

SEQUENCE LISTING

<110> GmbH, Medigene Immunotherapies
Bluebird bio, Inc.

<120> MAGE-A4-TCRs

<130> MED16702PCT

<160> 116

<170> PatentIn version 3.5

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Gln	Gly	Ser	Tyr	Asp	Glu	Gln	Asn
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Cys Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe

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Lys Gly His Asp Arg
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Ser Phe Asp Val Lys Asp
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Cys Ala Thr Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr
1 5 10 15

Phe

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Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly
115 120 125

Thr Arg Leu Met Val Lys Pro His
130 135

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<213> Homo sapiens

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Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Gln Ala Gln Ala Lys Phe Ser Leu Ser
85 90 95

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

Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr Phe Gly Pro
115 120 125

Gly Thr Arg Leu Leu Val Leu
130 135

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Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly
115 120 125

Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
180 185 190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Ser Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
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<400> 11

Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Gln Ala Gln Ala Lys Phe Ser Leu Ser
85 90 95

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

Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr Phe Gly Pro
115 120 125

Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
130 135 140

Glu Val Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala His Thr Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser
260 265 270

Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

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<400> 12

Thr Ser Asp Pro Ser Tyr Gly
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<210> 13
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<213> Homo sapiens

<400> 13

Gln Gly Ser Tyr Asp Gln Gln Asn
1 5

<210> 14
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<212> PRT
<213> Homo sapiens

<400> 14

Cys Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe
1 5 10 15

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<211> 5

<212> PRT

<213> Homo sapiens

<400> 15

Ser Gly Asp Leu Ser
1 5

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<212> PRT

<213> Homo sapiens

<400> 16

Tyr Tyr Asn Gly Glu Glu
1 5

<210> 17

<211> 13

<212> PRT

<213> Homo sapiens

<400> 17

Cys Ala Ser Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe
1 5 10

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<211> 137

<212> PRT

<213> Homo sapiens

<400> 18

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
115 120 125

Gly Thr Arg Leu Phe Val Lys Ala Asn
130 135

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<213> Homo sapiens

<400> 19

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
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Thr Val Leu
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<213> Artificial Sequence

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<223> with minimal murinized constant region

<400> 20

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
115 120 125

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Asp Pro Ala
130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
165 170 175

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225 230 235 240

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

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
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<213> Artificial Sequence

<220>
<223> with minimal murinized constant region

<400> 21

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

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

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

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Arg Ser Tyr His Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Ser Arg Gly
305 310

<210> 22
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<400> 22

Asp Ser Ala Ser Asn Tyr
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<210> 23
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<213> Homo sapiens

<400> 23

Ile Arg Ser Asn Val Gly Glu
1 5

<210> 24
<211> 14
<212> PRT
<213> Homo sapiens

<400> 24

Cys Ala Ala Ser Arg Gly Thr Gly Phe Gln Lys Leu Val Phe
1 5 10

<210> 25

<211> 5

<212> PRT

<213> Homo sapiens

<400> 25

Leu Gly His Asp Thr
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<210> 26

<211> 6

<212> PRT

<213> Homo sapiens

<400> 26

Tyr Asn Asn Lys Glu Leu
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<210> 27

<211> 16

<212> PRT

<213> Homo sapiens

<400> 27

Cys Ala Ser Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe
1 5 10 15

<210> 28

<211> 133

<212> PRT

<213> Homo sapiens

<400> 28

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

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

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

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

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

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

Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu
115 120 125

Leu Val Ser Pro Asn
130

<210> 29
<211> 134
<212> PRT
<213> Homo sapiens

<400> 29

Met Gly Cys Arg Leu Leu Cys Cys Val Val Phe Cys Leu Leu Gln Ala
1 5 10 15

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr
130

<210> 30

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> with minimal murinized constant region

<400> 30

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

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

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

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

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

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

Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu
115 120 125

Leu Val Ser Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145 150 155 160

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

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
180 185 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
195 200 205

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 31

<211> 311

<212> PRT

<213> Artificial Sequence

<220>

<223> with minimal murinized constant region

<400> 31

Met Gly Cys Arg Leu Leu Cys Cys Val Val Phe Cys Leu Leu Gln Ala
1 5 10 15

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
115 120 125

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

Val Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala His Thr Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr
260 265 270

His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Phe
305 310

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<220>
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<400> 32
accagcgatc agagctacgg c 21

<210> 33
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<400> 33
cagggcagct acgacgagca gaat 24

<210> 34
<211> 42

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> codon optimized

 <400> 34
 tgtgccatga gcggcgatag cgccggcaac atgcttacat tt 42

 <210> 35
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> codon optimized

 <400> 35
 aagggccacg accgg 15

 <210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> codon optimized

 <400> 36
 agcttcgacg tgaaggac 18

 <210> 37
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> codon optimized

 <400> 37
 tgcgccacca gcgactggga tagaagcggc gacaaagaga cacagtactt c 51

 <210> 38
 <211> 831
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> with minimal murinized constant region; codon optimized

<400> 38
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gccagaaga tcaccagac acagcccggc atgttcgtgc aagagaaaga agccgtgaca 120
ctggactgca cctacgacac cagcgatcag agctacggcc tgttctggta caagcagcct 180
agcagcggcg agatgatctt cctgatctac cagggcagct acgacgagca gaatgccacc 240
gagggcagat acagcctgaa cttccagaag gcccggaagt ccgccaacct ggtcatttct 300
gcttctcagc tgggcgacag cgccatgtac ttttgtgcca tgagcggcga tagcgccggc 360
aacatgctta catttggcgg cggaaccgg ctgatgggtca agcccatat tcagaacccc 420
gatcctgccg tgtaccagct gagagacagc aagagcagcg acaagagcgt gtgtctgttc 480
accgacttcg acagccagac caacgtgtcc cagagcaagg acagcgacgt gtacatcacc 540
gacaagaccg tgctggacat gcggagcatg gacttcaaga gcaacagcgc cgtggcctgg 600
tccaacaaga gcgatttcgc ctgcgccaac gccttcaaca atagcattat ccccgaggac 660
acattcttcc ccagctccga tgtgccctgc gacgtgaagc tgggtggaaaa gagcttcgag 720
acagacacca acctgaactt ccagaacctg agcgtgatcg gcttcagaat cctgctgctg 780
aaggtggccg gcttcaatct gctgatgacc ctgagactgt ggtccagctg a 831

