

SEQUENCE LISTING

<110> Hummingbird Bioscience Pte. Ltd (all states)
 Clegg, Richard (LS only)
 <120> Antigen-Binding Molecule Format
 <130> RIC/FP7409303
 <140> PCT/EP2018/083224
 <141> 2018-11-30
 <150> GB 1720028.8
 <151> 2017-12-01
 <160> 135
 <170> PatentIn version 3.5
 <210> 1
 <211> 153
 <212> PRT
 <213> Homo sapiens T-cell receptor delta chain C region (TRDC); UniProt:
 B7Z8K6-1, v2
 <400> 1

Ser Gln Pro His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr
 1 5 10 15

Asn Val Ala Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile
 20 25 30

Asn Leu Val Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val
 35 40 45

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

Asp Ser Asn Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val
 65 70 75 80

His Ser Thr Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys
 85 90 95

Pro Lys Glu Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Cys His Lys
 100 105 110

Pro Lys Ala Ile Val His Thr Glu Lys Val Asn Met Met Ser Leu Thr
 115 120 125

Val Leu Gly Leu Arg Met Leu Phe Ala Lys Thr Val Ala Val Asn Phe
 130 135 140

Leu Leu Thr Ala Lys Leu Phe Phe Leu
145 150

<210> 2
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Construct CD region (C110) (positions 4-110 of B7Z8K6-1, v2)
<400> 2

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Cys
100 105

<210> 3
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Construct CD region (C110A)
<400> 3

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala
100 105

<210> 4

<211> 173

<212> PRT

<213> Homo sapiens T-cell receptor gamma chain C region 1 (TRGC1); UniProt:
P0CF51-1, v1

<400> 4

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

Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys
20 25 30

Leu Leu Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu
35 40 45

Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys
50 55 60

Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Lys
65 70 75 80

Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys
85 90 95

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

Ile Thr Met Asp Pro Lys Asp Asn Cys Ser Lys Asp Ala Asn Asp Thr
115 120 125

Leu Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu
130 135 140

Leu Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys Cys Leu
145 150 155 160

Leu Arg Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
165 170

<210> 5
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC1 constant region (positions 10-138 of P0CF51-1, v1)

<400> 5

Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln
1 5 10 15

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

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

Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser
50 55 60

Trp Leu Thr Val Pro Glu Lys Ser Leu Asp Lys Glu His Arg Cys Ile
65 70 75 80

Val Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe
85 90 95

Pro Pro Ile Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys
100 105 110

Ser Lys Asp Ala Asn Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr Ser
115 120 125

Ala

<210> 6
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC1 Ig-like domain (positions 10-104 of P0CF51-1, v1)

<400> 6

Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln

1	5	10	15
Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Phe Pro Asp Val	20	25	30
Ile Lys Ile His Trp Gln Glu Lys Lys Ser Asn Thr Ile Leu Gly Ser	35	40	45
Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser	50	55	60
Trp Leu Thr Val Pro Glu Lys Ser Leu Asp Lys Glu His Arg Cys Ile	65	70	75
Val Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile Ile	85	90	95

<210> 7
 <211> 34
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRGC1 stem region (positions 105-138 of P0CF51-1, v1)
 <400> 7

Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn	1	5	10	15
Cys Ser Lys Asp Ala Asn Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr	20	25	30	

Ser Ala

<210> 8
 <211> 189
 <212> PRT
 <213> Homo sapiens T-cell receptor gamma-2 chain C region (TRGC2); UniProt: P03986-1, v1
 <400> 8

Asp Lys Gln Leu Asp Ala Asp Val Ser Pro Lys Pro Thr Ile Phe Leu	1	5	10	15
Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys	20	25	30	
Leu Leu Glu Lys Phe Phe Pro Asp Ile Ile Lys Ile His Trp Gln Glu	35	40	45	

Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys
50 55 60

Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu
65 70 75 80

Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys
85 90 95

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

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

Ile Thr Met Asp Pro Lys Asp Asn Trp Ser Lys Asp Ala Asn Asp Thr
130 135 140

Leu Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu
145 150 155 160

Leu Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys Cys Leu
165 170 175

Leu Gly Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
180 185

<210> 9
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2 constant region (positions 10-156 of P03986-1, v1)

<400> 9

Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln
1 5 10 15

Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Phe Pro Asp Ile
20 25 30

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

Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser
50 55 60

Trp Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile
65 70 75 80

Val Arg His Glu Asn Asn Lys Asn Gly Ile Asp Gln Glu Ile Ile Phe
85 90 95

Pro Pro Ile Lys Thr Asp Val Thr Thr Val Asp Pro Lys Asp Ser Tyr
100 105 110

Ser Lys Asp Ala Asn Asp Val Ile Thr Met Asp Pro Lys Asp Asn Trp
115 120 125

Ser Lys Asp Ala Asn Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr Ser
130 135 140

Ala
145

<210> 10
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2 Ig-like domain (positions 10-104)

<400> 10

Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln
1 5 10 15

Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Phe Pro Asp Ile
20 25 30

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

Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser
50 55 60

Trp Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile
65 70 75 80

Val Arg His Glu Asn Asn Lys Asn Gly Ile Asp Gln Glu Ile Ile
85 90 95

<210> 11
<211> 50
<212> PRT
<213> Artificial Sequence

<220>

<223> TRGC2 stem region (positions 105-156 of P03986-1, v1)

<400> 11

Phe Pro Pro Ile Lys Thr Asp Val Thr Thr Val Asp Pro Lys Asp Ser
1 5 10 15

Tyr Ser Lys Asp Ala Asn Asp Val Ile Thr Met Asp Pro Lys Asp Asn
20 25 30

Trp Ser Lys Asp Ala Asn Asp Thr Leu Leu Leu Gln Leu Thr Asn Thr
35 40 45

Ser Ala
50

<210> 12

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Construct CG region (C121)

