

SEQUENCE LISTING

<110> UCB BIOPHARMA spr1

<120> Tau-binding antibodies

<130> PF0031-WO-PCT

<160> 65

<170> PatentIn version 3.5

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR-L1

<400> 1

Gln Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> CDR-L2

<400> 2

Ala Ala Ser Tyr Leu Ala Ser
1 5

<210> 3

<211> 12

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<223> CDR-L3

<220>

<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa can be A or G

<400> 3

Gln Gln Xaa Tyr Thr Arg Thr Asp Ile Asp Asn Thr
1 5 10

<210> 4
<211> 10
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<213> Artificial Sequence

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<223> CDR-H1

<400> 4

Gly Ile Asp Leu Ser Thr Trp Arg Met Asn
1 5 10

<210> 5
<211> 16
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<213> Artificial Sequence

<220>
<223> CDR-H2

<400> 5

Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys Gly
1 5 10 15

<210> 6
<211> 12
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<223> CDR-H3

<220>
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<222> (6)..(6)

<223> Xaa can be A, Q, N, D or S

<400> 6

Leu Gly Ala Asn Asn Xaa Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 7

<211> 110

<212> PRT

<213> Rabbit

<220>

<221> MISC_FEATURE

<222> (91)..(91)

<223> Xaa can be A or G

<400> 7

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

Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Xaa Tyr Thr Arg Thr Asp
85 90 95

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

<210> 8

<211> 117
<212> PRT
<213> Rabbit

<220>
<221> MISC_FEATURE
<222> (100)..(100)
<223> Xaa can be A, Q, N, D or S

<400> 8

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

Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp Arg
20 25 30

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

Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys Gly
50 55 60

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

Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Leu Gly
85 90 95

Ala Asn Asn Xaa Gly Tyr Pro Leu Asp Leu Trp Gly Pro Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 9
<211> 110
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<213> Artificial Sequence

<220>

<223> murinised

<400> 9

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

Gln Arg Ala Thr Ile Ser Cys Gln Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Thr Arg Thr Asp
85 90 95

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

<210> 10

<211> 118

<212> PRT

<213> Artificial Sequence

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<223> murinised

<400> 10

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

Gly Arg Phe Ser Ile Ser Lys Asp Ser Thr Gln Val Phe Leu Lys Met
65 70 75 80

Asn Ser Leu Gln Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Leu
85 90 95

Gly Ala Asn Asn Asn Gly Tyr Pro Leu Asp Leu Trp Gly Ala Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 11
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 11

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Thr Arg Thr Asp
85 90 95

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

<210> 12
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<213> Artificial Sequence

<220>
<223> humanized

<400> 12

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Tyr Thr Arg Thr Asp
85 90 95

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

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

<220>
<223> humanized

<220>
<221> MISC_FEATURE
<222> (91)..(91)
<223> Xaa can be A or G

<400> 13

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Tyr Thr Arg Thr Asp
85 90 95

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

<210> 14
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> humanized

<400> 14

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Gln Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 15

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized

<400> 15

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Ala Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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

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<223> humanized

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Xaa can be A, Q, N, D or S

<400> 16

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Xaa Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 17
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 17

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Thr Arg Thr Asp
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 18

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized

<400> 18

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Tyr Thr Arg Thr Asp
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 19
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<220>
<221> MISC_FEATURE
<222> (91)..(91)
<223> Xaa can be A or G

<400> 19

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Xaa Tyr Thr Arg Thr Asp
85 90 95

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

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

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

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

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

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

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 20
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 20

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Gln Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

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

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

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

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

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

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

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

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

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

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

<210> 21
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 21

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Ala Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

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

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

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

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

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

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

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

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

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

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

<210> 22
<211> 447
<212> PRT
<213> Artificial Sequence

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<223> humanized

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Xaa can be A, Q, N, D or S

<400> 22

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Xaa Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

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

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

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

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

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

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

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

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

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

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

<210> 23
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 23

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Gln Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 24
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<220>
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<400> 24

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Ala Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 25
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Xaa can be A, Q, N, D or S

<400> 25

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Leu Gly Ala Asn Asn Xaa Gly Tyr Pro Leu Asp Leu Trp Gly Gln
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
450

