

pctgb2016052564-seq1.txt
SEQUENCE LISTING

<110> Autolus Ltd

<120> RECEPTOR

<130> P108038PCT

<150> GB1514875.2

<151> 2015-08-20

<160> 55

<170> PatentIn version 3.5

<210> 1

<211> 86

<212> PRT

<213> Artificial Sequence

<220>

<223> endodomain derived from IL-2 receptor common gamma-chain

<400> 1

Glu Arg Thr Met Pro Arg Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu
1 5 10 15

Val Thr Glu Tyr His Gly Asn Phe Ser Ala Trp Ser Gly Val Ser Lys
20 25 30

Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu
35 40 45

Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu Gly Glu Gly Pro Gly
50 55 60

Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr
65 70 75 80

Thr Leu Lys Pro Glu Thr
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<210> 2

<211> 286

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<213> Artificial Sequence

<220>

<223> endodomain derived from IL-2 receptor common beta-chain

<400> 2

Asn Cys Arg Asn Thr Gly Pro Trp Leu Lys Lys Val Leu Lys Cys Asn
1 5 10 15

Thr Pro Asp Pro Ser Lys Phe Phe Ser Gln Leu Ser Ser Glu His Gly
20 25 30

Gly Asp Val Gln Lys Trp Leu Ser Ser Pro Phe Pro Ser Ser Ser Phe
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Ser Pro Gly Gly Leu Ala Pro Glu Ile Ser Pro Leu Glu Val Leu Glu
 50 55 60

Arg Asp Lys Val Thr Gln Leu Leu Leu Gln Gln Asp Lys Val Pro Glu
 65 70 75 80

Pro Ala Ser Leu Ser Ser Asn His Ser Leu Thr Ser Cys Phe Thr Asn
 85 90 95

Gln Gly Tyr Phe Phe Phe His Leu Pro Asp Ala Leu Glu Ile Glu Ala
 100 105 110

Cys Gln Val Tyr Phe Thr Tyr Asp Pro Tyr Ser Glu Glu Asp Pro Asp
 115 120 125

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

Pro Leu Ser Gly Glu Asp Asp Ala Tyr Cys Thr Phe Pro Ser Arg Asp
 145 150 155 160

Asp Leu Leu Leu Phe Ser Pro Ser Leu Leu Gly Gly Pro Ser Pro Pro
 165 170 175

Ser Thr Ala Pro Gly Gly Ser Gly Ala Gly Glu Glu Arg Met Pro Pro
 180 185 190

Ser Leu Gln Glu Arg Val Pro Arg Asp Trp Asp Pro Gln Pro Leu Gly
 195 200 205

Pro Pro Thr Pro Gly Val Pro Asp Leu Val Asp Phe Gln Pro Pro Pro
 210 215 220

Glu Leu Val Leu Arg Glu Ala Gly Glu Glu Val Pro Asp Ala Gly Pro
 225 230 235 240

Arg Glu Gly Val Ser Phe Pro Trp Ser Arg Pro Pro Gly Gln Gly Glu
 245 250 255

Phe Arg Ala Leu Asn Ala Arg Leu Pro Leu Asn Thr Asp Ala Tyr Leu
 260 265 270

Ser Leu Gln Glu Leu Gln Gly Gln Asp Pro Thr His Leu Val
 275 280 285

<210> 3

<211> 195

<212> PRT

<213> Artificial Sequence

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<220>

<223> endodomain derived from IL-7 receptor alpha-chain

<400> 3

Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys
1 5 10 15

Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val
20 25 30

Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp
35 40 45

Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe
50 55 60

Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val
65 70 75 80

Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val Ile Thr Pro Glu Ser
85 90 95

Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala
100 105 110

Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu
115 120 125

Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu
130 135 140

Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly
145 150 155 160

Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser
165 170 175

Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr
180 185 190

Gln Asn Gln
195

<210> 4

<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<223> hinge-CH2CH3 of human IgG1

<400> 4

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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1              5              10              15
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
      20              25              30
Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
      35              40              45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
      50              55              60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
      65              70              75              80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
      85              90              95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
      100              105              110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
      115              120              125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
      130              135              140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
      145              150              155              160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
      165              170              175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
      180              185              190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
      195              200              205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
      210              215              220
Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp
      225              230

