> Homo sapiens

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<309> 1996-10-01
<313> (1)..(281)

<400> 16

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20 25 30

eolf-seql

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 17
<211> 150

eolf-seql

<212> PRT
<213> Homo sapiens

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<309> 2001-01-08
<313> (24)..(173)

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<309> 2001-01-08
<313> (24)..(173)

<400> 17

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
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Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130 135 140

Ala Glu Ile Met Arg Ser
145 150

<210> 18
<211> 124
<212> PRT
<213> Homo sapiens

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<309> 2002-05-16
<313> (2)..(125)

<300>
<308> GenBank/AAM28885.1
<309> 2002-05-16

eolf-seql

<313> (2)..(125)

<400> 18

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile His Glu
100 105 110

Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala
115 120

<210> 19

<211> 263

<212> PRT

<213> Homo sapiens

<300>

<308> PDB/1EKUA

<309> 2008-09-24

<313> (2)..(264)

<400> 19

Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn
1 5 10 15

Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
20 25 30

Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln
35 40 45

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

Ser Ile Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys
65 70 75 80

eo1f-seq1

Phe Phe Asn Ser Asn Lys Lys Lys Arg Asp Asp Phe Glu Lys Leu Thr
85 90 95

Asn Tyr Ser Val Thr Asp Leu Asn Val Gln Arg Lys Ala Ile Asp Glu
100 105 110

Leu Ile Gln Val Met Ala Glu Phe Ser Thr Glu Glu Gln Gln Glu Gly
115 120 125

Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr Phe Asn Ala Gly
130 135 140

His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile Leu Lys
145 150 155 160

Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val
165 170 175

Ser Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile
180 185 190

Gln Lys Ser Val Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe
195 200 205

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

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

Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys Thr Gly Lys Arg Lys
245 250 255

Arg Ser Gln Met Leu Phe Arg
260

<210> 20
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<220>
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<400> 20

Pro Leu Gly Leu Ala Gly
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<210> 21
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<212> PRT
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<220>

<223> artificial

<400> 21

Arg Val Val Arg
1

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial

<300>

<301> Tsutsumi Y, Onda M, Nagata S, Lee B, Kreitman RJ, Pastan I.

<302> Site-specific chemical modification with polyethylene glycol of recombinant immunotoxin anti-Tac(Fv)-PE38 (LMB-2) improves antitumor activity and reduces animal toxicity and immunogenicity.

<303> Proc Natl Acad Sci U S A.

<304> 97

<305> 15

<306> 8548-53

<307> 2000-07-18

<308> PMID/10890891

<309> 2000-07-18

<400> 22

Ala Ser Gly Cys Gly Pro Glu
1 5

<210> 23

<211> 5

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<400> 23

Ala Ala Cys Ala Ala
1 5

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<400> 24

Ser Gly Gly Cys Gly Gly Ser
1 5

<210> 25

<211> 5

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

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<400> 25

Ser Gly Cys Gly Ser
1 5

<210> 26

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> artificial

<400> 26

Gly Ser Gly Gly Gly
1 5

<210> 27

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

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<400> 27

Gly Gly Gly Ser
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<210> 28

<211> 4

<212> PRT

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<221> misc_feature

<222> (1)..(1)