<210> 26

<211> 330

<212> DNA

<213> Rabbit

<400> 26

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atcaagtgcc aggccagtca gaggcttagt agttacttag cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatgct gcatcctatc tggcatccgg ggtcccatca 180

cggttcaaag gcagtggatc tgggacagag ttactctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttatta ctgtcaacag ggttatacta ggactgatat tgataatact	300
ttcggcggag ggaccaaggt ggtggtcgaa	330

<210> 27
 <211> 351
 <212> DNA
 <213> Rabbit

<400> 27	
cagtcgctgg aggagtccgg gggtcgcctg gtcacgcctg ggacaccccct gacactcacc	60
tgcacagtct ctggaatcga cctcagtact tggagaatga actgggtccg ccaggctcca	120
gggaaggggc tggaatggat cggaatcatt ggtactggtg gtagaacata ctacgcgaac	180
tgggcaaaaag gccgattcac catctccaaa acctcgacca cggtggatct gaaggtcacc	240
agtccgacaa ccgaggacac ggccacctat ttctgtgcc aattgggtgc taataataat	300
ggttatcctt tggacttggt gggccgggg accctgggtca ccgtctcgag t	351

<210> 28
 <211> 330
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> murinised

<400> 28	
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atctcgtgcc aagcgtcca gtctgtctcc tcgtacttgg cctgggtatca gcagaagcca	120
ggacagccgc cgaaactcct catctacgcc gcctcatacc ttgcgtccgg agtgccttcg	180
agattcaaag gaagcggaag cggcactgag ttaccctga acatccaccc ggtggaagaa	240
gaggacgcag ccacgtacta ctgtcaacaa gggtacaccc gcaccgatat tgacaatacc	300
ttcggtggtg ggactaagct ggaaatcaag	330

<210> 29
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>

<223> murinised

<400> 29

caagtgcagc tgaaagaatc aggaccggga ctggtggcac caagccagtc cctgtcgatc	60
acctgtactg tgtccggaat cgacctctcc acctggcgca tgaattgggt ccggcagcct	120
cccggaaagg gcctcgaatg gattggcatc atcgggtactg ggggcagaac ttactacgcc	180
aattgggcga aggggcgctt ctcaatctcg aaagactcga cccaagtgtt cttgaagatg	240
aacagccttc agaccgagga taccgctacc tacttttgcg cgaggctggg agccaacaac	300
aacggttacc cgctcgatct gtggggagcc ggaacgactg tgactgtctc gagc	354

<210> 30

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> humanized

<400> 30

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ggaaaaggcgc ccaaactttt gatctacgcc gcctcgatc tggcatccgg cgtgccgtca	180
agattcagcg ggtcgggctc cggaactgac ttcaccctga ccatcagcag cctgcagcct	240
gaggactttg ccacttacta ctgccagcag ggatacacc ggaccgatat tgacaacacc	300
ttcggcgggg gaactaaggt cgaaatcaag	330

<210> 31

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> humanized

<400> 31

gatatccaaa tgaccagtc cccatcctcc ctgtccgctt ctgtcggatga ccgcgtgacc	60
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ggaaaggcgc ccaaactttt gatctacgcc gcctcgtacc tggcatccgg cgtgccgtca	180
agattcagcg ggtcgggctc cggaactgac ttcaccctga ccatcagcag cctgcagcct	240
gaggactttg ccacttacta ctgccagcag gcctacaccc ggaccgatat tgacaacacc	300
ttcggcgggg gaactaaggt cgaaatcaag	330

<210> 32
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 32	
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ccgggaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240
aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgccc gctgggagcc	300
aacaaccagg gctacccgct ggatcttttg ggacagggaa ccctcgtgac tgtctcgagt	360

<210> 33
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 33	
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acctgtactg tgtccgggat cgacttgagc acctggagga tgaactggat tcgccagcca	120
ccgggaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240

aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgcccg gctgggagcc	300
aacaacgccc gctacccgct ggatctttgg ggacagggaa ccctcgtgac tgtctcgagt	360