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<210> 5
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<220>
<223> human CD8 stalk

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<400> 5

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Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

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

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
35 40 45

<210> 6
<211> 20
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<220>
<223> human IgG1 hinge

<400> 6

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Lys Asp Pro Lys
20

<210> 7
<211> 21
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<220>
<223> transmembrane derived from human common gamma chain

<400> 7

Val Val Ile Ser Val Gly Ser Met Gly Leu Ile Ile Ser Leu Leu Cys
1 5 10 15

Val Tyr Phe Trp Leu
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<210> 8
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<220>
<223> transmembrane derived from human IL-2Rbeta

<400> 8

Ile Pro Trp Leu Gly His Leu Leu Val Gly Leu Ser Gly Ala Phe Gly
1 5 10 15

Phe Ile Ile Leu Val Tyr Leu Leu Ile
20 25

<210> 9

pctgb2016052564-seq1.txt

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> transmembrane derived from human IL-7Ralpha

<400> 9

Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu
1 5 10 15

Leu Val Ile Leu Ala Cys Val Leu Trp
20 25

<210> 10

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> transmembrane derived from human IL-15Ralpha

<400> 10

Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser
1 5 10 15

Leu Leu Ala Cys Tyr Leu
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<210> 11

<211> 118

<212> PRT

<213> Artificial sequence

<220>

<223> sequence of 5D3D11 VH

<400> 11

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

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

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

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Lys Tyr Asn Gly Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
85 90 95

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

Ser Val Thr Val Ser Ser
115

<210> 12
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of 5D3D11 VL

<400> 12

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

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Val Thr Phe Gly Ala Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 13
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of 5D5A5 VH

<400> 13

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

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ser Ser Tyr
20 25 30

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

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Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Asn Asn Gln Lys Phe
50 55 60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

Val Thr Val Ser Ser
115

<210> 14
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of 5D5A5 VL

<400> 14

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

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

Gly Phe Thr Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr His
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 15
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> ScFv based on 5D5A5

<400> 15

pctgb2016052564-seq1.txt

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

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ser Ser Tyr
20 25 30

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

Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Asn Asn Gln Lys Phe
50 55 60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
130 135 140

Pro Pro Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Ile Asp Leu Tyr Gly Phe Thr Phe Met His Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Ile Leu Ile Tyr Arg Ala
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

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

Gly Gly Thr Lys Leu Glu Ile Lys
245

<210> 16
<211> 250
<212> PRT

<213> Artificial sequence

<220>

<223> ScFv based on 5D3D11

<400> 16

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

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

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

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Lys Tyr Asn Gly Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Val Asp Ser Ala Val Tyr Phe Cys
85 90 95

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

Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
130 135 140

Thr Ala Pro Ser Val Phe Val Thr Pro Gly Glu Ser Val Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu
165 170 175

Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
180 185 190

Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu
210 215 220

Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr Pro Val Thr
225 230 235 240

Phe Gly Ala Gly Thr Lys Val Glu Ile Lys

<210> 17
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 <223> sequence of CXCR4

<400> 17

Met Ser Ile Pro Leu Pro Leu Leu Gln Ile Tyr Thr Ser Asp Asn Tyr
 1 5 10 15

Thr Glu Glu Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys
 20 25 30

Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile
 35 40 45

Tyr Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
 50 55 60

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

Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro
 85 90 95

Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu
 100 105 110

Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val
 115 120 125

Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val
 145 150 155 160

Tyr Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe
 165 170 175

Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg
 180 185 190

Phe Tyr Pro Asn Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile
 195 200 205

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

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Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys
225 230 235 240

Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp
245 250 255

Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu
260 265 270

Ile Ile Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile
275 280 285

Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
290 295 300

Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala
305 310 315 320

Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly
325 330 335

Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser
340 345 350

Phe His Ser Ser
355

<210> 18
<211> 374
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<213> Artificial Sequence

<220>
<223> sequence of cell surface receptor CCR2
<400> 18

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1 5 10 15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
20 25 30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
Page 12