<223> Xaa can be any naturally occurring amino acid

<400> 28

Xaa Gly Gly Ser
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<210> 29

<211> 1034

<212> DNA

<213> Artificial Sequence

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<400> 29

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60

eolf-seql

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gaagaattttg gtaatcagtt tcagaaagcc gaaaccattc cggttctgca tgaaatgatt      180
cagcagatttt ttaacctggt tagcaccaaa gatagcagcg cagcatggga tgaaaccctg      240
ctggataaat tttataccga actgtatcag cagctgaatg atctggaagc atgtgttatt      300
caggggtgttg gtgttaccga aacaccgctg atgaaagaag atagcattct ggccgtgcgt      360
aaatatatttc agcgcattac cctgtatctg aaagaaaaaa aatatagccc gtgtgcatgg      420
gaagtgtttc gtgcagaaat tatgcgtagc tttagcctga gcaccaatct gcaggaaagc      480
ctgcgtagca aagaaccgct ggggtctggca ggtcgtgttg ttcgtccgct ggcctggctg      540
gccgtgtggt gcgtgttgca gcacatatta ccggcacccg tggtcgtagc aataccctga      600
gcagcccga tagcaaaaat gaaaaagccc tgggtcgcaa aattaatagc tgggaaagca      660
gccgtagcgg tcatagcttt ctgagcaatc tgcattctgcg taatggtgaa ctggtgattc      720
atgaaaaagg cttttattat atttatagcc agacctatct tcgctttcag gaagaaatta      780
aagaaaatac caaaaatgat aaacaaatgg tgcagtatat ctataaatat accagctatc      840
cggatccgat tctgctgatg aaaagcgcac gtaatagctg ttggagcaaa gatgcagaat      900
atggcctgta tagcatttat caggggtggca tttttgaact gaaagaaaat gatcgcatct      960
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catttctggt gggt                                           1034

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<212> DNA
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<220>
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agcggtcata gctttctgag caatctgcat ctgcgtaatg gtgaactggg gattcatgaa      180
aaaggctttt attatatatta tagccagacc tattttcgtc ttcaggaaga aattaaagaa      240
aataccaaaa atgataaaca aatggtgcag tataatctata aatataccag ctatccggat      300
ccgattctgc tgatgaaaag cgcacgtaat agctgttgga gcaaagatgc agaatatggc      360
ctgtatagca tttatcaggg tggcattttt gaactgaaag aaaatgatcg catttttgtg      420
agcgtgacca atgaacatct gattgatatg gatcatgaag ccagcttttt tgggtgcattt      480
ctggtgggtc cgctgggtct ggcaggctcg gttgttcgtc cgctgggcct gctggccgtg      540
tgggtgtgta tctgccgcag acccatagcc tgggtagccg tcgtaccctg atgctgctgg      600
cacagatgcg tcgtattagc ctgttttagc gcctgaaaga tcgtcatgat tttggttttc      660
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eolf-seql

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ttattcaggg tgttggtggt accgaaacac cgctgatgaa agaagatagc attctggccg	900
tgcgtaaata ttttcagcgc attaccctgt atctgaaaga aaaaaaatat agcccgtgtg	960
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gaagaatttg gtaatcagtt tcagaaagcc gaaaccattc cggttctgca tgaaatgatt	180
cagcagattt ttaacctggt tagcaccaa gatagcagcg cagcatggga tgaaaccctg	240
ctggataaat ttataccga actgtatcag cagctgaatg atctggaagc atgtgttatt	300
caggggtgtg gtgttaccga aacaccgctg atgaaagaag atagcattct ggccgtgctg	360
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aattaatagc tgggaaagca gccgtagcgg tcatagcttt ctgagcaatc tgcattctgcg	720
taatggtgaa ctggtgattc atgaaaaagg cttttattat atttatagcc agacctat	780
tcgctttcag gaagaaatta aagaaaatac caaaaatgat aaacaaatgg tgcagtatat	840
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gaaagaaaat gatcgcat	1020
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 <211> 1057
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificial

eolf-seql

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ggcatagct ttctgagcaa tctgcatctg cgtaatggtg aactggtgat tcatgaaaaa 180
ggcttttatt atatttatag ccagacctat tttcgctttc aggaagaaat taaagaaaat 240
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attctgctga tgaaaagcgc acgtaatagc tgttggagca aagatgcaga atatggcctg 360
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tcatgatttt ggttttccgc aggaagaatt tggtaatcag tttcagaaaag ccgaaaccat 720
tccggttctg catgaaatga ttcagcagat ttttaacctg tttagcacca aagatagcag 780
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aaaatatagc ccgtgtgcat gggaagttgt tcgtgcagaa attatgcgta gcttttagcct 1020
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<212> DNA
<213> Artificial Sequence

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<220>
<223> artificial

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gctttctgag caatctgcat ctgcgtaatg gtgaactggt gattcatgaa aaaggctttt 600
attatattta tagccagacc tattttcgct ttcaggaaga aattaaagaa aacacaaaaa 660