<210> 34
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 34	
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attacttgtc aagccagcca gtcgggtgtcc tcatacctcg cctggatatca gcagaagccg	120
ggaaaggcgc ccaaactttt gatctacgcc gcctcgtacc tggcatccgg cgtgccgtca	180
agattcagcg ggtcgggctc cggaactgac ttcaccctga ccatcagcag cctgcagcct	240
gaggactttg ccacttacta ctgccagcag ggatacacc ggaccgatat tgacaacacc	300
ttcggcgggg gaactaaggt cgaaatcaag cggaccgtgg ccgctccctc cgtgttcac	360
ttcccaccct ccgacgagca gcttaagtcc ggcaccgcct ccgtcgtgtg cctgctgaac	420
aacttctacc cccgcgaggc caagggtgcag tggaagggtg acaacgccct gcagtccggc	480
aactcccagg aatccgtcac cgagcaggac tccaaggaca gcacctactc cctgtcctcc	540
accctgaccc tgtccaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc	600
caccagggcc tgtccagccc cgtgaccaag tccttcaacc ggggcgagtg c	651

<210> 35
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 35	
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attacttgtc aagccagcca gtcgggtgtcc tcatacctcg cctggatatca gcagaagccg	120

ggaaaggcgc ccaaactttt gatctacgcc gcctcgtacc tggcatccgg cgtgccgtca	180
agattcagcg ggtcgggctc cggaactgac ttcaccctga ccatcagcag cctgcagcct	240
gaggactttg ccacttacta ctgccagcag gcctacaccc ggaccgatat tgacaacacc	300
ttcggcgggg gaactaaggt cgaaatcaag cgtacggtag cggcccatc tgtcttcac	360
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat	420
aacttctatc ccagagaggc caaagtacag tggaaggtagg ataacgccct ccaatcgggt	480
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc	540
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc	600
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t	651

<210> 36
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 36	
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acctgtactg tgtccgggat cgacttgagc acctggagga tgaactggat tcgccagcca	120
ccgggaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240
aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgcccg gctgggagcc	300
aacaaccagg gctacccgct ggatcttttg ggacagggaa ccctcgtgac tgtctcgagt	360
gcctccacca agggcccctc cgtgttccct ctggcccctt gctcccggtc cacctccgag	420
tctaccgccg ctctgggctg cctggtcaag gactacttcc ccgagcccgt gacagtgtcc	480
tggaactctg gcgccctgac ctccggcgtg cacaccttcc ctgccgtgct gcagtcctcc	540
ggcctgtact ccctgtcctc cgtcgtgacc gtgccctcct ccagcctggg caccaagacc	600
tacacctgta acgtggacca caagccctcc aacaccaagg tggacaagcg ggtggaatct	660

aagtacggcc ctccctgccc cccctgccct gcccctgaat ttctgggcgg accttccgtg	720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatct cccggacccc cgaagtgacc	780
tgcgtgggtg tggacgtgtc ccaggaagat cccgagggtcc agttcaattg gtacgtggac	840
ggcgtggaag tgcacaatgc caagaccaag cccagagagg aacagttcaa ctccacctac	900
cgggtgggtg ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag	960
tgcaagggtg ccaacaaggg cctgccctcc agcatcgaaa agaccatctc caaggccaag	1020
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aaccaggtgt ccctgacctg tctggtcaag ggcttctacc cctccgacat tgccgtggaa	1140
tgggagtcca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc	1200
gacggctcct tcttcctgta ctctcggctg accgtggaca agtcccgggtg gcaggaaggc	1260
aacgtcttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc	1320
ctgtccctga gcctgggcaa g	1341