<400> 12

Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys
1 5 10 15

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

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

Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp
50 55 60

Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile Val
65 70 75 80

Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro
85 90 95

Pro Ile Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys Ser
100 105 110

<210> 13

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Construct CG region (C121A)

<400> 13

Lys Pro Thr Ile Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys
1 5 10 15

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

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

Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp
50 55 60

Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile Val
65 70 75 80

Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro
85 90 95

Pro Ile Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Ala Ser
100 105 110

<210> 14

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGC joint

<400> 14

Thr Asp Lys Gln Leu Asp Ala Asp Val Ser Pro
1 5 10

<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Optimised TRGC joint 1

<400> 15

Leu Asp Ser Asp Gly Ser Pro
1 5

<210> 16
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL-CG joint

<400> 16

Arg Thr Leu Asp Ser Asp Gly Ser Pro
 1 5

<210> 17
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRDC joint

<400> 17

Glu Pro Arg Ser Gln Pro His Thr
 1 5

<210> 18
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Optimised TRDC joint

<400> 18

Leu Thr Val Ser Ser Ala Ser
 1 5

<210> 19
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH-CD joint

<400> 19

Leu Thr Val Ser Ser Ala Ser His Thr
 1 5

<210> 20
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD-CH2 hinge

<400> 20

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

<210> 21

<211> 330

<212> PRT

<213> Homo sapiens IgG1 constant region (IGHG1; UniProt:P01857-1, v1)

<400> 21

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

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

195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

 <210> 22
 <211> 98
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> CH1 IgG1 (positions 1-98 of P01857-1, v1)

 <400> 22

 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15

 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 23
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge IgG1 (positions 99-110 of P01857-1, v1)

<400> 23

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

<210> 24
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2 IgG1 (positions 111-223 of P01857-1, v1)

<400> 24

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 25
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH3 IgG1 (positions 224-330 of P01857-1, v1)

<400> 25

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60

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

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 26
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH anti-CD33

<400> 26

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

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

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 27
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL anti-CD33

<400> 27

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

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

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 28
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> IL-2 signal peptide

<400> 28

Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu
1				5					10					15	

Val	Thr	Asn	Ser
			20

<210> 29

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Partial H joint

<400> 29

Ala	Ser
1	

<210> 30

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> CH3 (D356E, L358M; positions numbered according to EU numbering)

<400> 30

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

Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			20					25					30		

Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		35					40					45			

Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	50					55					60				

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

Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85					90					95	

Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
				100				105		

<210> 31
 <211> 481
 <212> PRT
 <213> Artificial Sequence

<220>

<223> SignalP-anti-CD33 VH-CD (C110A)-hinge-CH2-CH3

<400> 31

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1 5 10 15

Val Thr Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 20 25 30

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
 35 40 45

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
 50 55 60

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

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
 85 90 95

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

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
 115 120 125

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

Phe Val Met Lys Asn Gly Thr Asn Val Ala Cys Leu Val Lys Glu Phe
 145 150 155 160

Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr
 165 170 175

Glu Phe Asp Pro Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala
 180 185 190

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

Gln His Asp Asn Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr
 210 215 220
 Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln
 225 230 235 240
 Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys
 245 250 255
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 260 265 270
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 275 280 285
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 290 295 300
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 305 310 315 320
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 325 330 335
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 340 345 350
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 355 360 365
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 370 375 380
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 385 390 395 400
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 405 410 415
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 420 425 430
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 435 440 445
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 32
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VH-CD (C110A)-hinge-CH2-CH3

<400> 32

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser His Thr Lys Pro Ser Val Phe Val Met Lys
115 120 125

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

Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro
145 150 155 160

Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly
165 170 175

Lys Tyr Glu Asp Ser Asn Ser Val Thr Cys Ser Val Gln His Asp Asn
 180 185 190

Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr Asp Ser Thr Asp
 195 200 205

His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser
 210 215 220

Ala Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys Thr His Thr Cys
 225 230 235 240

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 340 345 350

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 355 360 365

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 405 410 415

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 33
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> SignalP-anti-CD33 VH-CD (C110)-hinge-CH2-CH3

<400> 33

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
20 25 30

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
35 40 45

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
50 55 60

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

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
85 90 95

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

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
115 120 125

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

Phe Val Met Lys Asn Gly Thr Asn Val Ala Cys Leu Val Lys Glu Phe
145 150 155 160

Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr
165 170 175

Glu Phe Asp Pro Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala
 180 185 190

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

Gln His Asp Asn Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr
 210 215 220

Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln
 225 230 235 240

Pro Ser Lys Ser Cys Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys
 245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 370 375 380

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 34
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VH-CD (C110)-hinge-CH2-CH3

<400> 34

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser His Thr Lys Pro Ser Val Phe Val Met Lys
115 120 125

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

Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro
 145 150 155 160

Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly
 165 170 175

Lys Tyr Glu Asp Ser Asn Ser Val Thr Cys Ser Val Gln His Asp Asn
 180 185 190

Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr Asp Ser Thr Asp
 195 200 205

His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser
 210 215 220

Cys Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys Thr His Thr Cys
 225 230 235 240

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 340 345 350

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 355 360 365

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
405 410 415

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 35

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> SignalP-anti-CD33 VL-CG (C121A)

<400> 35

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser
35 40 45

Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro
50 55 60

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

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

Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile
130 135 140

Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr
145 150 155 160

Leu Cys Leu Leu Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp
165 170 175

Gln Glu Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr
180 185 190

Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro
195 200 205

Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn
210 215 220

Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr
225 230 235 240

Asp Val Ile Thr Met Asp Pro Lys Asp Asn Ala Ser Gly
245 250

<210> 36
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VL-CG (C121A)

<400> 36

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

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

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser
115 120 125

Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu
130 135 140

Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys
145 150 155 160

Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn
165 170 175

Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu
180 185 190

Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly
195 200 205

Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr
210 215 220

Met Asp Pro Lys Asp Asn Ala Ser Gly
225 230

<210> 37
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> SignalP-anti-CD33 VL-CG (C121)