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eolf-seql

atgataaaca aatggtgcag tatatctata aatataccag ctatccggat ccgattctgc	720
tgatgaaaag cgcacgtaat agctgttggg gcaaagatgc agaatatggc ctgtatagca	780
tttatcaggg tggcattttt gaactgaaag aaaatgatcg cttttttgtg agcgtgacca	840
atgaacatct gattgatatg gatcatgaag ccagcttttt tggtgcattt ctggtgggt	899

<210> 34
 <211> 857
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificial

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 <211> 928
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificial

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gatcgtaaaa tcatgcagag ccagattgtg agcttctatt ttaaactgtt caaaaatttt	180
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eolf-seql

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 <213> Artificial Sequence

<220>
 <223> artificial

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<210> 37
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eolf-seql

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<210> 38
<211> 1014
<212> DNA
<213> Artificial Sequence

<220>
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eolf-seql

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 <211> 951
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificial

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 <212> DNA
 <213> Artificial Sequence

<220>
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eolf-seql

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<212> DNA
<213> Artificial Sequence
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eolf-seql

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 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificial

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eolf-seql

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 <213> Artificial Sequence

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eolf-seql

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<210> 44
 <211> 538
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> none

<400> 44

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Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
 145 150 155 160

Leu Arg Ser Lys Glu Gly Gly Gly Gly Ser Pro Leu Gly Leu Ala Gly
 165 170 175

Arg Val Val Arg Ser Gly Gly Gly Gly Ser Glu Lys Ser Arg Leu Ser
 180 185 190

eolf-seql

Glu Gln Leu Asn Thr Ser Leu Ser Phe Ser Arg Met Ile Glu Ala Arg
195 200 205

Val Val Glu Trp Ala Cys Pro Ser Tyr Lys Lys Glu Lys Leu Tyr Leu
210 215 220

Thr Ile Arg Gln Phe Tyr Phe Arg Val Ala Leu Ile Ser Asp Glu Lys
225 230 235 240

Met Leu Pro Thr Glu Thr Val Gly Val Gly Gln Ile Val Cys Ala Glu
245 250 255

Leu Asp Asn Leu Gln Gln Tyr Leu Glu Thr Tyr Phe Lys Asp Leu Leu
260 265 270

Thr Glu Asp Trp Ala Ala Ser Ser Asp Lys Thr Ser Phe Leu Asn Phe
275 280 285

Ile Gln Gln Ile Met Glu His Leu Val Pro Ile Thr Glu Ala Lys Gln
290 295 300

Phe Gln Asn Gly Phe Glu Glu Gln Pro Phe Gly Phe Asp His Arg Asp
305 310 315 320

Lys Leu Cys Ser Phe Leu Ser Ile Arg Arg Met Gln Ala Leu Leu Met
325 330 335

Leu Thr Arg Arg Ser Gly Leu Ser His Thr Gln Pro Leu Asp Cys Pro
340 345 350

Leu Gly Leu Ala Gly Arg Val Val Arg Ala Ser Gly Cys Gly Pro Glu
355 360 365

Pro Leu Gly Leu Ala Gly Arg Val Val Arg Val Ala Ala His Ile Thr
370 375 380

Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
385 390 395 400

Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
405 410 415

Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
420 425 430

Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
435 440 445

Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
450 455 460

Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
 465 470 475 480

Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 485 490 495

Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
 500 505 510

Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
 515 520 525

Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 530 535

<210> 45
 <211> 384
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> none

<400> 45

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

Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser
 65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
 100 105 110

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

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Ile Ser Thr Asn Leu Gln Glu
 145 150 155 160