<210> 37
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 37	
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acctgtactg tgtccgggat cgacttgagc acctggagga tgaactggat tcgccagcca	120
ccgggaaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240
aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgcccc gctgggagcc	300
aacaacgccg gctacccgct ggatcttttg ggacagggaa ccctcgtgac tgtctcgagt	360
gcctccacca agggccccctc cgtgttccct ctggccccctt gctcccgggtc cacctccgag	420
tctaccgccg ctctgggctg cctggtcaag gactacttcc ccgagcccgt gacagtgtcc	480

tggaactctg gcgccctgac ctccggcgtg cacaccttcc ctgccgtgct gcagtcctcc	540
ggcctgtact ccctgtcctc cgtcgtgacc gtgccctcct ccagcctggg caccaagacc	600
tacacctgta acgtggacca caagccctcc aacaccaagg tggacaagcg ggtggaatct	660
aagtacggcc ctccctgccc cccctgccct gccctgaat ttctgggcgg accttccgtg	720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatct cccggacccc cgaagtgacc	780
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cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag	960
tgcaaggtgt ccaacaaggg cctgccctcc agcatcgaag agaccatctc caaggccaag	1020
ggccagcccc gcgagcccca ggtgtacacc ctgcccccta gccaggaaga gatgaccaag	1080
aaccaggtgt ccctgacctg tctggtcaag ggcttctacc cctccgacat tgccgtggaa	1140
tgggagtcca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc	1200
gacggctcct tcttcctgta ctctcggctg accgtggaca agtcccgggtg gcaggaaggc	1260
aacgtcttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc	1320
ctgtccctga gcctgggcaa g	1341

<210> 38
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 38	
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ccgggaaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240
aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgcccc gctgggagcc	300

aacaaccagg gctacccgct ggatcttttg ggacaggga cctcgtgac tgtctcgagt	360
gcctccacca agggccctc cgtgttcccg ctcgctccat catcgaagtc taccagcgga	420
ggcactgcgg ctctcggttg cctcgtgaag gactacttcc cggagccggt gaccgtgtcg	480
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ggcctttact ccctgtcatc agtggtgact gtcccgcca gctcattggg aacccaaacc	600
tacatctgca atgtgaatca caaacctagc aacaccaagg ttgacaagaa agtcgagccc	660
aaatcgtgtg acaagactca cacttgtccg ccgtgcccgg caccgaact gctgggaggt	720
cccagcgtct ttctgttccc tccaaagccg aaagacacgc tgatgatctc ccgcaccccg	780
gaggtcactt gcgtggtcgt ggacgtgtca catgaggacc cagaggtgaa gttcaattgg	840
tacgtggatg gcgtcgaagt ccacaatgcc aaaactaagc ccagagaaga acagtacaat	900
tcgacctacc gcgtcgtgtc cgtgctcacg gtgttgcatc aggattggct gaacgggaag	960
gaatacaagt gcaaagtgtc caacaaggcg ctgccggcac cgatcgagaa aactatctcc	1020
aaagcgaagg gacagcctag ggaacctcaa gtctacacgc tgccaccatc acgggatgaa	1080
ctgactaaga atcaagtctc actgacttgt ctggtgaagg ggttttaccc tagcgacatt	1140
gccgtggagt gggaatccaa cggccagcca gagaacaact acaagactac ccctccagtg	1200
ctcgactcgg atggatcgtt cttcctttac tcgaagctca ccgtggataa gtcccgggtg	1260
cagcaggga acgtgttctc ctgctcgggtg atgcatgaag ccctccataa ccactatacc	1320
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<210> 39
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> humanized

<400> 39	
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acctgtactg tgtccgggat cgacttgagc acctggagga tgaactggat tcgccagcca	120

ccgggaaagg gactggagtg gatcggcatt atcgggtactg ggggacggac ctactacgcc	180
aattgggcaa agggcagagt gacgatttca aaggacacct cgaagaacca ggtgtccctg	240
aaactgtcct ccgtgactgc ggctgacacc gccgtgtact attgcgccccg gctgggagcc	300
aacaacgccg gctacccgct ggatcttttg ggacagggaa ccctcgtgac tgtctcgagt	360
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tggaacagcg gagccctgac cagcgggggtg cacacctttc cggccgtctt gcagtcaagc	540
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tacatctgca atgtgaatca caaacctagc aacaccaagg ttgacaagaa agtcgagccc	660
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cccagcgtct ttctgttccc tccaaagccg aaagacacgc tgatgatctc ccgcacccccg	780
gaggtcactt gcgtggtcgt ggacgtgtca catgaggacc cagaggtgaa gttcaattgg	840
tacgtggatg gcgtcgaagt ccacaatgcc aaaactaagc ccagagaaga acagtacaat	900
tcgacctacc gcgtcgtgtc cgtgctcacg gtgttgcac aggattggct gaacgggaag	960
gaatacaagt gcaaagtgtc caacaaggcg ctgccggcac cgatcgagaa aactatctcc	1020
aaagcgaagg gacagcctag ggaacctcaa gtctacacgc tgccaccatc acgggatgaa	1080
ctgactaaga atcaagtctc actgacttgt ctggtgaagg ggttttacct tagcgacatt	1140
gccgtggagt gggaatccaa cggccagcca gagaacaact acaagactac ccctccagtg	1200
ctcgactcgg atggatcgtt cttcctttac tcgaagctca ccgtggataa gtcccggtgg	1260
cagcagggaa acgtgttctc ctgctcgggtg atgcatgaag ccctccataa ccactatacc	1320
caaaagtcgc tgtccctgtc gccgggaaag	1350