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

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

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

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

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

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

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

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
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pctgb2016052564-seq1.txt
360 365Gln Asp Lys Glu Gly Ala
370

<210> 19

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> sequence of cell surface receptor CCR4

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Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 170 175Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
180 185 190Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
195 200 205

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

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300

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

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350

Asp His Asp Leu His Asp Ala Leu
 355 360

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 <223> scFv based on J591
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Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Thr
 1 5 10 15

Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30

Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
 50 55 60

Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Glu Leu Arg Ser₈₅ Leu Thr Ser Glu Asp₉₀ Ser Ala Val Tyr Tyr₉₅ Cys

Ala Ala Gly Trp₁₀₀ Asn Phe Asp Tyr Trp₁₀₅ Gly Gln Gly Thr Thr₁₁₀ Leu Thr

Val Ser Ser₁₁₅ Gly Gly Gly Gly Ser₁₂₀ Gly Gly Gly Gly Ser₁₂₅ Gly Gly Gly

Gly Ser₁₃₀ Asp Ile Val Met Thr₁₃₅ Gln Ser His Lys Phe₁₄₀ Met Ser Thr Ser

Val Gly Asp Arg Val Ser₁₅₀ Ile Ile Cys Lys Ala₁₅₅ Ser Gln Asp Val Gly₁₆₀

Thr Ala Val Asp Trp₁₆₅ Tyr Gln Gln Lys Pro₁₇₀ Gly Gln Ser Pro Lys₁₇₅ Leu

Leu Ile Tyr Trp₁₈₀ Ala Ser Thr Arg His₁₈₅ Thr Gly Val Pro Asp₁₉₀ Arg Phe

Thr Gly Ser₁₉₅ Gly Ser Gly Thr Asp₂₀₀ Phe Thr Leu Thr Ile₂₀₅ Thr Asn Val

Gln Ser₂₁₀ Glu Asp Leu Ala Asp₂₁₅ Tyr Phe Cys Gln Gln₂₂₀ Tyr Asn Ser Tyr

Pro Leu Thr Phe Gly Ala₂₃₀ Gly Thr Met Leu Asp₂₃₅ Leu Lys Arg

<210> 21

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> signal peptide derived from TCR beta chain

<400> 21

Met Gly Thr Ser₅ Leu Leu Cys Trp Met Ala₁₀ Leu Cys Leu Leu Gly₁₅ Ala

Asp His Ala Asp Gly₂₀

<210> 22

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> signal peptide derived from IgG1

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<400> 22

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 23

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> signal peptide derived from CD8a

<400> 23

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

Asp Ala Arg Cys
20

<210> 24

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> CD3 Z endodomain

<400> 24

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 25

<211> 152

<212> PRT

<213> Artificial sequence

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<223> CD28 and CD3 Zeta endodomains

<400> 25

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 1 5 10 15

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 20 25 30

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
 35 40 45

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 50 55 60

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 65 70 75 80

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 85 90 95

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 100 105 110

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 115 120 125

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 130 135 140

His Met Gln Ala Leu Pro Pro Arg
 145 150

<210> 26

<211> 188

<212> PRT

<213> Artificial sequence

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<223> CD28, OX40 and CD3 Zeta endodomains

<400> 26

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 1 5 10 15

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 20 25 30

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp
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35

40

45

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu
 50 55 60

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe
 65 70 75 80

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 85 90 95

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 100 105 110

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 115 120 125

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 130 135 140

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 145 150 155 160

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 165 170 175

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 180 185

<210> 27
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ICOS endodomain

<400> 27

Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn
 1 5 10 15

Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg
 20 25 30

Leu Thr Asp Val Thr Leu
 35

<210> 28
 <211> 48
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD27 endodomain

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<400> 28

Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro
1 5 10 15

Ala Glu Pro Cys His Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr
20 25 30

Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
35 40 45

<210> 29

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> BTLA endodomain

<400> 29

Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala Gly Arg
1 5 10 15

Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr Glu Ala
20 25 30

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

Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser Glu Val
50 55 60

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

Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg Leu Ala Arg Asn
85 90 95

Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg Ser
100 105 110

<210> 30

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> CD30 endodomain

<400> 30

His Arg Arg Ala Cys Arg Lys Arg Ile Arg Gln Lys Leu His Leu Cys
1 5 10 15

Tyr Pro Val Gln Thr Ser Gln Pro Lys Leu Glu Leu Val Asp Ser Arg
Page 20

20

25

30

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

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

Cys His Ser Val Gly Ala Ala Tyr Leu Glu Ser Leu Pro Leu Gln Asp
 65 70 75 80

Ala Ser Pro Ala Gly Gly Pro Ser Ser Pro Arg Asp Leu Pro Glu Pro
 85 90 95

Arg Val Ser Thr Glu His Thr Asn Asn Lys Ile Glu Lys Ile Tyr Ile
 100 105 110

Met Lys Ala Asp Thr Val Ile Val Gly Thr Val Lys Ala Glu Leu Pro
 115 120 125

Glu Gly Arg Gly Leu Ala Gly Pro Ala Glu Pro Glu Leu Glu Glu Glu
 130 135 140

Leu Glu Ala Asp His Thr Pro His Tyr Pro Glu Gln Glu Thr Glu Pro
 145 150 155 160

Pro Leu Gly Ser Cys Ser Asp Val Met Leu Ser Val Glu Glu Glu Gly
 165 170 175

Lys Glu Asp Pro Leu Pro Thr Ala Ala Ser Gly Lys
 180 185

<210> 31

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> GITR endodomain

<400> 31

Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp Pro
 1 5 10 15

Arg Glu Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
 20 25 30

Arg Ser Cys Gln Phe Pro Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu
 35 40 45

Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
 50 55

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<210> 32
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVEM endodomain

<400> 32

Cys Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val
 1 5 10 15

Ser Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile
 20 25 30

Glu Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu
 35 40 45

Thr Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
 50 55 60

<210> 33
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 33

Tyr His Ala Asp Tyr Tyr Lys Gln Arg Leu Ile His Asp Val Glu Met
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 34
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 34

His Tyr Ala Gly Tyr Phe Ala Asp Leu Leu Ile His Asp Ile Glu Thr
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 35
 <211> 20
 <212> PRT
 <213> Artificial Sequence

pctgb2016052564-seq1.txt

<220>

<223> cleavage site, 2A-like sequence

<400> 35

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 36

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> cleavage site, 2A-like sequence

<400> 36

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 37

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> cleavage site, 2A-like sequence

<400> 37

Ala Ala Arg Gln Met Leu Leu Leu Leu Ser Gly Asp Val Glu Thr Asn
1 5 10 15

Pro Gly Pro

<210> 38

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> cleavage site, 2A-like sequence

<400> 38

Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
1 5 10 15

Asn Pro Gly Pro
20

<210> 39

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

<220>
 <223> cleavage site, 2A-like sequence

<400> 39

Thr Arg Ala Glu Ile Glu Asp Glu Leu Ile Arg Ala Gly Ile Glu Ser
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 40
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 40

Thr Arg Ala Glu Ile Glu Asp Glu Leu Ile Arg Ala Asp Ile Glu Ser
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 41
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 41

Ala Lys Phe Gln Ile Asp Lys Ile Leu Ile Ser Gly Asp Val Glu Leu
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 42
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 42

Ser Ser Ile Ile Arg Thr Lys Met Leu Val Ser Gly Asp Val Glu Glu
 1 5 10 15

Asn Pro Gly Pro

20

<210> 43
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 43

Cys Asp Ala Gln Arg Gln Lys Leu Leu Leu Ser Gly Asp Ile Glu Gln
 1 5 10 15

Asn Pro Gly Pro
 20

<210> 44
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cleavage site, 2A-like sequence

<400> 44

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

Asn Pro Gly Pro
 20

<210> 45
 <211> 1722
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion construct with IL-2R beta chain

<400> 45

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Thr Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
 35 40 45

Thr Glu Tyr Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
 50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn
 65 70 75 80

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Gln Lys Phe Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe Met
145 150 155 160

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln
165 170 175

Asp Val Gly Thr Ala Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser
180 185 190