<400> 37

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser
35 40 45

Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro
50 55 60

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser

65

70

75

80

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

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

Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile
130 135 140

Phe Leu Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr
145 150 155 160

Leu Cys Leu Leu Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp
165 170 175

Gln Glu Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr
180 185 190

Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro
195 200 205

Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn
210 215 220

Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr
225 230 235 240

Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys Ser Gly
245 250

<210> 38

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-CD33 VL-CG (C121)

<400> 38

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

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

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser
115 120 125

Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu
130 135 140

Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys
145 150 155 160

Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn
165 170 175

Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu
180 185 190

Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly
195 200 205

Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr
210 215 220

Met Asp Pro Lys Asp Asn Cys Ser Gly
225 230

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> C? CL (IGCK; UniProt: P01834-1, v2)

<400> 39

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 40
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VL-Ckappa

<400> 40

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

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

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

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

Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

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

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

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

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

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

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

<210> 41
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VH-IgG1

<400> 41

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 42
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> SignalP-anti-CD33 VH-CD (C110A)-hinge-CH2-CH3_hole
<400> 42

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
20 25 30

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
35 40 45

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
50 55 60

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

Asn Gln Lys Phe Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr
85 90 95

Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala

100

105

110

Val Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln
 115 120 125

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

Phe Val Met Lys Asn Gly Thr Asn Val Ala Cys Leu Val Lys Glu Phe
 145 150 155 160

Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr
 165 170 175

Glu Phe Asp Pro Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala
 180 185 190

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

Gln His Asp Asn Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr
 210 215 220

Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln
 225 230 235 240

Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys
 245 250 255

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 260 265 270

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 275 280 285

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 290 295 300

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 305 310 315 320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
370 375 380

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

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 43
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VH-CD (C110A)-hinge-CH2-CH3_hole

<400> 43

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
340 345 350

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
405 410 415

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 44
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> SignalP-anti-CD33 VH-CD (C110)-hinge-CH2-CH3_hole

<400> 44

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
20 25 30

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
35 40 45

Phe Thr Asp Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
50 55 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr

65					70						75				80
Asn	Gln	Lys	Phe	Lys	Ser	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr
				85					90					95	
Asn	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala
			100					105					110		
Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Arg	Pro	Ala	Met	Asp	Tyr	Trp	Gly	Gln
		115					120					125			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	His	Thr	Lys	Pro	Ser	Val
	130					135					140				
Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala	Cys	Leu	Val	Lys	Glu	Phe
145					150					155					160
Tyr	Pro	Lys	Asp	Ile	Arg	Ile	Asn	Leu	Val	Ser	Ser	Lys	Lys	Ile	Thr
				165				170						175	
Glu	Phe	Asp	Pro	Ala	Ile	Val	Ile	Ser	Pro	Ser	Gly	Lys	Tyr	Asn	Ala
			180					185					190		
Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn	Ser	Val	Thr	Cys	Ser	Val
		195					200					205			
Gln	His	Asp	Asn	Lys	Thr	Val	His	Ser	Thr	Asp	Phe	Glu	Val	Lys	Thr
	210					215					220				
Asp	Ser	Thr	Asp	His	Val	Lys	Pro	Lys	Glu	Thr	Glu	Asn	Thr	Lys	Gln
225					230					235					240
Pro	Ser	Lys	Ser	Cys	Ser	Gly	Gly	Gly	Arg	Pro	Lys	Ser	Ala	Asp	Lys
				245					250					255	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
			260					265					270		
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
		275					280					285			
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
	290					295					300				
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
305					310					315					320

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
340 345 350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
370 375 380

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

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 45
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD33 VH-CD (C110)-hinge-CH2-CH3_hole

<400> 45

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

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

Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser His Thr Lys Pro Ser Val Phe Val Met Lys
115 120 125

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

Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro
145 150 155 160

Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly
165 170 175

Lys Tyr Glu Asp Ser Asn Ser Val Thr Cys Ser Val Gln His Asp Asn
180 185 190

Lys Thr Val His Ser Thr Asp Phe Glu Val Lys Thr Asp Ser Thr Asp
195 200 205

His Val Lys Pro Lys Glu Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser
210 215 220

Cys Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp Lys Thr His Thr Cys
225 230 235 240

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 340 345 350

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
 370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 405 410 415

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455 460

<210> 46

<211> 141

<212> PRT

<213> Homo sapiens TRAC (UniProt: A0N8L7-1, v1)

<400> 46

Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
 20 25 30

Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
 35 40 45

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
 50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
 65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
 85 90 95

Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
 100 105 110

Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
 115 120 125

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 130 135 140

<210> 47
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRBC1 (GenBank Accession No. AAA60661.1; GI:338834)
 <400> 47

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

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

Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
 35 40 45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
 50 55 60

Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
 65 70 75 80

Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
 85 90 95

Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
 100 105 110

Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala

115 120 125
 Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala
 130 135 140

 Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
 145 150 155 160

 Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Phe
 165 170 175

 <210> 48
 <211> 178
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> TRBC2 (GenBank Accession No. AAA60662.1; GI:338836)

 <400> 48

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

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

 Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
 35 40 45

 Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
 50 55 60

 Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
 65 70 75 80

 Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
 85 90 95

 Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
 100 105 110

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

 Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
 130 135 140

 Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
 145 150 155 160

Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
165 170 175

Arg Gly

<210> 49
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2 (2x) (GenBank Accession No. M15002.1; GI:339083)

<400> 49

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

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

Leu Glu Lys Phe Phe Pro Asp Ile Ile Lys Ile His Trp Gln Glu Lys
35 40 45

Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr
50 55 60

Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser
65 70 75 80

Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn
85 90 95

Gly Ile Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr
100 105

<210> 50
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2 (3x) (GenBank Accession No. AAB63312.1; GI:2072750;)