<210> 40
 <211> 132
 <212> PRT
 <213> Rabbit

<220>

<221> MISC_FEATURE

<222> (1)..(22)

<223> Signal sequence

<400> 40

Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
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Leu Pro Gly Ala Arg Cys Asp Val Val Met Thr Gln Thr Pro Ala Ser
20 25 30

Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
35 40 45

Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60

Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Ala Ser Gly Val
65 70 75 80

Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

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

Gly Tyr Thr Arg Thr Asp Ile Asp Asn Thr Phe Gly Gly Gly Thr Lys
115 120 125

Val Val Val Glu
130

<210> 41

<211> 136

<212> PRT

<213> Rabbit

<220>

<221> MISC_FEATURE

<222> (1)..(19)

<223> Signal sequence

<400> 41

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
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Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30

Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser
35 40 45

Thr Trp Arg Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp
65 70 75 80

Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95

Lys Val Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110

Arg Leu Gly Ala Asn Asn Asn Gly Tyr Pro Leu Asp Leu Trp Gly Pro
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 42

<211> 396

<212> DNA

<213> Rabbit

<220>

<221> misc_feature

<222> (1)..(66)

<223> Signal sequence

<400> 42

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atggacatga gggccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc      60
agatgtgatg ttgtgatgac ccagactcca gcctccgtgg aggcagctgt gggaggcaca      120
gtcaccatca agtgccaggc cagtcagagc gttagtagtt acttagcctg gtatcagcag      180
aaaccagggc agcctcccaa gtcctgatc tatgctgcat cctatctggc atccggggtc      240
ccatcacggt tcaaaggcag tggatctggg acagagttca ctctcaccat cagcgacctg      300
gagtgtgccg atgctgccac ttattactgt caacagggtt atactaggac tgatattgat      360
aatactttcg gcggagggac caaggtggtg gtcgaa                                396
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<210> 43

<211> 408

<212> DNA

<213> Rabbit

<220>

<221> misc_feature

<222> (1)..(57)

<223> Signal sequence

<400> 43

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atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaagggtg ccagtgtcag      60
tcgctggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc      120
acagtctctg gaatcgacct cagtacttgg agaatgaact gggtcgccca ggctccaggg      180
aaggggctgg aatggatcgg aatcattggt actggtggta gaacatacta cgcgaactgg      240
gcaaaaggcc gattcaccat ctcaaaaacc tcgaccacgg tggatctgaa ggtcaccagt      300
ccgacaaccg aggacacggc cacctatttc tgtgccagat tgggtgctaa taataatggt      360
tatcctttgg acttgtgggg cccggggacc ctggtcaccg tctcgagt                                408
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<210> 44

<211> 107

<212> PRT

<213> Homo sapiens

<400> 44

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 45

<211> 114

<212> PRT

<213> Homo sapiens

<400> 45

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

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

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

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

Ser Ser

<210> 46
<211> 321
<212> DNA
<213> Homo sapiens

<400> 46
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 47
<211> 342
<212> DNA
<213> Homo sapiens

<400> 47
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120
cagccccag ggaaggggct ggagtggatt gggagtatct attatagtgg gagcacctac 180

tacaacccgt ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcgagatac 300
tttgactact ggggccaagg aaccctgggtc accgtctcct ca 342