<210> 39
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> with minimal murinized constant region; codon optimized

<400> 39
atggccagcc tgctgttctt ctgcggcgcc ttttatctgc tcggcaccgg ctctatggac 60
gccgacgtta cacagacccc tcggaacaga atcaccaaga ccggcaagcg gatcatgctg 120
gaatgcagcc agaccaaggg ccacgaccgg atgtactggc acagacagga ccctggcctg 180
ggcctgagac tgatctacta cagcttcgac gtgaaggaca tcaacaaggg cgagatcagc 240
gacggctaca gcgtgtcaag acaggctcag gccaaagtta gcctgtctct ggaaagcgct 300
atccccaacc agacagccct gtacttctgc gccaccagcg actgggatag aagcggcgac 360
aaagagacac agtacttcgg ccctggcacc agactgctgg tgctggaaga tctgaacaag 420
gtgttccctc cagaggtggc cgtgttcgag ctttctaagg ccgagattgc ccacacacag 480

aaagccacac tcgtgtgcct ggctaccggc ttctttcctg accacgtgga actgtcttgg	540
tgggtcaacg gcaaagaggt gcacagcggc gtcagcacag atccccagcc tctgaaagaa	600
cagcccgtc tgaacgacag ccggtactgt ctgagcagca gactgagagt gtccgccaca	660
ttctggcaga accccagaaa ccacttcaga tgccaggtgc agttctacgg cctgagcgag	720
aacgatgagt ggaccagga tagagccaag cctgtgacac agatcgtgtc tgccgaagcc	780
tggggcagag ccgattgtgg aattaccagc gccagctacc atcagggcgt gctgtctgcc	840
acaatcctgt acgagatcct gctgggcaaa gccactctgt acgccgtgct ggtgtctgcc	900
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<220>
 <223> codon optimized

<400> 40	
accagcgatc ctagctacgg c	21

<210> 41
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<400> 41	
cagggcagct acgaccagca gaat	24

<210> 42
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 <212> DNA
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<220>
 <223> codon optimized

<400> 42	
tgtgccatga gcggcggcta caccggcggc ttcaagacaa tcttt	45

<210>	43	
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<212>	DNA	
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<223>	codon optimized	
<400>	43	
	agcggcgacc tgagc	15
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<213>	Artificial Sequence	
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<223>	codon optimized	
<400>	44	
	tactacaacg gcgaggaa	18
<210>	45	
<211>	39	
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<213>	Artificial Sequence	
<220>		
<223>	codon optimized	
<400>	45	
	tgtgccagct ctggcggaga tggcgacgag cagtttttt	39
<210>	46	
<211>	834	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	with minimal murinized constant region; codon optimized	
<400>	46	
	atgagcctga gcagcctgct gaaggtcgtg acagcctctc tgtggctcgg acctggaatc	60
	gcccagaaga tcaccagac acagcccggc atgttcgtgc aagagaaaga agccgtgaca	120
	ctggactgca cctacgacac cagcgatcct agctacggcc tgttctggta caagcagcct	180
	agcagcggcg agatgatctt cctgatctac cagggcagct acgaccagca gaatgccacc	240
	gagggcagat acagcctgaa cttccagaag gcccggaagt ccgccaacct ggtcattttct	300

gctagccagc tgggcgacag cgccatgtac ttttgtgcca tgagcggcgg ctacaccggc	360
ggcttcaaga caatcttttg cgccggaacc agactgttcg tgaaggccaa tattcagaac	420
cccgatcctg ccgtgtacca gctgagagac agcaagagca gcgacaagag cgtgtgtctg	480
ttcaccgact tcgacagcca gaccaacgtg tcccagagca aggacagcga cgtgtacatc	540
accgacaaga ccgtgctgga catgcggagc atggacttca agagcaacag cgccgtggcc	600
tggtccaaca agagcgattt cgcctgcgcc aacgccttca acaatagcat tatccccgag	660
gacacattct tccccagctc cgatgtgccc tgcgacgtga agctggtgga aaagagcttc	720
gagacagaca ccaacctgaa cttccagaac ctgagcgtga tcggcttcag aatcctgctg	780
ctgaaggtgg ccggcttcaa tctgctgatg accctgagac tgtggtccag ctga	834

<210> 47
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> with minimal murinized constant region; codon optimized

<400> 47	
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agcggcggtta cccagacacc taagcacctg atcacagcca caggccagcg cgtgaccctg	120
agatgtttctc ctagaagcgg cgacctgagc gtgtactggt atcagcagtc tctggaccag	180
ggcctgcagt tcctgatcca gtactacaac ggcgaggaaa gagccaaggg caacatcctg	240
gaacggttca gcgcccagca gttcccagat ctgcacagcg agctgaacct gagcagcctg	300
gaactgggag atagcgccct gtactttctgt gccagctctg gcggagatgg cgacgagcag	360
ttttttggcc ctggcaccag actgaccgtg ctggaggacc tgaagaacgt gttccctccg	420
gaggtggccg tgttcgagcc cagcaaagcc gagatcgcg acaccagaa ggccaccctg	480
gtgtgcctgg ccaccggctt ctaccccgac cacgtggagc tgagctggtg ggtgaacggc	540
aaggaggtgc acagcggcgt gagcaccgac cccagcccc tgaaggagca gcccgccctg	600
aacgacagcc gctactgcct gagcagccgc ctgcgcgtga gcgccacctt ctggcagaac	660
ccccgcaacc acttccgctg ccaggtgcag ttctacggcc tgagcgagaa cgacgagtgg	720
acccaggacc gcgccaagcc cgtgaccag atcgtgagcg ccgaggcctg gggccgcgcc	780

gactgctggca ttaccagccg cagctaccat cagggcgtgc tgagcgccac catcctgtac	840
gagatcctgc tgggcaaggc caccctgtac gccgtgctgg tgagcgccct ggtgctgatg	900
gcgatggtga agcgcaagga cagccgcggc tga	933