eolf-seql

Arg Leu Arg Arg Lys₁₆₅ Glu Gly Gly Ser Gly₁₇₀ Pro Leu Gly Leu Ala Gly₁₇₅

Arg Val Val Arg₁₈₀ Ala Ser Gly Cys₁₈₅ Gly₁₈₅ Pro Glu Pro Leu Gly₁₉₀ Leu Ala

Gly Arg Val₁₉₅ Val Arg Thr Ser Glu₂₀₀ Glu Thr Ile Ser Thr₂₀₅ Val Gln Glu

Lys Gln₂₁₀ Gln Asn Ile Ser Pro₂₁₅ Leu Val Arg Glu Arg₂₂₀ Gly Pro Gln Arg

Val Ala Ala His Ile Thr₂₃₀ Gly Thr Arg Gly Arg₂₃₅ Ser Asn Thr Leu Ser₂₄₀

Ser Pro Asn Ser Lys₂₄₅ Asn Glu Lys Ala Leu₂₅₀ Gly Arg Lys Ile Asn Ser₂₅₅

Trp Glu Ser Ser₂₆₀ Arg Ser Gly His Ser₂₆₅ Phe Leu Ser Asn Leu₂₇₀ His Leu

Arg Asn Gly₂₇₅ Glu Leu Val Ile His₂₈₀ Glu Lys Gly Phe Tyr₂₈₅ Tyr Ile Tyr

Ser Gln₂₉₀ Thr Tyr Phe Arg Phe₂₉₅ Gln Glu Glu Ile Lys₃₀₀ Glu Asn Thr Lys

Asn Asp Lys Gln Met Val₃₁₀ Gln Tyr Ile Tyr Lys₃₁₅ Tyr Thr Ser Tyr Pro₃₂₀

Asp Pro Ile Leu Leu₃₂₅ Met Lys Ser Ala Arg₃₃₀ Asn Ser Cys Trp Ser₃₃₅ Lys

Asp Ala Glu Tyr₃₄₀ Gly Leu Tyr Ser Ile₃₄₅ Tyr Gln Gly Gly Ile₃₅₀ Phe Glu

Leu Lys Glu₃₅₅ Asn Asp Arg Ile Phe₃₆₀ Val Ser Val Thr Asn₃₆₅ Glu His Leu

Ile Asp Met Asp His Glu Ala₃₇₅ Ser Phe Phe Gly Ala₃₈₀ Phe Leu Val Gly

<210> 46
 <211> 351
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> none

<400> 46

eolf-seql

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
 145 150 155 160

Leu Arg Ser Lys Glu Gly Gly Gly Gly Ser Pro Leu Gly Leu Ala Gly
 165 170 175

Arg Val Val Arg Ser Gly Gly Gly Gly Ser Glu Lys Ser Arg Leu Ser
 180 185 190

Glu Gln Leu Asn Thr Ser Leu Ser Phe Ser Arg Met Ile Glu Ala Arg
 195 200 205

Val Val Glu Trp Ala Cys Pro Ser Tyr Lys Lys Glu Lys Leu Tyr Leu
 210 215 220

Thr Ile Arg Gln Phe Tyr Phe Arg Val Ala Leu Ile Ser Asp Glu Lys
 225 230 235 240

Met Leu Pro Thr Glu Thr Val Gly Val Gly Gln Ile Val Cys Ala Glu
 245 250 255

Leu Asp Asn Leu Gln Gln Tyr Leu Glu Thr Tyr Phe Lys Asp Leu Leu
 260 265 270

self-seq1

Thr Glu Asp Trp Ala Ala Ser Ser Asp Lys Thr Ser Phe Leu Asn Phe
275 280 285

Ile Gln Gln Ile Met Glu His Leu Val Pro Ile Thr Glu Ala Lys Gln
290 295 300

Phe Gln Asn Gly Phe Glu Glu Gln Pro Phe Gly Phe Asp His Arg Asp
305 310 315 320

Lys Leu Cys Ser Phe Leu Ser Ile Arg Arg Met Gln Ala Leu Leu Met
325 330 335

Leu Thr Arg Arg Ser Gly Leu Ser His Thr Gln Pro Leu Asp Cys
340 345 350

<210> 47

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> none

<400> 47

Ser Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

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

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Ile Ser Thr Asn Leu Gln Glu
145 150 155 160