<400> 50

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

Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu

20

25

30

Leu Glu Lys Phe Phe Pro Asp Ile Ile Lys Ile His Trp Gln Glu Lys
 35 40 45

Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr
 50 55 60

Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser
 65 70 75 80

Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn
 85 90 95

Gly Ile Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Thr
 100 105 110

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

Thr Val Asp Pro Lys Tyr Asn Tyr Ser Lys Asp Ala Asn Asp Val Ile
 130 135 140

Thr Met Asp Pro Lys Asp Asn Trp Ser Lys Asp Ala Asn Asp Thr Leu
 145 150 155 160

Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu Leu
 165 170 175

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

Gly Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
 195 200

<210> 51
 <211> 189
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRGC2*01 (2x) (GenBank Accession No. M13231)

<400> 51

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

Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys
 20 25 30

Leu Leu Glu Lys Phe Phe Pro Asp Ile Ile Lys Ile His Trp Gln Glu
35 40 45

Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys
50 55 60

Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu
65 70 75 80

Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys
85 90 95

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

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

Ile Thr Met Asp Pro Lys Asp Asn Trp Ser Lys Asp Ala Asn Asp Thr
130 135 140

Leu Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu
145 150 155 160

Leu Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys Cys Leu
165 170 175

Leu Gly Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
180 185

<210> 52
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2*02 (2x) (GenBank Accession No. M15004)

<400> 52

Val Thr Thr Val Asp Pro Lys Tyr Asn Tyr Ser Lys Asp Ala Asn
1 5 10 15

<210> 53
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> TRGC2*08 (2x) (GenBank Accession No. M27332)

<400> 53

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

Pro Ser Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys
20 25 30

Leu Leu Glu Lys Phe Phe Pro Asp Ile Ile Lys Ile His Trp Gln Glu
35 40 45

Lys Lys Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys
50 55 60

Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu
65 70 75 80

Ser Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys
85 90 95

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

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

Ile Thr Met Asp Pro Lys Asp Asn Trp Ser Lys Asp Ala Asn Asp Thr
130 135 140

Leu Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu Leu
145 150 155 160

Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys Cys Leu Leu
165 170 175

Gly Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
180 185

<210> 54

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Optimised TRGC joint 2

<400> 54

Leu Asp Ala Asp Val Ser Pro
1 5

<210> 55
 <211> 4
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Optimised TRGC joint 3
 <400> 55

Val Ala Ser Pro
 1

<210> 56
 <211> 2
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Partial joint
 <400> 56

Ser Gly
 1

<210> 57
 <211> 82
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> CD region consensus sequence

<220>
 <221> MISC_FEATURE
 <222> (1) .. (1)
 <223> Xaa = H or T

<220>
 <221> MISC_FEATURE
 <222> (2) .. (2)
 <223> Xaa = T or K

<220>
 <221> MISC_FEATURE
 <222> (3) .. (3)
 <223> Xaa = K or G

<220>
 <221> MISC_FEATURE
 <222> (9) .. (9)
 <223> Xaa = M or C

<220>
 <221> MISC_FEATURE
 <222> (11) .. (11)
 <223> Xaa = N or A

<220>
<221> MISC_FEATURE
<222> (23) .. (23)
<223> Xaa = Y, F or L

<220>
<221> MISC_FEATURE
<222> (25) .. (25)
<223> Xaa = K, E or D

<220>
<221> MISC_FEATURE
<222> (26) .. (26)
<223> Xaa = D, P or S

<220>
<221> MISC_FEATURE
<222> (27) .. (27)
<223> Xaa = I or V

<220>
<221> MISC_FEATURE
<222> (43) .. (43)
<223> Xaa = A or S

<220>
<221> MISC_FEATURE
<222> (44) .. (44)
<223> Xaa = I, V or absent

<220>
<221> MISC_FEATURE
<222> (45) .. (45)
<223> Xaa = V or L

<220>
<221> MISC_FEATURE
<222> (46) .. (46)
<223> Xaa = I, Q or L

<220>
<221> MISC_FEATURE
<222> (47) .. (47)
<223> Xaa = S or absent

<220>
<221> MISC_FEATURE
<222> (48) .. (48)
<223> Xaa = P, S or R

<220>
<221> MISC_FEATURE
<222> (49) .. (49)
<223> Xaa = S or G

<220>
<221> MISC_FEATURE
<222> (50) .. (50)
<223> Xaa = G or L

<220>
<221> MISC_FEATURE

<222> (51) .. (51)
 <223> Xaa = K or absent

<220>
 <221> MISC_FEATURE
 <222> (82) .. (82)
 <223> Xaa = F or C

<400> 57

Xaa Xaa Xaa Pro Ser Val Phe Val Xaa Lys Xaa Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Xaa Pro Xaa Xaa Xaa Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Xaa

<210> 58
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 1 (dTCR_1)

<400> 58

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
 1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Cys Ser Gly Gly Gly Arg Pro Lys
 20 25 30

Ser Ala Asp Lys Thr His Thr Cys Pro
 35 40

<210> 59
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 2 (dTCR_2)

<400> 59

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Cys Ser Gly
20 25

<210> 60

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> CD Stem region 3 (dTCR_3; dTCR_5; dTCR_6; dTCR_10; dTCR_11;
dTCR_14; dTCR_15; dTCR_16; dTCR_17; dTCR_18; dTCR_19; dTCR_20;
dTCR_21)

<400> 60

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro Lys
20 25 30

Ser Ala Asp Lys Thr His Thr Cys Pro
35 40

<210> 61

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> CD Stem region 4 (dTCR_4)

<400> 61

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly
20 25

<210> 62

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CD Stem region 5 (dTCR_7; dTCR_12; dTCR_13)

<400> 62

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

<210> 63
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 6 (dTCR_8)

<400> 63

Glu Val Ser Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 1 5 10

<210> 64
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 7 (dTCR_9)

<400> 64

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

<210> 65
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 8 (dTCR_22)

<400> 65

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

<210> 66
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 9 (Construct CD region (C110) SEQ ID NO:2)

<400> 66

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
 1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Cys
 20 25