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro
195 200 205

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
210 215 220

Thr Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr
225 230 235 240

Asn Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
245 250 255

Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys
260 265 270

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
275 280 285

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

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

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

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Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 355 360 365
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 370 375 380
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Phe Trp Val Leu
 485 490 495
 Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
 500 505 510
 Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg Ser Ala
 515 520 525
 Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 530 535 540
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 545 550 555 560
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 565 570 575
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 580 585 590
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 595 600 605
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 610 615 620

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His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly Ser Leu
 625 630 635 640
 Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Asp
 645 650 655
 Thr Leu Ile Leu Trp Val Leu Leu Leu Leu Val Pro Gly Ser Thr Gly
 660 665 670
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
 675 680 685
 Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ser Ser Tyr
 690 695 700
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 705 710 715 720
 Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Asn Asn Gln Lys Phe
 725 730 735
 Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 740 745 750
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 755 760 765
 Ala Arg Ser Gly Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
 770 775 780
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 785 790 795 800
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
 805 810 815
 Pro Pro Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 820 825 830
 Arg Ala Ser Glu Ser Ile Asp Leu Tyr Gly Phe Thr Phe Met His Trp
 835 840 845
 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Ile Leu Ile Tyr Arg Ala
 850 855 860
 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 865 870 875 880
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 885 890 895

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Ala Thr Tyr Tyr Cys Gln Gln Thr His Glu Asp Pro Tyr Thr Phe Gly
900 905 910

Gly Gly Thr Lys Leu Glu Ile Lys Ser Asp Pro Ala Thr Thr Thr Pro
915 920 925

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
930 935 940

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
945 950 955 960

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Val Val Ile Ser Val Gly
965 970 975

Ser Met Gly Leu Ile Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu
980 985 990

Arg Thr Met Pro Arg Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val
995 1000 1005

Thr Glu Tyr His Gly Asn Phe Ser Ala Trp Ser Gly Val Ser Lys
1010 1015 1020

Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser Glu Arg Leu Cys
1025 1030 1035

Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu Gly Glu Gly
1040 1045 1050

Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp Ala Pro
1055 1060 1065

Pro Cys Tyr Thr Leu Lys Pro Glu Thr Gln Cys Thr Asn Tyr Ala
1070 1075 1080

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met
1085 1090 1095

Glu Thr Asp Thr Leu Ile Leu Trp Val Leu Leu Leu Leu Val Pro
1100 1105 1110

Gly Ser Thr Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
1115 1120 1125

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Val Ser Gly
1130 1135 1140

Tyr Ala Ile Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro
1145 1150 1155

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Gly	Gln 1160	Gly	Leu	Glu	Trp	Ile 1165	Gly	Arg	Ile	Tyr	Pro 1170	Gly	Asp	Gly
Asp	Thr 1175	Lys	Tyr	Asn	Gly	Lys 1180	Phe	Lys	Asp	Lys	Ala 1185	Thr	Leu	Thr
Val	Asp 1190	Lys	Ser	Ser	Ser	Thr 1195	Ala	Tyr	Met	Gln	Leu 1200	Ser	Ser	Leu
Thr	Ser 1205	Val	Asp	Ser	Ala	Val 1210	Tyr	Phe	Cys	Ala	Arg 1215	Asp	Gly	Tyr
Arg	Tyr 1220	Tyr	Phe	Asp	Tyr	Trp 1225	Gly	Gln	Gly	Thr	Ser 1230	Val	Thr	Val
Ser	Ser 1235	Gly	Gly	Gly	Gly	Ser 1240	Gly	Gly	Gly	Gly	Ser 1245	Gly	Gly	Gly
Gly	Ser 1250	Gly	Gly	Gly	Gly	Ser 1255	Asp	Ile	Val	Met	Thr 1260	Gln	Thr	Ala
Pro	Ser 1265	Val	Phe	Val	Thr	Pro 1270	Gly	Glu	Ser	Val	Ser 1275	Ile	Ser	Cys
Arg	Ser 1280	Ser	Lys	Ser	Leu	Leu 1285	His	Ser	Asn	Gly	Asn 1290	Thr	Tyr	Leu
Tyr	Trp 1295	Phe	Leu	Gln	Arg	Pro 1300	Gly	Gln	Ser	Pro	Gln 1305	Leu	Leu	Ile
Tyr	Arg 1310	Met	Ser	Asn	Leu	Ala 1315	Ser	Gly	Val	Pro	Asp 1320	Arg	Phe	Ser
Gly	Ser 1325	Gly	Ser	Gly	Thr	Asp 1330	Phe	Thr	Leu	Arg	Ile 1335	Ser	Arg	Val
Glu	Ala 1340	Glu	Asp	Val	Gly	Val 1345	Tyr	Tyr	Cys	Met	Gln 1350	His	Leu	Glu
Tyr	Pro 1355	Val	Thr	Phe	Gly	Ala 1360	Gly	Thr	Lys	Val	Glu 1365	Ile	Lys	Ser
Asp	Pro 1370	Ala	Lys	Ile	Glu	Val 1375	Met	Tyr	Pro	Pro	Pro 1380	Tyr	Leu	Asp
Asn	Glu 1385	Lys	Ser	Asn	Gly	Thr 1390	Ile	Ile	His	Val	Lys 1395	Gly	Lys	His
Leu	Cys 1400	Pro	Ser	Pro	Leu	Phe 1405	Pro	Gly	Pro	Ser	Lys 1410	Pro	Ile	Pro