<210> 48
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<400> 48	
gacagcgcca gcaactac	18

<210> 49
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<400> 49	
atccggtcca acgtgggcga g	21

<210> 50
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<400> 50	
tgcgctgcca gcagaggcac cggcttccag aaactggtgt tt	42

<210> 51
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized

<400> 51	
ctgggccacg acacc	15

<210>	52	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	codon optimized	
<400>	52	
tacaacaaca aagagctg		18
<210>	53	
<211>	48	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	codon optimized	
<400>	53	
tgtgccagca gccagttctg ggatggcgct ggcgacgagc agtatattt		48
<210>	54	
<211>	822	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	with minimal murinized constant region; codon optimized	
<400>	54	
atgaccagca tccggggcgt gttcatcttc ctgtggctgc agctggacct ggtcaacggc		60
gagaatgtgg aacagcaccc cagcacactg agcgtgcaag agggcgattc tgccgtgatc		120
aagtgcacct acagcgacag cgccagcaac tactttccct ggtacaagca agagctgggc		180
aaaagacccc agctgatcat cgacatccgg tccaacgtgg gcgagaagaa ggaccagaga		240
atcgccgtga cactgaacaa gaccgccaag cacttcagcc tgcacatcac cgagacacag		300
cctgaggata gcgccgtgta cttttgcgct gccagcagag gcaccggctt ccagaaactg		360
gtgtttggca ccggcaccag actgctggtg tccccaaata ttcagaacct cgatcctgcc		420
gtgtaccagc tgagagacag caagagcagc gacaagagcg tgtgtctgtt caccgacttc		480
gacagccaga ccaacgtgtc ccagagcaag gacagcgacg tgtacatcac cgacaagacc		540
gtgctggaca tgcggagcat ggacttcaag agcaacagcg ccgtggcctg gtccaacaag		600

agcgatttcg cctgcgcaa cgccttcaac aatagcatta tccccgagga cacattcttc	660
cccagctccg atgtgccctg cgacgtgaag ctgggtggaaa agagcttcga gacagacacc	720
aacctgaact tccagaacct gagcgtgatc ggcttcagaa tcctgctgct gaaggtggcc	780
ggcttcaatc tgctgatgac cctgagactg tggtccagct ga	822

<210> 55
 <211> 936
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> with minimal murinized constant region; codon optimized

<400> 55	
atgggctgca gactgctgtg ctgtgtggtg ttctgcctgc tgcaagccgg acctctggat	60
acagccgtgt ctcagacccc taagtacctg gtcaccaga tgggcaacga caagagcatc	120
aagtgcgagc agaacctggg ccacgacacc atgtactggt acaagcagga cagcaagaaa	180
ttcctgaaga tcatgttcag ctacaacaac aaagagctga tcatcaacga gacagtgtccc	240
aacagattca gccctaagag ccccgataag gccacctga acctgcacat caacagcctg	300
gaactgggcg acagcgccgt gtacttttgt gccagcagcc agttctggga tggcgctggc	360
gacgagcagt attttggccc tggcaccaga ctgaccgtga ccgaggacct gaacaagggtg	420
ttccctccgg aggtggccgt gttcgagccc agcaaagccg agatcgcgca caccagaag	480
gccaccctgg tgtgcctggc caccggcttc ttccccgacc acgtggagct gagctggtgg	540
gtgaacggca aggaggtgca cagcggcgtg agcaccgacc ccagcccct gaaggagcag	600
cccgcccctga acgacagccg ctactgcctg agcagccgcc tgcgcgtgag cgccaccttc	660
tggcagaacc cccgcaacca cttccgctgc caggtgcagt tctacggcct gagcgagaac	720
gacgagtgga ccagggaccg cgccaagccc gtgaccaga tcgtgagcgc cgaggcctgg	780
ggccgcgccg actgcggcat taccagcgcg agctaccatc agggcgtgct gagcgccacc	840
atcctgtacg agatcctgct gggcaaggcc accctgtacg ccgtgctggt gagcgccctg	900
gtgctgatgg cgatggtgaa gcgcaaggac ttctga	936

<210> 56
 <211> 10

<212> PRT
<213> Homo sapiens

<400> 56

Lys Leu Tyr Gly Leu Asp Trp Ala Glu Leu
1 5 10

<210> 57
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> murinized

<400> 57

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly
115 120 125

Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro Glu Pro Ala Val
130 135 140

Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly
165 170 175

Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser
180 185 190

Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys
195 200 205

Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val
210 215 220

Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn
225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu
245 250 255

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265 270

<210> 58
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> murinized

<400> 58

Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Gln Ala Gln Ala Lys Phe Ser Leu Ser
85 90 95

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

Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr Phe Gly Pro
115 120 125

Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro
130 135 140

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

Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp
225 230 235 240

Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly

260

265

270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
 275 280 285

Leu Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys
 290 295 300

Lys Lys Asn Ser
 305

<210> 59
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> murinized

<400> 59

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
 1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
 20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
 35 40 45

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
 50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
 65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
 85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
 100 105 110

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala

115

120

125

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Glu Pro Ala
 130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
 145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
 165 170 175

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
 180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
 195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
 210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
 225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu
 245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
 260 265 270

Ser

<210> 60

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> murinized

<400> 60

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala

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

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
225 230 235 240

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
245 250 255

Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala
260 265 270

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
275 280 285

Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
290 295 300

<210> 61
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> murinized

<400> 61

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

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

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

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

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

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

Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu
115 120 125

Leu Val Ser Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

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

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala
245 250 255

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 62
<211> 307
<212> PRT
<213> Artificial Sequence