<210> 67
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD Stem region 10 (Construct CD region (C110A) SEQ ID NO:3)

<400> 67

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
 1 5 10 15

Asn Thr Lys Gln Pro Ser Lys Ser Ala
 20 25

<210> 68
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_1

<400> 68

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
 85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Cys Ser Gly Gly Gly Arg
 100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
 115 120

<210> 69
 <211> 109

<212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_2

<400> 69

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
 85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Cys Ser Gly
 100 105

<210> 70
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_3

<400> 70

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr

65

70

75

80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 71

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> dTCR_4

<400> 71

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly
100 105

<210> 72

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> dTCR_5

<400> 72

His Thr Lys Pro Ser Val Phe Val Cys Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
 85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Arg
 100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
 115 120

<210> 73
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_6

<400> 73

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Cys Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu

85

90

95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
 100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
 115 120

<210> 74
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_7

<400> 74

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
 35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
 50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
 65 70 75 80

Asp Phe Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 85 90

<210> 75
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> dTCR_8

<400> 75

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
 1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
 20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Ser Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
85 90 95

<210> 76
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_9

<400> 76

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Ser Thr Asp Pro Lys Ser Cys Asp Lys Thr His Thr
85 90 95

Cys Pro

<210> 77
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_10

<400> 77

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 78
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_11

<400> 78

His Thr Lys Pro Ser Val Phe Val Met Lys Ala Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 79
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_12

<400> 79

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
85 90

<210> 80
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_13

<400> 80

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
85 90

<210> 81
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_14

<400> 81

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Phe Pro Glu Pro Val Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 82
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> dTCR_15

<400> 82

Thr	Lys	Gly	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Phe	Pro	Glu	Pro	Val	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ala	Ile	Val	Ile	Ser	Pro
		35					40					45			

Ser	Gly	Lys	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn
	50					55					60				

Ser	Val	Thr	Cys	Ser	Val	Gln	His	Asp	Asn	Lys	Thr	Val	His	Ser	Thr
65					70					75					80

Asp	Cys	Glu	Val	Lys	Thr	Asp	Ser	Thr	Asp	His	Val	Lys	Pro	Lys	Glu
				85					90					95	

Thr	Glu	Asn	Thr	Lys	Gln	Pro	Ser	Lys	Ser	Ala	Ser	Gly	Gly	Gly	Arg
			100					105					110		

Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro
		115					120			

<210> 83

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> dTCR_16

<400> 83

His	Thr	Lys	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Phe	Pro	Glu	Pro	Val	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ser	Val	Leu	Gln	Ser	Ser
		35					40					45			

Gly	Leu	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn	Ser
	50					55					60				

Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr Asp
65 70 75 80

Cys Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr
85 90 95

Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro
100 105 110

Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 84
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_17

<400> 84

Thr Lys Gly Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Phe Pro Glu Pro Val Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ser Val Leu Gln Ser Ser
35 40 45

Gly Leu Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn Ser
50 55 60

Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr Asp
65 70 75 80

Cys Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr
85 90 95

Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro
100 105 110

Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 85
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<223> dTCR_18

<400> 85

His	Thr	Lys	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Leu	Pro	Asp	Ser	Ile	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ala	Ile	Val	Ile	Ser	Pro
		35					40					45			

Ser	Gly	Lys	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn
	50					55					60				

Ser	Val	Thr	Cys	Ser	Val	Gln	His	Asp	Asn	Lys	Thr	Val	His	Ser	Thr
65					70					75					80

Asp	Cys	Glu	Val	Lys	Thr	Asp	Ser	Thr	Asp	His	Val	Lys	Pro	Lys	Glu
				85					90					95	

Thr	Glu	Asn	Thr	Lys	Gln	Pro	Ser	Lys	Ser	Ala	Ser	Gly	Gly	Gly	Arg
			100					105					110		

Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro
		115					120			

<210> 86

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> dTCR_19

<400> 86

Thr	Lys	Gly	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Leu	Pro	Asp	Ser	Ile	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ala	Ile	Val	Ile	Ser	Pro
		35					40					45			

Ser	Gly	Lys	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn
	50					55					60				

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu
85 90 95

Thr Glu Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 87
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_20

<400> 87

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Leu Pro Asp Ser Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ser Val Leu Arg Gly Gly
35 40 45

Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn Ser Val
50 55 60

Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr Asp Cys
65 70 75 80

Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr Glu
85 90 95

Asn Thr Lys Gln Pro Ser Lys Ser Ala Ser Gly Gly Gly Arg Pro Lys
100 105 110

Ser Ala Asp Lys Thr His Thr Cys Pro
115 120

<210> 88
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> dTCR_21

<400> 88

Thr	Lys	Gly	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Leu	Pro	Asp	Ser	Ile	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ser	Val	Leu	Arg	Gly	Gly
		35					40					45			

Lys	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn	Ser	Val
	50					55					60				

Thr	Cys	Ser	Val	Gln	His	Asp	Asn	Lys	Thr	Val	His	Ser	Thr	Asp	Cys
65					70					75					80

Glu	Val	Lys	Thr	Asp	Ser	Thr	Asp	His	Val	Lys	Pro	Lys	Glu	Thr	Glu
				85					90					95	

Asn	Thr	Lys	Gln	Pro	Ser	Lys	Ser	Ala	Ser	Gly	Gly	Gly	Arg	Pro	Lys
			100					105					110		

Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro
		115					120	

<210> 89

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> dTCR_22

<400> 89

His	Thr	Lys	Pro	Ser	Val	Phe	Val	Met	Lys	Asn	Gly	Thr	Asn	Val	Ala
1				5					10					15	

Cys	Leu	Val	Lys	Glu	Phe	Tyr	Pro	Lys	Asp	Ile	Arg	Ile	Asn	Leu	Val
			20					25					30		

Ser	Ser	Lys	Lys	Ile	Thr	Glu	Phe	Asp	Pro	Ala	Ile	Val	Ile	Ser	Pro
		35					40					45			