eof-seql

Arg Leu Arg Arg Lys Glu
165

<210> 48
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> none

<400> 48
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gaagaatttg gaaatcaatt tcaaaaggca gaaacaatac cagtgttaca tgaaatgata 180
caacaaatat ttaattttatt ttcaacaaag gattcatcag cagcatggga tgaaacatta 240
ttagataagt ttatatacaga attatatcaa caattaaatg atttagaagc atgtgtgata 300
caaggagtgg gaggtagaca aacaccatta atgaaggaag attcaatatt agcagtgaga 360
aagtattttc aaagaataac atttatattta aaggaaaaga agtattcacc atgtgcatgg 420
gaagtgggtga gaggcagaat aatgagatca ttttcattat caacaaattt acaagaatca 480
ttaagatcaa aggaaggagg agggagatca ccattaggat tagcaggaag agtgggtgaga 540
tcaggaggag gaggatcaga aaagtcaaga ttatcagaac aattaaatac atcattatca 600
ttttcaagaa tgatagaagc aagagtgggtg gaatgggcat gtccatcata taagaaggaa 660
aagttatatt taacaataag acaattttat ttttagagtgg cattaatatc agatgaaaag 720
atgttaccaa cagaaacagt gggagtggga caaatagtgt gtgcagaatt agataattta 780
caacaatatt tagaaacata ttttaaggat ttattaacag aagattgggc agcatcatca 840
gataagacat ctttttttaa ttttatacaa caaataatgg aacatttagt gccataaaca 900
gaagcaaagc aatttcaaaa tggatttgaa gaacaacat ttggatttga tcatagagat 960
aagttatggt cttttttatc aataagaaga atgcaagcat tattaatggt aacaagaaga 1020
tcaggattat cacatacaca accattagat tgtccattag gattagcagg aagagtgggtg 1080
agagcatcag gatgtggacc agaaccatta ggattagcag gaagagtggg gagagtggca 1140
gcacataata caggaacaag aggaagatca aatacattat catcaccaa ttcaaagaat 1200
gaaaaggcat taggaagaaa gataaattca tgggaatcat caagatcagg acattcattt 1260
ttatcaaatt tacatttaag aaatggagaa ttagtgatac atgaaaaggg attttattat 1320
atatattcac aaacatattt tagattttcaa gaagaaataa aggaaaatac aaagaatgat 1380
aagcaaattg tgcaatatat atataagtat acatcatatc cagatccaat attattaatg 1440
aagtcagcaa gaaattcatg ttggtcaaag gatgcagaat atggattata ttcaatatat 1500
caaggaggaa tatttgaatt aaaggaaaat gatagaatat ttgtgtcagt gacaaatgaa 1560
catttaatag atatggatca tgaagcatca ttttttggag cttttttagt ggga 1614

eolf-seql

<210> 49
 <211> 1152
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> none

<400> 49
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 gaagaatttg atggaaatca atttcaaaag gcacaagcaa tatcagtgtt acatgaaatg 180
 atacaacaaa catttaattt attttcaaca aaggattcat cagcagcatg ggatgaatca 240
 ttattagaaa agttttatac agaattatat caacaattaa atgattttaga agcatgtgtg 300
 atacaagaag tgggagtggg agaaacacca ttaatgaatg tggattcaat attagcagtg 360
 aagaagtatt ttcaaagaat aacattatat ttaacagaaa agaagtattc accatgtgca 420
 tgggaagtgg tgagagcaga aataatgaga tcattttcaa tatcaacaaa ttacaagaa 480
 agattaagaa gaaaggaagg aggatcagga ccattaggat tagcaggaag agtggtgaga 540
 gcatcaggat gtggaccaga accattagga ttagcaggaa gagtggtgag aacatcagaa 600
 gaaacaatat caacagtgcg agaaaagcaa caaaatatat caccattagt gagagaaaga 660
 ggaccacaaa gagtggcagc acatataaca ggaacaagag gaagatcaaa tacattatca 720
 tcaccaaatt caaagaatga aaaggcatta ggaagaaaga taaattcatg ggaatcatca 780
 agatcaggac attcattttt atcaaattta catttaagaa atggagaatt agtgatacat 840
 gaaaagggat tttattatat atattcacia acatatttta gatttcaaga agaaataaag 900
 gaaaatacaa agaattgataa gcaaatggtg caatatatat ataagtatac atcatatcca 960
 gatccaatat tattaatgaa gtcagcaaga aattcatgtt ggtcaaagga tgcagaatat 1020
 ggattatatt caatatatca aggaggaata tttgaattaa aggaaaatga tagaatattt 1080
 gtgtcagtga caaatgaaca tttaatagat atggatcatg aagcatcatt ttttggagca 1140
 tttttagtgg ga 1152

<210> 50
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> none

<400> 50

Gly Gly Ser Gly
 1