<220>
<223> murinized

<400> 62

Met Gly Cys Arg Leu Leu Cys Cys Val Val Phe Cys Leu Leu Gln Ala
1 5 10 15

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
115 120 125

Thr Arg Leu Thr Val Thr Glu Asp Leu Arg Asn Val Thr Pro Pro Lys
130 135 140

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

Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser
195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe

210

215

220

Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro
 225 230 235 240

Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp
 245 250 255

Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val
 260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
 275 280 285

Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys
 290 295 300

Lys Asn Ser
 305

<210> 63
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> human optimized

<400> 63
 acttcagacc agtcgtacgg t

21

<210> 64
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> human optimized

<400> 64
 cagggatcgt acgacgagca gaac

24

<210> 65
 <211> 42
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> human optimized
 <400> 65
 tgcgcaatgt ccggcgatag cgcaggaaac atgctgactt tc 42

<210> 66
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human optimized
 <400> 66
 aagggccacg accgc 15

<210> 67
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human optimized
 <400> 67
 tccttcgacg tgaaggac 18

<210> 68
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> human optimized
 <400> 68
 tgtgccacct cggattggga ccgatccggc gacaaggaaa ctcagtactt c 51

<210> 69
 <211> 831
 <212> DNA
 <213> human optimized
 <400> 69
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 gcccagaaga tcactcagac ccagcctgga atgttcgtgc aagagaaaga ggccgtgacc 120

ctggattgta cttatgacac ttcagaccag tcgtacggtt tgttcttgga caagcagccg	180
tcctccggag aaatgatctt cctgatctac cagggatcgt acgacgagca gaacgctacc	240
gagggcagat attccctcaa cttccaaaag gcccggaat ccgcgaacct cgtgatctcg	300
gcctcacaac ttggggactc cgctatgtat ttctgcgcaa tgtccggcga tagcgcagga	360
aacatgctga ctttcggcgg tggaactagg ctgatggtca agccccacat tcaaaacct	420
gaccagcag tctaccagtt gcgggattcc aagtcttccg ataaatccgt gtgtctcttt	480
acagacttcg atagccagac caacgtgtcc cagagcaaag acagcgacgt gtacattact	540
gacaagactg tgctggacat gcggtccatg gacttcaaga gcaactccgc cgtcgcttgg	600
tccaacaagt ctgactttgc gtgcgcgaac gctttcaaca acagcattat cccggaggac	660
acctttttcc cttccccga gtcaagctgc gatgtcaagc ttgtggaaaa gtcgttcgaa	720
accgacacca acctgaactt ccagaacctg tccgtcatcg ggttccgcat tctgctgctg	780
aaggtcgccg gcttcaatct cctgatgact ctccgcttgt ggtcctcata a	831

<210> 70
 <211> 936
 <212> DNA
 <213> human optimized

<400> 70	
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gccgacgtga cccaaacccc tcgcaaccgc atcaccaaga ctggaaagcg gatcatgctg	120
gaatgctccc agaccaaggg ccacgaccgc atgtactggt acagacagga cccgggtctg	180
ggattgcgcc tgatctacta ctccttcgac gtgaaggaca tcaacaaggg ggagatctcc	240
gatggatact cagtctcgag acaagcccag gctaagtttt ccctgtccct cgaatccgcc	300
attcccaatc agaccgcgct gtacttctgt gccacctcgg attgggaccg atccggcgac	360
aaggaaactc agtacttcgg accaggaacc aggctcctgg tgctggagga tctgaacaag	420
gtgttcccgc cggaagtggc agtgttcgag ccatccgaag ccgagatctc gcatacgag	480
aaggccaccc tcgtgtgcct ggccactggg tttttccctg accacgtgga gctctcgtgg	540
tgggtcaacg gaaaggaagt gcacagcggg gtctcaaccg acccgcaacc tctcaaggaa	600
cagcccgcgc tcaatgattc gcggtactgc ctgagcagcc ggctcagagt gtccgccact	660

ttctggcaaa acccgcgga ccatttccgg tgccaagtgc aattctacgg gctgtcggaa	720
aacgacgaat ggaccagga cagggccaaag cccgtgacct agattgtgtc cgctgaagcc	780
tgggggagag ctgattgcgg tttcaccagc gtgtcgtatc agcagggcgt gctgtcagcc	840
accattctgt acgaaatcct cctggggaag gccacactgt acgccgtgct cgtgtccgcc	900
ctggtgctga tggccatggt caagcggaag gacttc	936

<210> 71
 <211> 21
 <212> DNA
 <213> human optimized

<400> 71	
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<400> 72	
caaggctcct atgatcagca gaac	24

<210> 73
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<220>
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<400> 73	
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<220>
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<400> 74	
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<210> 75

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	ctcgactgca cttacgacac ctccgacctg tcctacgggc tgttctggta caagcagccg	180
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	gcatcccaac tgggggacag cgccatgtac ttctgtgcca tgtcgggcgg atacaccggg	360
	ggattcaaga ccattttcgg ggccggcact agactgttcg tgaaggccaa catccagaat	420
	cctgatccgg cgggtgatca gctgcgcgac tccaagtctt ccgataaatc cgtgtgtctc	480
	tttacagact tcgactccca aaccaacgtg tcacagtcca aggacagcga tgtgtacatc	540
	accgacaaaa ccgtgctgga catgcggtcc atggacttca agtcaaacag cgcagtcgcc	600
	tggccaaca agtccgactt cgcctgtgcg aacgccttca acaactccat cattccggaa	660

gataacctttt tcccttcacc tgagtcgagc tgtgatgtga agctcgtgga aaagtcgttt	720
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gactgcggat tcacctcca gtcctaccaa caaggcgtcc tctcggcgac cattctgtac	840
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<210> 79
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	gactcagcat caaactat	18
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	atccgctcca acgtcggaga g	21
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<223>	human optimized	
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	tgtgcggcct cgaggggcac tgggtttcag aagctcgtgt tc	42
<210>	82	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	human optimized	
<400>	82	
	ctcggacacg acacc	15
<210>	83	
<211>	18	
<212>	DNA	
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<220>		
<223>	human optimized	
<400>	83	
	tacaacaaca aggaactg	18