Ser	Gly	Lys	Tyr	Asn	Ala	Val	Lys	Leu	Gly	Lys	Tyr	Glu	Asp	Ser	Asn
	50					55					60				

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr
85 90

<210> 90
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> dTCR_23

<400> 90

His Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala
1 5 10 15

Cys Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val
20 25 30

Ser Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro
35 40 45

Ser Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn
50 55 60

Ser Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr
65 70 75 80

Asp Cys

<210> 91
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> CG region consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = P or absent

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = F or C

<220>

<221> MISC_FEATURE
<222> (11) .. (11)
<223> Xaa = A or C

<220>
<221> MISC_FEATURE
<222> (29) .. (29)
<223> Xaa = F or Y

<220>
<221> MISC_FEATURE
<222> (31) .. (31)
<223> Xaa = D or R

<220>
<221> MISC_FEATURE
<222> (32) .. (32)
<223> Xaa = V, E or I

<220>
<221> MISC_FEATURE
<222> (52) .. (52)
<223> Xaa = N or V

<220>
<221> MISC_FEATURE
<222> (54) .. (54)
<223> Xaa = M or E

<220>
<221> MISC_FEATURE
<222> (55) .. (55)
<223> Xaa = K or Q

<220>
<221> MISC_FEATURE
<222> (56) .. (56)
<223> Xaa = T or D

<220>
<221> MISC_FEATURE
<222> (57) .. (57)
<223> Xaa = N or S

<220>
<221> MISC_FEATURE
<222> (58) .. (58)
<223> Xaa = D or K

<220>
<221> MISC_FEATURE
<222> (59) .. (59)
<223> Xaa = D or absent

<220>
<221> MISC_FEATURE
<222> (60) .. (60)
<223> Xaa = S or absent

<220>
<221> MISC_FEATURE
<222> (73) .. (73)
<223> Xaa = K or E

<220>

<221> MISC_FEATURE

<222> (92)..(92)

<223> Xaa = V or I

<400> 91

Xaa	Lys	Pro	Thr	Ile	Xaa	Leu	Pro	Ser	Ile	Xaa	Glu	Thr	Lys	Leu	Gln
1				5					10					15	

Lys	Ala	Gly	Thr	Tyr	Leu	Cys	Leu	Leu	Glu	Lys	Phe	Xaa	Pro	Xaa	Xaa
			20					25					30		

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

Gln	Glu	Gly	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Tyr	Met	Lys
	50					55						60			

Phe	Ser	Trp	Leu	Thr	Val	Pro	Glu	Xaa	Ser	Leu	Asp	Lys	Glu	His	Arg
65					70					75					80

Cys	Ile	Val	Arg	His	Glu	Asn	Asn	Lys	Asn	Gly	Xaa	Asp	Gln	Glu	Ile
				85					90					95	

Ile	Phe	Pro	Pro	Ile
				100

<210> 92

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> CG Stem region 1 (gTCR_1; gTCR_3)

<400> 92

Lys	Thr	Asp	Val	Ile	Thr	Met	Asp	Pro	Lys	Asp	Asn	Cys	Ser	Gly	Gly
1				5					10					15	

Gly	Arg	Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro
			20					25				

<210> 93

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> CG Stem region 2 (gTCR_5; gTCR_7)

<400> 93

Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Ala Ser Gly Gly
 1 5 10 15

Gly Arg Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
 20 25

<210> 94
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 3 (gTCR_2; gTCR_4)

<400> 94

Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Cys Ser Gly
 1 5 10 15

<210> 95
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 4 (gTCR_6; gTCR_8; gTCR_9; gTCR_10; gTCR_13;
 gTCR_16; gTCR_17; gTCR_18; gTCR_19; gTCR_20; gTCR_21)

<400> 95

Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Ala Ser Gly
 1 5 10 15

<210> 96
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 5 (gTCR_11; gTCR_22)

<400> 96

Gly Glu Cys
 1

<210> 97
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 6 (gTCR_12; gTCR_14)

<400> 97

Ser Gly Glu Cys

1

<210> 98
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 7 (TRGC1 constant region SEQ ID NO:5)

<400> 98

Lys	Thr	Asp	Val	Ile	Thr	Met	Asp	Pro	Lys	Asp	Asn	Cys	Ser	Lys	Asp
1				5					10					15	

Ala	Asn	Asp	Thr	Leu	Leu	Leu	Gln	Leu	Thr	Asn	Thr	Ser	Ala
			20					25					30

<210> 99
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 8 (TRGC2 constant region SEQ ID NO:9)

<400> 99

Lys	Thr	Asp	Val	Thr	Thr	Val	Asp	Pro	Lys	Asp	Ser	Tyr	Ser	Lys	Asp
1				5					10					15	

Ala	Asn	Asp	Val	Ile	Thr	Met	Asp	Pro	Lys	Asp	Asn	Trp	Ser	Lys	Asp
			20					25					30		

Ala	Asn	Asp	Thr	Leu	Leu	Leu	Gln	Leu	Thr	Asn	Thr	Ser	Ala
			35				40					45	

<210> 100
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CG Stem region 9 (Construct CG region (C121) SEQ ID NO:12)

<400> 100

Lys	Thr	Asp	Val	Ile	Thr	Met	Asp	Pro	Lys	Asp	Asn	Cys	Ser
1				5					10				

<210> 101
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CG Stem region 10 (Construct CG region (C121A) SEQ ID NO:13)

<400> 101

Lys Thr Asp Val Ile Thr Met Asp Pro Lys Asp Asn Ala Ser
1 5 10

<210> 102

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> gTCR_1

<400> 102

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Cys Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp
115 120 125

Lys Thr His Thr Cys Pro
130

<210> 103

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> gTCR_2

<400> 103

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
 1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
 50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
 65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
 85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
 100 105 110

Asp Pro Lys Asp Asn Cys Ser Gly
 115 120

<210> 104
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_3

<400> 104

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

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
 50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
 65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Cys Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp
115 120 125