<210> 48
<211> 12
<212> PRT
<213> Rabbit

<400> 48

Leu Gly Ala Asn Asn Asn Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 49

Leu Gly Ala Asn Asn Gln Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 50
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized

<400> 50

Leu Gly Ala Asn Asn Ala Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 51
<211> 12
<212> PRT

<213> Artificial Sequence

<220>

<223> humanized

<400> 51

Leu Gly Ala Asn Asn Asp Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 52

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized

<400> 52

Leu Gly Ala Asn Asn Ser Gly Tyr Pro Leu Asp Leu
1 5 10

<210> 53

<211> 12

<212> PRT

<213> Rabbit

<400> 53

Gln Gln Gly Tyr Thr Arg Thr Asp Ile Asp Asn Thr
1 5 10

<210> 54

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized

<400> 54

Gln Gln Ala Tyr Thr Arg Thr Asp Ile Asp Asn Thr
1 5 10

<210> 55
<211> 441
<212> PRT
<213> Homo sapiens

<400> 55

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1 5 10 15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
20 25 30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
35 40 45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
50 55 60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65 70 75 80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
85 90 95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
100 105 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
115 120 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
130 135 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145 150 155 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
165 170 175

Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
180 185 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
195 200 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
210 215 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225 230 235 240

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

Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
260 265 270

Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
275 280 285

Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
290 295 300

Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305 310 315 320

Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
325 330 335

Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
340 345 350

Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
355 360 365

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala

370

375

380

Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385 390 395 400

Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
405 410 415

Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
420 425 430

Ser Ala Ser Leu Ala Lys Gln Gly Leu
435 440

<210> 56
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> modified

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> ACETYLATION and NYTROSYLATION

<220>
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<223> NYTROSYLATION

<220>
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<222> (2)..(2)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> PHOSPHORYLATION

<220>
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<222> (5)..(6)
<223> Position of Biotin Conjugation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> AMIDATION

<400> 56

Tyr Ser Ser Pro Cys Ser Pro Gly Thr Pro
1 5 10

<210> 57
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> modified

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> PHOSPHORYLATION

<220>
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<222> (8)..(8)
<223> PHOSPHORYLATION

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Position of Biotin Conjugation

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> AMIDATION

<400> 57

Arg Thr Pro Pro Lys Ser Pro Ser Ser Cys
1 5 10

<210> 58
<211> 217
<212> PRT
<213> Mouse

<400> 58

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

Gln Arg Ala Thr Ile Ser Cys Gln Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Thr Arg Thr Asp
85 90 95

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

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

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

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

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

Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
180 185 190

Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
195 200 205

Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 59
<211> 442
<212> PRT
<213> Mouse

<400> 59

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Ile Asp Leu Ser Thr Trp
20 25 30

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

Gly Ile Ile Gly Thr Gly Gly Arg Thr Tyr Tyr Ala Asn Trp Ala Lys
50 55 60

Gly Arg Phe Ser Ile Ser Lys Asp Ser Thr Gln Val Phe Leu Lys Met
65 70 75 80

Asn Ser Leu Gln Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Leu
85 90 95

Gly Ala Asn Asn Asn Gly Tyr Pro Leu Asp Leu Trp Gly Ala Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro
115 120 125

Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly
130 135 140

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

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

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

Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser
195 200 205

Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro
210 215 220

Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro
225 230 235 240

Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys

245

250

255

Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp
 260 265 270

Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu
 275 280 285

Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met
 290 295 300

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

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

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

Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe
 355 360 365

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

Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe
 385 390 395 400

Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn
 405 410 415

Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr
 420 425 430

Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440

<210> 60
<211> 651
<212> DNA
<213> Mouse

<400> 60
gatgtcgtga tgactcagtc acccgcaagc ctggctgtgt cgctgggaca gcgggctact 60
atctcgtgcc aagcgtccca gtctgtctcc tcgtacttgg cctggatatca gcagaagcca 120
ggacagccgc cgaaactcct catctacgcc gcctcatacc ttgcgtccgg agtgccttcg 180
agattcaaag gaagcggaag cggcactgag tttaccctga acatccaccc ggtggaagaa 240
gaggacgcag ccacgtacta ctgtcaacaa gggtacaccc gcaccgatat tgacaatacc 300
ttcggtggcg ggactaagct ggaaatcaag cgtacggatg ctgcaccaac tgtatccatc 360
ttcccaccat ccagtgagca gttaacatct ggaggtgcct cagtcgtgtg cttcttgaac 420
aacttctacc ccaaagacat caatgtcaag tggaagattg atggcagtga acgacaaaat 480
ggcgtcctga acagttggac tgatcaggac agcaaagaca gcacctacag catgagcagc 540
accctcacgt tgaccaagga cgagtatgaa cgacataaca gctatacctg tgaggccact 600
cacaagacat caacttcacc cattgtcaag agcttcaaca ggaatgagtg t 651

<210> 61
<211> 1326
<212> DNA
<213> Mouse

<400> 61
caagtgcagc tgaaagaatc aggaccggga ctggtggcac caagccagtc cctgtcgatc 60
acctgtactg tgtccggaat cgacctctcc acctggcgca tgaattgggt ccggcagcct 120
cccggaaagg gcctcgaatg gattggcatc atcgggtactg ggggcagaac ttactacgcc 180
aattgggcga aggggcgctt ctcaatctcg aaagactcga cccaagtgtt cttgaagatg 240
aacagccttc agaccgagga taccgctacc tacttttgcg cgaggctggg agccaacaac 300
aacggttacc cgctcgatct gtggggagcc ggaacgactg tgactgtctc gagtgccaaa 360
acgacacccc catctgtcta tccactggcc cctggatctg ctgccccaac taactccatg 420

gtgaccttgg gatgcctggt caagggctat ttccctgagc cagtgcagct gacctggaac	480
tctggatccc tgtccagcgg tgtgcacacc ttcccagctg tcctgcagtc tgacctctac	540
actctgagca gctcagtgac tgtccccctcc agcacctggc ccagcgagac cgtcacctgc	600
aacgttgccc acccggccag cagcaccaag gtggacaaga aaattgtgcc cagggattgt	660
ggttgtaagc cttgcatatg tacagtccca gaagtatcat ctgtcttcat cttcccccca	720
aagcccaagg atgtgctcac cattactctg actcctaagg tcacgtgtgt tgtggtagac	780
atcagcaagg atgatcccga ggtccagttc agctggtttg tagatgatgt ggaggtgcac	840
acagctcaga cgcaaccccg ggaggagcag ttcaacagca ctttccgctc agtcagtga	900
cttcccatca tgcaccagga ctggctcaat ggcaaggagt tcaaatgcag ggtcaacagt	960
gcagctttcc ctgcccccat cgagaaaacc atctccaaaa ccaaaggcag accgaaggct	1020
ccacaggtgt acaccattcc acctcccaag gagcagatgg ccaaggataa agtcagtctg	1080
acctgcatga taacagactt cttccctgaa gacattactg tggagtggca gtggaatggg	1140
cagccagcgg agaactacaa gaacactcag cccatcatgg acacagatgg ctcttacttc	1200
gtctacagca agctcaatgt gcagaagagc aactggggagg caggaaatac tttcacctgc	1260
tctgtgttac atgagggcct gcacaaccac catactgaga agagcctctc ccactctcct	1320
ggtaaa	1326

<210> 62
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> ACETYLATION

<220>
 <221> MISC_FEATURE
 <222> (1)..(2)

<223> Position of Biotin Conjugation

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> AMIDATION

<400> 62

Cys Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro
1 5 10

<210> 63

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> modified

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> ACETYLATION

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Position of Biotin Conjugation

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> AMIDATION

<400> 63

Arg Thr Pro Ser Leu Pro Thr Pro Cys
1 5

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> modified

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> ACETYLATION

<220>

<221> MISC_FEATURE

<222> (1)..(2)

<223> Position of Biotin Conjugation

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> PHOSPHORYLATION

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> AMIDATION

<400> 64

Cys Ser Pro Val Val Ser Gly Asp Thr Ser
1 5 10

<210> 65

<211> 10

<212> PRT

<213> Artificial Sequence

<400> 65

Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro
1 5 10