<210> 84
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> human optimized

<400> 84
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<210> 85
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> human optimized

<400> 85
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<210> 86
<211> 930
<212> DNA

<213> Artificial Sequence

<220>

<223> human optimized

<400> 86

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gacgagtgga ctcaggacag agcgaagccc gtgacccaaa tcgtgtccgc cgaggcctgg      780
ggacgcgccg actgcggttt cacctccgtg agctaccaac agggcgtgct gtcagctacc      840
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<210> 87

<211> 276

<212> PRT

<213> Homo sapiens

<400> 87

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          20          25          30
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Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly
115 120 125

Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
180 185 190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
275

<210> 88
<211> 312
<212> PRT
<213> Homo sapiens

<400> 88

Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Gln Ala Gln Ala Lys Phe Ser Leu Ser
85 90 95

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

Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr Phe Gly Pro
115 120 125

Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
130 135 140

Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln

145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
260 265 270

Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 89
<211> 277
<212> PRT
<213> Homo sapiens

<400> 89

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
115 120 125

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Asp Pro Ala
130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
165 170 175

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
210 215 220

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225 230 235 240

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

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
275

<210> 90
<211> 310
<212> PRT
<213> Homo sapiens

<400> 90

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val

130

135

140

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

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
 165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
 180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
 195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
 210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
 225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
 245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
 260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
 275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
 290 295 300

Arg Lys Asp Ser Arg Gly
 305 310

<210> 91

<211> 273

<212> PRT

<213> Homo sapiens

<400> 91

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
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Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
20 25 30

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

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

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

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
85 90 95

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

Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu
115 120 125

Leu Val Ser Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
145 150 155 160

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

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
180 185 190

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
195 200 205

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
210 215 220

Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
245 250 255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
260 265 270

Ser

<210> 92
<211> 310
<212> PRT
<213> Homo sapiens

<400> 92

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly

115

120

125

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

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
 145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
 165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
 245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr
 260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
 275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
 290 295 300

Met Val Lys Arg Lys Asp
 305 310

<210> 93

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> human optimized

<400> 93

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<210> 94
 <211> 610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human optimized

<400> 94

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Gly	Ser	Met	Asp	Ala	Asp	Val	Thr	Gln	Thr	Pro	Arg	Asn	Arg	Ile	Thr
			20					25					30		

Lys	Thr	Gly	Lys	Arg	Ile	Met	Leu	Glu	Cys	Ser	Gln	Thr	Lys	Gly	His
		35					40					45			

Asp	Arg	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Leu
	50					55					60				

Ile	Tyr	Tyr	Ser	Phe	Asp	Val	Lys	Asp	Ile	Asn	Lys	Gly	Glu	Ile	Ser
65					70					75				80	

Asp	Gly	Tyr	Ser	Val	Ser	Arg	Gln	Ala	Gln	Ala	Lys	Phe	Ser	Leu	Ser
				85					90					95	

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

Ser	Asp	Trp	Asp	Arg	Ser	Gly	Asp	Lys	Glu	Thr	Gln	Tyr	Phe	Gly	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
 130 135 140

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

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
 165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
 180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
 195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
 210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
 225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
 245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
 260 265 270

Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
 275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
 290 295 300

Ala Met Val Lys Arg Lys Asp Phe Gly Ser Gly Ala Thr Asn Phe Ser
 305 310 315 320

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser
 325 330 335

Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu Gly Pro
340 345 350

Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe Val Gln
355 360 365

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

Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu Met Ile
385 390 395 400

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

Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn Leu Val
420 425 430

Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys Ala Met
435 440 445

Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg
450 455 460

Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
465 470 475 480

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
485 490 495

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
500 505 510

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
515 520 525

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
530 535 540

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro

545		550		555		560
Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp						
		565		570		575
Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu						
		580		585		590
Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp						
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Ser Ser						
610						

<210> 95
 <211> 1842
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<220>
 <223> human optimized

<400> 95	
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aacgactcgc ggtactgtct gtcctcccgg ctgagagtgt cggccacctt ctggcaaaac	660
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<210> 96
<211> 613
<212> PRT
<213> Artificial Sequence

<220>
<223> human optimized

<400> 96

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			20					25					30		

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

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

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

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala

245

250

255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
 260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
 275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
 290 295 300

Arg Lys Asp Ser Arg Gly Arg Ala Lys Arg Gly Ser Gly Ala Thr Asn
 305 310 315 320

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
 325 330 335

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
 340 345 350

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
 355 360 365

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

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
 385 390 395 400

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
 405 410 415

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
 420 425 430

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
 435 440 445

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
 450 455 460

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Asp Pro Ala
465 470 475 480

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
485 490 495

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
500 505 510

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
515 520 525

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
530 535 540

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
545 550 555 560

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
565 570 575

Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe
580 585 590

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
595 600 605

Arg Leu Trp Ser Ser
610

<210> 97
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> human optimized

<400> 97
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aaatgcgaac agaacctcgg acacgacacc atgtactggg acaaacagga ttccaagaag	180
ttcctgaaga ttatgttctc atacaacaac aaggaactga ttatcaacga aactgtgccg	240
aaccggttct caccgaagtc gcctgacaag gctcatctca acttgcatat caactcgctg	300
gagctcggcg actccgccgt gtactttctgc gcgtccagcc agttctggga cggagcgggc	360
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gccactctgg tctgcctggc caccggtttc ttccccgatc acgtggaact gtcttggtgg	540
gtgaacggaa aagaagtgca ctcgggggtg tccacggacc ccagcctct gaaggaacag	600
ccggcactga atgactcacg ctactgtctg tcgtcacggc tgcgcgtgtc ggccaccttc	660
tggcaaaacc cgcgaaacca ctttcgctgc caagtgcagt ttacgggct ttccgagaac	720
gacgagtgga ctcaggacag agcgaagccc gtgacccaaa tcgtgtccgc cgaggcctgg	780
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<210> 98
 <211> 610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human optimized