Lys Thr His Thr Cys Pro
130

<210> 105
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_4

<400> 105

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

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Cys Ser Gly
115 120

<210> 106
<211> 134
<212> PRT
<213> Artificial Sequence

<220>

<223> gTCR_5

<400> 106

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp
115 120 125

Lys Thr His Thr Cys Pro
130

<210> 107

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> gTCR_6

<400> 107

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly
115 120

<210> 108
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_7

<400> 108

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

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly Gly Gly Arg Pro Lys Ser Ala Asp
115 120 125

Lys Thr His Thr Cys Pro

130

<210> 109
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_8

<400> 109

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

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
 50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
 65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
 85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
 100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly
 115 120

<210> 110
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_9

<400> 110

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Cys Leu Pro Ser Ile
 1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly
115 120

<210> 111
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_10

<400> 111

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly

115

120

<210> 112
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_11

<400> 112

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
 1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
 50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
 65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
 85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Gly Glu Cys
 100 105

<210> 113
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_12

<400> 113

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
 1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Ser Gly Glu Cys
100 105

<210> 114
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_13

<400> 114

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly
115 120

<210> 115
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> gTCR_14

<400> 115

Leu	Asp	Ser	Asp	Gly	Ser	Pro	Lys	Pro	Thr	Ile	Phe	Leu	Pro	Ser	Ile
1				5					10					15	

Cys	Glu	Thr	Lys	Leu	Gln	Lys	Ala	Gly	Thr	Tyr	Leu	Cys	Leu	Leu	Glu
			20					25					30		

Lys	Phe	Phe	Pro	Asp	Val	Ile	Lys	Ile	His	Trp	Gln	Glu	Lys	Lys	Ser
		35					40					45			

Asn	Thr	Ile	Leu	Gly	Ser	Gln	Glu	Gly	Asn	Thr	Met	Lys	Thr	Asn	Asp
	50					55					60				

Thr	Tyr	Met	Lys	Phe	Ser	Trp	Leu	Thr	Val	Pro	Glu	Glu	Ser	Leu	Asp
65					70					75					80

Lys	Glu	His	Arg	Cys	Ile	Val	Arg	His	Glu	Asn	Asn	Lys	Asn	Gly	Val
				85					90					95	

Asp	Gln	Glu	Ile	Ile	Phe	Pro	Pro	Ile	Ser	Gly	Glu	Cys
			100					105				

<210> 116

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> gTCR_15

<400> 116

Leu	Asp	Ser	Asp	Gly	Ser	Pro	Lys	Pro	Thr	Ile	Phe	Leu	Pro	Ser	Ile
1				5					10					15	

Cys	Glu	Thr	Lys	Leu	Gln	Lys	Ala	Gly	Thr	Tyr	Leu	Cys	Leu	Leu	Glu
			20					25					30		

Lys	Phe	Phe	Pro	Asp	Val	Ile	Lys	Ile	His	Trp	Gln	Glu	Lys	Lys	Ser
		35					40					45			

Asn	Thr	Ile	Leu	Gly	Ser	Gln	Glu	Gly	Asn	Thr	Met	Lys	Thr	Asn	Asp
	50					55					60				

Thr	Tyr	Met	Lys	Phe	Ser	Trp	Leu	Thr	Val	Pro	Glu	Glu	Ser	Leu	Asp
65					70					75					80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile
100 105

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

<220>
<223> gTCR_16

<400> 117

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

Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Phe
20 25 30

Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser Asn Thr Ile
35 40 45

Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met
50 55 60

Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His
65 70 75 80

Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu
85 90 95

Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met Asp Pro Lys
100 105 110

Asp Asn Ala Ser Gly
115

<210> 118
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_17

<400> 118

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Tyr Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
100 105 110

Asp Pro Lys Asp Asn Ala Ser Gly
115 120

<210> 119
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_18

<400> 119

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
1 5 10 15

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
20 25 30

Lys Phe Tyr Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Val Thr Glu Gln Asp Ser Lys
50 55 60

Asp Ser Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser
65 70 75 80

Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn
85 90 95

Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile
 100 105 110

Thr Met Asp Pro Lys Asp Asn Ala Ser Gly
 115 120

<210> 120
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_19

<400> 120

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
 1 5 10 15

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Tyr Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Asp Ser Lys
 50 55 60

Asp Ser Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser
 65 70 75 80

Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn
 85 90 95

Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile
 100 105 110

Thr Met Asp Pro Lys Asp Asn Ala Ser Gly
 115 120

<210> 121
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_20

<400> 121

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

Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Tyr
20 25 30

Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser Asn Thr Ile
35 40 45

Leu Gly Ser Gln Glu Gly Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp Lys
65 70 75 80

Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val Asp
85 90 95

Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met Asp
100 105 110

Pro Lys Asp Asn Ala Ser Gly
115

<210> 122

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> gTCR_21

<400> 122

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

Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu Lys Phe Tyr
20 25 30

Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser Asn Thr Ile
35 40 45

Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp Lys
65 70 75 80

Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val Asp
85 90 95

Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met Asp
 100 105 110

Pro Lys Asp Asn Ala Ser Gly
 115

<210> 123
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_22

<400> 123

Leu Asp Ser Asp Gly Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser Ile
 1 5 10 15

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Tyr Pro Arg Glu Ile Lys Ile His Trp Gln Glu Lys Lys Ser
 35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Asp Ser Lys
 50 55 60

Asp Ser Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser
 65 70 75 80

Leu Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn
 85 90 95

Gly Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Ser Gly Glu Cys
 100 105 110

<210> 124
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> gTCR_23

<400> 124

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

Cys Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu Glu
 20 25 30

Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Gln Glu Lys Lys Ser
35 40 45

Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn Asp
50 55 60

Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Glu Ser Leu Asp
65 70 75 80

Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val
85 90 95

Asp Gln Glu Ile Ile Phe Pro Pro Ile Gly Glu Cys
100 105

<210> 125
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> gTCR_24

<400> 125

Lys Pro Thr Ile Phe Leu Pro Ser Ile Cys Glu Thr Lys Leu Gln Lys
1 5 10 15

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

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

Glu Gly Asn Thr Met Lys Thr Asn Asp Thr Tyr Met Lys Phe Ser Trp
50 55 60

Leu Thr Val Pro Glu Glu Ser Leu Asp Lys Glu His Arg Cys Ile Val
65 70 75 80

Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile Ile Phe Pro
85 90 95

Pro Ile

<210> 126
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> DC-Hinge Linker 1

<400> 126

Ser Gly Gly Gly

1

<210> 127

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> DC-Hinge Linker 2

<400> 127

Ser Gly Gly Gly Arg

1

5

<210> 128

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CD Stem region 11

<400> 128

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro

1

5

10

<210> 129

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> TRDC transmembrane region

<400> 129

Leu Gly Leu Arg Met Leu Phe Ala Lys Thr Val Ala Val Asn Phe Leu

1

5

10

15

Leu Thr Ala Lys Leu Phe Phe

20

<210> 130

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGC1 transmembrane region

<400> 130

Tyr Tyr Met Tyr Leu Leu Leu Leu Lys Ser Val Val Tyr Phe Ala
1 5 10 15

Ile Ile Thr Cys Cys Leu Leu
20

<210> 131

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGC2 transmembrane region

<400> 131

Met Tyr Leu Leu Leu Leu Lys Ser Val Val Tyr Phe Ala Ile Ile
1 5 10 15

Thr Cys Cys Leu Leu
20

<210> 132

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGC1 cytoplasmic tail

<400> 132

Arg Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
1 5 10

<210> 133

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TRGC2 cytoplasmic tail

<400> 133

Gly Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser
1 5 10

<210> 134

<211> 251

<212> PRT

<213> Homo sapiens TCR gamma chains

<400> 134

Glu	Thr	Gly	Ser	Ser	Asn	Leu	Glu	Gly	Gly	Thr	Lys	Ser	Val	Thr	Arg	1	5	10	15
Pro	Thr	Arg	Ser	Ser	Ala	Glu	Ile	Thr	Cys	Asp	Leu	Thr	Val	Ile	Asn	20	25	30	
Ala	Phe	Tyr	Ile	His	Trp	Tyr	Leu	His	Gln	Glu	Gly	Lys	Ala	Pro	Gln	35	40	45	
Arg	Leu	Leu	Tyr	Tyr	Asp	Val	Ser	Asn	Ser	Lys	Asp	Val	Leu	Glu	Ser	50	55	60	
Gly	Leu	Ser	Pro	Gly	Lys	Tyr	Tyr	Thr	His	Thr	Pro	Arg	Arg	Trp	Ser	65	70	75	80
Trp	Ile	Leu	Ile	Leu	Arg	Asn	Leu	Ile	Glu	Asn	Asp	Ser	Gly	Val	Tyr	85	90	95	
Tyr	Cys	Ala	Thr	Trp	Asp	Arg	Gly	Asn	Pro	Lys	Thr	His	Tyr	Tyr	Lys	100	105	110	
Lys	Leu	Phe	Gly	Ser	Gly	Thr	Thr	Leu	Val	Val	Thr	Asp	Lys	Gln	Leu	115	120	125	
Asp	Ala	Asp	Val	Ser	Pro	Lys	Pro	Thr	Ile	Phe	Leu	Pro	Ser	Ile	Ala	130	135	140	
Glu	Thr	Lys	Leu	Gln	Lys	Ala	Gly	Thr	Tyr	Leu	Cys	Leu	Leu	Glu	Lys	145	150	155	160
Phe	Phe	Pro	Asp	Val	Ile	Lys	Ile	His	Trp	Gln	Glu	Lys	Lys	Ser	Asn	165	170	175	
Thr	Ile	Leu	Gly	Ser	Gln	Glu	Gly	Asn	Thr	Met	Lys	Thr	Asn	Asp	Thr	180	185	190	
Tyr	Met	Lys	Phe	Ser	Trp	Leu	Thr	Val	Pro	Glu	Glu	Ser	Leu	Asp	Lys	195	200	205	
Glu	His	Arg	Cys	Ile	Val	Arg	His	Glu	Asn	Asn	Lys	Asn	Gly	Val	Asp	210	215	220	
Gln	Glu	Ile	Ile	Phe	Pro	Pro	Ile	Lys	Thr	Asp	Val	Ile	Thr	Met	Asp	225	230	235	240
Pro	Lys	Asp	Asn	Ala	Ser	Gly	Leu	Val	Pro	Arg	245	250							

<210> 135
 <211> 236
 <212> PRT
 <213> Homo sapiens TCR delta chain

<400> 135

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

Pro Val Arg Lys Ala Val Thr Leu Asn Cys Leu Tyr Glu Thr Ser Trp
 20 25 30

Trp Ser Tyr Tyr Ile Phe Trp Tyr Lys Gln Leu Pro Ser Lys Glu Met
 35 40 45

Ile Phe Leu Ile Arg Gln Gly Ser Asp Glu Gln Asn Ala Lys Ser Gly
 50 55 60

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

Ile Ser Ala Leu Gln Leu Glu Asp Ser Ala Lys Tyr Phe Cys Ala Leu
 85 90 95

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

Thr Arg Val Thr Val Glu Pro Arg Ser Gln Pro His Thr Lys Pro Ser
 115 120 125

Val Phe Val Met Lys Asn Gly Thr Asn Val Ala Cys Leu Val Lys Glu
 130 135 140

Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val Ser Ser Lys Lys Ile
 145 150 155 160

Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro Ser Gly Lys Tyr Asn
 165 170 175

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

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

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

Gln	Pro	Ser	Lys	Ser	Ala	Ser	Gly	Leu	Val	Pro	Arg
225					230					235	