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Trp	Leu 1415	Gly	His	Leu	Leu	Val 1420	Gly	Leu	Ser	Gly	Ala 1425	Phe	Gly	Phe
Ile	Ile 1430	Leu	Val	Tyr	Leu	Leu 1435	Ile	Asn	Cys	Arg	Asn 1440	Thr	Gly	Pro
Trp	Leu 1445	Lys	Lys	Val	Leu	Lys 1450	Cys	Asn	Thr	Pro	Asp 1455	Pro	Ser	Lys
Phe	Phe 1460	Ser	Gln	Leu	Ser	Ser 1465	Glu	His	Gly	Gly	Asp 1470	Val	Gln	Lys
Trp	Leu 1475	Ser	Ser	Pro	Phe	Pro 1480	Ser	Ser	Ser	Phe	Ser 1485	Pro	Gly	Gly
Leu	Ala 1490	Pro	Glu	Ile	Ser	Pro 1495	Leu	Glu	Val	Leu	Glu 1500	Arg	Asp	Lys
Val	Thr 1505	Gln	Leu	Leu	Leu	Gln 1510	Gln	Asp	Lys	Val	Pro 1515	Glu	Pro	Ala
Ser	Leu 1520	Ser	Ser	Asn	His	Ser 1525	Leu	Thr	Ser	Cys	Phe 1530	Thr	Asn	Gln
Gly	Tyr 1535	Phe	Phe	Phe	His	Leu 1540	Pro	Asp	Ala	Leu	Glu 1545	Ile	Glu	Ala
Cys	Gln 1550	Val	Tyr	Phe	Thr	Tyr 1555	Asp	Pro	Tyr	Ser	Glu 1560	Glu	Asp	Pro
Asp	Glu 1565	Gly	Val	Ala	Gly	Ala 1570	Pro	Thr	Gly	Ser	Ser 1575	Pro	Gln	Pro
Leu	Gln 1580	Pro	Leu	Ser	Gly	Glu 1585	Asp	Asp	Ala	Tyr	Cys 1590	Thr	Phe	Pro
Ser	Arg 1595	Asp	Asp	Leu	Leu	Leu 1600	Phe	Ser	Pro	Ser	Leu 1605	Leu	Gly	Gly
Pro	Ser 1610	Pro	Pro	Ser	Thr	Ala 1615	Pro	Gly	Gly	Ser	Gly 1620	Ala	Gly	Glu
Glu	Arg 1625	Met	Pro	Pro	Ser	Leu 1630	Gln	Glu	Arg	Val	Pro 1635	Arg	Asp	Trp
Asp	Pro 1640	Gln	Pro	Leu	Gly	Pro 1645	Pro	Thr	Pro	Gly	Val 1650	Pro	Asp	Leu
Val	Asp 1655	Phe	Gln	Pro	Pro	Pro 1660	Glu	Leu	Val	Leu	Arg 1665	Glu	Ala	Gly