<400> 98

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

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
 50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
 85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
 115 120 125

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

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
 145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr
260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Phe Arg Ala Lys Arg Gly Ser Gly Ala Thr
305 310 315 320

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
325 330 335

Pro Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu
340 345 350

Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser
355 360 365

Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser Asp Ser

370

375

380

Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys Arg Pro
 385 390 395 400

Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys Asp Gln
 405 410 415

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

Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ala
 435 440 445

Ser Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg
 450 455 460

Leu Leu Val Ser Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 465 470 475 480

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 485 490 495

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 500 505 510

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 515 520 525

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 530 535 540

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
 545 550 555 560

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
 565 570 575

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
 580 585 590

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
595 600 605

Ser Ser
610

<210> 99
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-7 a complete

<400> 99
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aaggtcgccg gcttcaatct cctgatgact ctccgcttgt ggtcctca 828

<210> 100
<211> 936
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-7 b complete

<400> 100
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gaatgctccc agaccaaggg ccacgaccgc atgtactggt acagacagga cccgggtctg 180
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ctggtgctga tggccatggt caagcggaag gacttc 936

<210> 101
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-7 polycistronic construct

<400> 101
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gaatgctccc agaccaaggg ccacgaccgc atgtactggt acagacagga cccgggtctg 180
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attcccaatc agaccgcgct gtactttctgt gccacctcgg attgggaccg atccggcgac	360
aaggaaactc agtacttcgg accaggaacc aggctcctgg tgctggagga tctgaacaag	420
gtgttcccg cggaaagtggt agtggttcgag ccatccaagg cggagatcgc ccatacgacg	480
aaggccaccc tcgtgtgcct ggccactggg tttttccctg accacgtgga gctctcgtgg	540
tgggtcaacg gaaaggaagt gcacagcggg gtctcaaccg acccgcaacc tctcaaggaa	600
cagcccgcg tcaatgattc gcggtactgc ctgagcagcc ggctcagagt gtccgccact	660
ttctggcaaa acccgcgga ccatctccgg tgccaagtgc aattctacgg gctgtcggaa	720
aacgacgaat ggaccagga caggccaag cccgtgaccc agattgtgtc cgctgaagcc	780
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atgcggtcca tggacttcaa gagcaactcc gccgtcgctt ggtccaacaa gtctgacttt	1620
gcgtgcgca acgctttcaa caacagcatt atcccggagg acacctttt ccttccagc	1680
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<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR-7 a complete

<400> 102

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
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Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
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Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly
115 120 125

Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val
130 135 140

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe

180

185

190

Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
 195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
 210 215 220

Ser Ser Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
 225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg
 245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
 260 265 270

Leu Trp Ser Ser
 275

<210> 103
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR-7 b complete

<400> 103

Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
 1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
 20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
 35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
 50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser

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

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 104
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR-7 polyprotein

<400> 104

Met Ala Ser Leu Leu Phe Phe Cys Gly Ala Phe Tyr Leu Leu Gly Thr
1 5 10 15

Gly Ser Met Asp Ala Asp Val Thr Gln Thr Pro Arg Asn Arg Ile Thr
20 25 30

Lys Thr Gly Lys Arg Ile Met Leu Glu Cys Ser Gln Thr Lys Gly His
35 40 45

Asp Arg Met Tyr Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Phe Asp Val Lys Asp Ile Asn Lys Gly Glu Ile Ser
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Gln Ala Gln Ala Lys Phe Ser Leu Ser
85 90 95

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

Ser Asp Trp Asp Arg Ser Gly Asp Lys Glu Thr Gln Tyr Phe Gly Pro
115 120 125

Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro
130 135 140

Glu Val Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala His Thr Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser
260 265 270

Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe Gly Ser Gly Ala Thr Asn Phe Ser
305 310 315 320

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser
325 330 335

Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu Gly Pro
340 345 350

Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe Val Gln

355

360

365

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

Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu Met Ile
 385 390 395 400

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

Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn Leu Val
 420 425 430

Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys Ala Met
 435 440 445

Ser Gly Asp Ser Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg
 450 455 460

Leu Met Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 465 470 475 480

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 485 490 495

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 500 505 510

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 515 520 525

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 530 535 540

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Ser
 545 550 555 560

Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
 565 570 575

Thr Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu
580 585 590

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
595 600 605

Ser Ser
610

<210> 105
<211> 831
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-8 a complete

<400> 105
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tcctccggag agatgatctt cctcatctac caaggctcct atgatcagca gaacgccacc 240
gaaggacgct acagcctgaa cttccagaag gctcggaagt cggcgaacct cgtgatcagc 300
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ggattcaaga ccattttcgg ggccggcact agactgttcg tgaaggccaa catccagaat 420
cctgatccgg cgggtgatca gctgcgcgac tccaagtctt ccgataaatc cgtgtgtctc 480
tttacagact tcgactccca aaccaacgtg tcacagtcca aggacagcga tgtgtacatc 540
accgacaaaa ccgtgctgga catgcggtcc atggacttca agtcaaacag cgcagtcgcc 600
tggtccaaca agtccgactt cgcctgtgcg aacgccttca acaactccat cattccggaa 660
gatacctttt tcccttcaag cgacgtcccc tgtgatgtga agctcgtgga aaagtcgttt 720
gaaacggaca ccaacctgaa ctttcagaac ctgctagtga ttgtgctccg catcctgctg 780
ctgaaggtcg ccggcttcaa cttgctgatg acgctccggc tgtggtcctc g 831

<210> 106
<211> 930
<212> DNA

<213> Artificial Sequence

<220>

<223> TCR-8 b complete

<400> 106

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cgatgctcac cacggtctgg cgacctctcc gtgtactggg atcagcagag cctggaccag      180
ggactgcagt tcctgatcca gtactacaac ggagaggagc gggctaaggg aaacatactg      240
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gaattgggag actccgccct gtacttctgc gcaagcagcg gtggtgacgg ggatgaacag      360
ttctttggcc ctggaaccag actcaccgtg ctcgaggacc tcaagaacgt gttcccaccc      420
gaagtcgcgg tgttcgagcc ctccaaggcg gagatcgccc atactcagaa agccactctc      480
gtgtgcctgg ccaccggatt ctaccgggac cacgtcgagc tctcttggtg ggtgaacggg      540
aaagagggtc acagcggcgt gagcactgat ccgcagccgc tgaaggaaca acccgcttg      600
aacgactcgc ggtactgtct gtcctcccgg ctgagagtgt cggccacctt ctggcaaaac      660
cccaggaacc actttaggtg ccaagtccag ttctacggcc tgagcgaaaa cgatgagtgg      720
accaggaca gagccaagcc tgtgaccagc attgtgtcag ccgaggcttg gggtagagca      780
gactgcggaa tcaccagcgc cagctaccac caaggcgtcc tctcggcgac cattctgtac      840
gaaatcctgc ttgggaaggc cactctgtac gccgtgctgg tgtccgccct ggtgctgatg      900
gcatggtca agcggaagga ctccggggg      930
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<210> 107

<211> 1842

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR-8 polycistronic construct

<400> 107

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cgatgctcac cacggtctgg cgacctctcc gtgtactggg atcagcagag cctggaccag      180
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gagcggttct cggcgcaaca attccccgat ctgcactccg aactgaacct gtcctccctg	300
gaattgggag actccgccct gtactttctgc gcaagcagcg gtggtgacgg ggatgaacag	360
ttctttggcc ctggaaccag actcaccgtg ctcgaggacc tcaagaacgt gttcccaccc	420
gaagtgcgcg tgttcgagcc ctccaaggcg gagatcgccc atactcagaa agccactctc	480
gtgtgcctgg ccaccggatt ctacccggac cacgtcgagc tctcttggtg ggtgaacggg	540
aaagagggtcc acagcggcgt gagcactgat ccgcagccgc tgaaggaaca acccgcttg	600
aacgactcgc ggtactgtct gtcctcccgg ctgagagtgt cggccacctt ctggcaaaac	660
cccaggaacc actttaggtg ccaagtccag ttctacggcc tgagcgaaaa cgatgagtgg	720
accaggaca gagccaagcc tgtgaccag attgtgtcag ccgaggcttg gggtagagca	780
gactgcggaa tcaccagcgc cagctaccac caaggcgtcc tctcggcgac cattctgtac	840
gaaatcctgc ttgggaaggc cactctgtac gccgtgctgg tgtccgccct ggtgctgatg	900
gccatggtca agcggaaagga ctcccggggg agagcaaaga ggggatcggg agccaccaat	960
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accagactc agcctgggat gttcgtgcaa gagaaggaag ccgtgaccct cgactgcact	1140
tacgacacct ccgaccgctc ctacgggctg ttctggtaca agcagccgtc ctccggagag	1200
atgatcttcc tcatctacca aggctcctat gatcagcaga acgccaccga aggacgtac	1260
agcctgaact tccagaaggc tcggaagtcg gcgaacctcg tgatcagcgc atcccaactg	1320
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atthtcgggg ccggcactag actgttcgtg aaggccaaca tccagaatcc tgatccggcg	1440
gtgtatcagc tgcgcgactc caagtcttcc gataaatccg tgtgtctctt tacagacttc	1500
gactcccaa ccaacgtgtc acagtccaag gacagcgatg tgtacatcac cgacaaaacc	1560
gtgctggaca tgcggtccat ggacttcaag tcaaacagcg cagtcgcctg gtccaacaag	1620
tccgacttcg cctgtgcgaa cgccttcaac aactccatca ttccggaaga tacctttttc	1680
ccttcaagcg acgtcccctg tgatgtgaag ctctgtgaaa agtcgtttga aacggacacc	1740
aacctgaact ttcagaacct gctagtgatt gtgctccgca tcctgctgct gaaggtcgcc	1800

ggcttcaact tgctgatgac gctccggctg tggtcctcgt aa

1842

<210> 108
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR-8 a complete

<400> 108

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
1 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
35 40 45

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
100 105 110

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
115 120 125

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Asp Pro Ala
130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser

165

170

175

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
 180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
 195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
 210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe
 225 230 235 240

Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu
 245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
 260 265 270

Arg Leu Trp Ser Ser
 275

<210> 109
 <211> 310
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR-8 b complete

<400> 109

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
 1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
 20 25 30

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe

50

55

60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

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

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

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Ser Arg Gly
305 310

<210> 110
<211> 613
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR-8 polyprotein

<400> 110

Met Gly Phe Arg Leu Leu Cys Cys Val Ala Phe Cys Leu Leu Gly Ala
1 5 10 15

Gly Pro Val Asp Ser Gly Val Thr Gln Thr Pro Lys His Leu Ile Thr
20 25 30

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

Leu Ser Val Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe
50 55 60

Leu Ile Gln Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu
65 70 75 80

Glu Arg Phe Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn
85 90 95

Leu Ser Ser Leu Glu Leu Gly Asp Ser Ala Leu Tyr Phe Cys Ala Ser
100 105 110

Ser Gly Gly Asp Gly Asp Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu
115 120 125

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

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

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Ser Arg Gly Arg Ala Lys Arg Gly Ser Gly Ala Thr Asn
305 310 315 320

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
325 330 335

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu

340

345

350

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
 355 360 365

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

Asp Pro Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
 385 390 395 400

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Gln Gln Asn Ala Thr
 405 410 415