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Glu Glu Val Pro Asp Ala Gly Pro Arg Glu Gly Val Ser Phe Pro
1670 1675 1680

Trp Ser Arg Pro Pro Gly Gln Gly Glu Phe Arg Ala Leu Asn Ala
1685 1690 1695

Arg Leu Pro Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln Glu Leu
1700 1705 1710

Gln Gly Gln Asp Pro Thr His Leu Val
1715 1720

<210> 46
<211> 1631
<212> PRT
<213> Artificial sequence

<220>
<223> fusion construct with IL-7R alpha chain

<400> 46

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30

Pro Gly Thr Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
35 40 45

Thr Glu Tyr Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
50 55 60

Glu Trp Ile Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn
65 70 75 80

Gln Lys Phe Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe Met
145 150 155 160

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln

165

170

175

Asp Val Gly Thr Ala Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser
 180 185 190

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro
 195 200 205

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 210 215 220

Thr Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr
 225 230 235 240

Asn Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
 245 250 255

Arg Ser Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
 275 280 285

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

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

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 340 345 350

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

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
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435

440

445

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Phe Trp Val Leu
 485 490 495

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
 500 505 510

Ala Phe Ile Ile Phe Trp Val Arg Arg Val Lys Phe Ser Arg Ser Ala
 515 520 525

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 530 535 540

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 545 550 555 560

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 565 570 575

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 580 585 590

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 595 600 605

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 610 615 620

His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly Ser Leu
 625 630 635 640

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Asp
 645 650 655

Thr Leu Ile Leu Trp Val Leu Leu Leu Leu Val Pro Gly Ser Thr Gly
 660 665 670

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
 675 680 685

Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ser Ser Tyr
 690 695 700

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 Page 34

705 710 715 720
 Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Asn Asn Gln Lys Phe
 725 730 735
 Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr
 740 745 750
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 755 760 765
 Ala Arg Ser Gly Arg Leu Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
 770 775 780
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 785 790 795 800
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
 805 810 815
 Pro Pro Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 820 825 830
 Arg Ala Ser Glu Ser Ile Asp Leu Tyr Gly Phe Thr Phe Met His Trp
 835 840 845
 Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Ile Leu Ile Tyr Arg Ala
 850 855 860
 Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
 865 870 875 880
 Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 885 890 895
 Ala Thr Tyr Tyr Cys Gln Gln Thr His Glu Asp Pro Tyr Thr Phe Gly
 900 905 910
 Gly Gly Thr Lys Leu Glu Ile Lys Ser Asp Pro Ala Thr Thr Thr Pro
 915 920 925
 Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
 930 935 940
 Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 945 950 955 960
 Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Val Val Ile Ser Val Gly
 965 970 975
 Ser Met Gly Leu Ile Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu
 980 985 990

Arg Thr Met Pro Arg Ile Pro Thr Leu Lys Asn Leu Glu Asp Leu Val
 995 1000 1005

Thr Glu Tyr His Gly Asn Phe Ser Ala Trp Ser Gly Val Ser Lys
 1010 1015 1020

Gly Leu Ala Glu Ser Leu Gln Pro Asp Tyr Ser Glu Arg Leu Cys
 1025 1030 1035

Leu Val Ser Glu Ile Pro Pro Lys Gly Gly Ala Leu Gly Glu Gly
 1040 1045 1050

Pro Gly Ala Ser Pro Cys Asn Gln His Ser Pro Tyr Trp Ala Pro
 1055 1060 1065

Pro Cys Tyr Thr Leu Lys Pro Glu Thr Gln Cys Thr Asn Tyr Ala
 1070 1075 1080

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met
 1085 1090 1095

Glu Thr Asp Thr Leu Ile Leu Trp Val Leu Leu Leu Leu Val Pro
 1100 1105 1110

Gly Ser Thr Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
 1115 1120 1125

Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Val Ser Gly
 1130 1135 1140

Tyr Ala Ile Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro
 1145 1150 1155

Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly
 1160 1165 1170

Asp Thr Lys Tyr Asn Gly Lys Phe Lys Asp Lys Ala Thr Leu Thr
 1175 1180 1185

Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 1190 1195 1200

Thr Ser Val Asp Ser Ala Val Tyr Phe Cys Ala Arg Asp Gly Tyr
 1205 1210 1215

Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
 1220 1225 1230

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

1235						1240						1245			
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Thr	Ala	
1250						1255					1260				
Pro	Ser	Val	Phe	Val	Thr	Pro	Gly	Glu	Ser	Val	Ser	Ile	Ser	Cys	
1265						1270					1275				
Arg	Ser	Ser	Lys	Ser	Leu	Leu	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	
1280						1285					1290				
Tyr	Trp	Phe	Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	
1295						1300					1305				
Tyr	Arg	Met	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	
1310						1315					1320				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	
1325						1330					1335				
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	His	Leu	Glu	
1340						1345					1350				
Tyr	Pro	Val	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Val	Glu	Ile	Lys	Ser	
1355						1360					1365				
Asp	Pro	Ala	Lys	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	
1370						1375					1380				
Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	
1385						1390					1395				
Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Pro	Ile	
1400						1405					1410				
Leu	Leu	Thr	Ile	Ser	Ile	Leu	Ser	Phe	Phe	Ser	Val	Ala	Leu	Leu	
1415						1420					1425				
Val	Ile	Leu	Ala	Cys	Val	Leu	Trp	Lys	Lys	Arg	Ile	Lys	Pro	Ile	
1430						1435					1440				
Val	Trp	Pro	Ser	Leu	Pro	Asp	His	Lys	Lys	Thr	Leu	Glu	His	Leu	
1445						1450					1455				
Cys	Lys	Lys	Pro	Arg	Lys	Asn	Leu	Asn	Val	Ser	Phe	Asn	Pro	Glu	
1460						1465					1470				
Ser	Phe	Leu	Asp	Cys	Gln	Ile	His	Arg	Val	Asp	Asp	Ile	Gln	Ala	
1475						1480					1485				
Arg	Asp	Glu	Val	Glu	Gly	Phe	Leu	Gln	Asp	Thr	Phe	Pro	Gln	Gln	

1490

1495

1500

Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser
 1505 1510 1515

Pro Asn Cys Pro Ser Glu Asp Val Val Ile Thr Pro Glu Ser Phe
 1520 1525 1530

Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala
 1535 1540 1545

Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg
 1550 1555 1560

Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu
 1565 1570 1575

Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu
 1580 1585 1590

Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro
 1595 1600 1605

Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr
 1610 1615 1620

Met Ser Ser Phe Tyr Gln Asn Gln
 1625 1630

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<211> 19

<212> PRT

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<220>

<223> signal sequence derived from human CD8a

<400> 47

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala

<210> 48

<211> 4

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<220>

<223> linker

<400> 48

Ser Asp Pro Ala

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<210> 49
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<400> 49

Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

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

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

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

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

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

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

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

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

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 165 170 175

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

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

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

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Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 50
<211> 27
<212> PRT
<213> Artificial Sequence

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Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
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Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 51
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> endodomain derived from TCRz

<400> 51

Arg Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
1 5 10 15

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
20 25 30

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
35 40 45

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
50 55 60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
100 105 110

Arg

<210> 52
<211> 20
<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence derived from mouse kappa VIII

<400> 52

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

Gly Ser Thr Gly
20

<210> 53

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> human CD28STK spacer

<400> 53

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
1 5 10 15

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
20 25 30

Leu Phe Pro Gly Pro Ser Lys Pro
35 40

<210> 54

<211> 4

<212> PRT

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<223> furin cleavage site

<220>

<221> misc_feature

<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa can be Arg or Lys

<400> 54

Arg Xaa Xaa Arg
1

<210> 55

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

pctgb2016052564-seq1.txt

<223> consensus Tobacco Etch Virus (TEV) cleavage site

<400> 55

Glu Asn Leu Tyr Phe Gln Ser
1 5