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
 420 425 430

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
 435 440 445

Ala Met Ser Gly Gly Tyr Thr Gly Gly Phe Lys Thr Ile Phe Gly Ala
 450 455 460

Gly Thr Arg Leu Phe Val Lys Ala Asn Ile Gln Asn Pro Asp Pro Ala
 465 470 475 480

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
 485 490 495

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
 500 505 510

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
 515 520 525

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
 530 535 540

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
 545 550 555 560

Pro Ser Ser Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe
565 570 575

Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu
580 585 590

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
595 600 605

Arg Leu Trp Ser Ser
610

<210> 111
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-9 a complete

<400> 111
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cccgaggaca gcgccgtcta cttttgtgcg gcctcgaggg gcactgggtt tcagaagctc 360
gtgttcggca ctgggacccg gctgctggtg tcgccaaaca tccagaatcc agaccccgcg 420
gtgtaccagc tgagagactc gaagtcttcc gataaatccg tgtgtctctt tacagacttc 480
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gtgctggata tgcggagcat ggactttaag tccaattcag cggtcgcgtg gagcaacaag 600
tccgacttcg cctgcgctaa cgctttcaac aactccatta tcccggagga taccttcttc 660
ccgtcaagcg acgtcccctg cgacgtgaag ctggctcgaga agtccttcga aaccgatacc 720
aacctgaact tcaaaaacct cctagtgatt gtgctcagaa tcctgctgct gaaagtggct 780
ggcttcaatt tgctgatgac cctgcggctc tggagcagc 819

<210> 112
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-9 b complete

<400> 112
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aaatgcgaac agaacctcgg acacgacacc atgtactggg acaaacagga ttccaagaag 180
ttcctgaaga ttatgttctc atacaacaac aaggaactga ttatcaacga aactgtgccg 240
aaccggttct caccgaagtc gcctgacaag gctcatctca acttgcatat caactcgctg 300
gagctcggcg actccgccgt gtacttctgc gcgtccagcc agttctggga cggagcgggc 360
gacgaacagt acttcggccc gggcactcgg ctgaccgtga ccgaagatct gaacaaagtg 420
ttcccccccg aagtggccgt gttcgaacct tccaaggcgg agatcgccca caccctaaag 480
gccactctgg tctgcctggc caccggtttc ttccccgata acgtggaact gtcttggtgg 540
gtgaacggaa aagaagtgca ctcggggggtg tccacggacc ccagcctct gaaggaacag 600
ccggcactga atgactcacg ctactgtctg tcgtcacggc tgcgcgtgtc ggccaccttc 660
tggcaaaacc cgcgaaacca ctttcgctgc caagtgcagt ttacgggct ttccgagaac 720
gacgagtggg ctgaggacag agcgaagccc gtgacccaaa tcgtgtccgc cgaggcctgg 780
ggacgcgccg actgcggtat caccagcgcc agctaccacc agggcgtgct gtcagctacc 840
atcctttacg agatcctcct gggaaaggcc accctctacg ccgtcctggt gtccgcactg 900
gtgctgatgg ctatggtcaa gcggaaggat 930

<210> 113
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR-9 polycistronic construct

<400> 113
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<210> 114
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR-9 a complete

<400> 114

Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu Asp
 1 5 10 15

Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser Val
 20 25 30

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

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

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

Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser Leu His Ile
 85 90 95

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

Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg Leu
 115 120 125

Leu Val Ser Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
 130 135 140

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe

145		150		155		160
Asp Ser Gln Thr	Asn Val Ser Gln Ser	Lys Asp Ser Asp	Val Tyr Ile			
	165	170	175			
Thr Asp Lys Thr	Val Leu Asp Met	Arg Ser Met Asp	Phe Lys Ser Asn			
	180	185	190			
Ser Ala Val Ala	Trp Ser Asn Lys	Ser Asp Phe Ala	Cys Ala Asn Ala			
	195	200	205			
Phe Asn Asn Ser	Ile Ile Pro Glu	Asp Thr Phe Phe	Pro Ser Ser Asp			
	210	215	220			
Val Pro Cys Asp	Val Lys Leu Val	Glu Lys Ser Phe	Glu Thr Asp Thr			
225	230	235	240			
Asn Leu Asn Phe	Gln Asn Leu Leu	Val Ile Val Leu	Arg Ile Leu Leu			
	245	250	255			
Leu Lys Val Ala	Gly Phe Asn Leu	Leu Met Thr Leu	Arg Leu Trp Ser			
	260	265	270			

Ser

<210> 115
 <211> 310
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR-9 b complete

<400> 115

Met Gly Cys Arg	Leu Leu Cys Cys	Val Val Phe Cys	Leu Leu Gln Ala
1	5	10	15

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His

35

40

45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
 50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
 85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
 115 120 125

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

Val Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala His Thr Gln Lys
 145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
 165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
 245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr
260 265 270

His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp
305 310

<210> 116
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR-9 polyprotein

<400> 116

Met Gly Cys Arg Leu Leu Cys Cys Val Val Phe Cys Leu Leu Gln Ala
1 5 10 15

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

Gln Met Gly Asn Asp Lys Ser Ile Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Phe Leu Lys Ile
50 55 60

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

Asn Arg Phe Ser Pro Lys Ser Pro Asp Lys Ala His Leu Asn Leu His
85 90 95

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

Ser Gln Phe Trp Asp Gly Ala Gly Asp Glu Gln Tyr Phe Gly Pro Gly
115 120 125

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

Val Ala Val Phe Glu Pro Ser Lys Ala Glu Ile Ala His Thr Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr
260 265 270

His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Phe Arg Ala Lys Arg Gly Ser Gly Ala Thr
305 310 315 320

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly

325

330

335

Pro Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu Gln Leu
340 345 350

Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr Leu Ser
355 360 365

Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser Asp Ser
370 375 380

Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys Arg Pro
385 390 395 400

Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys Asp Gln
405 410 415

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

Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ala
435 440 445

Ser Arg Gly Thr Gly Phe Gln Lys Leu Val Phe Gly Thr Gly Thr Arg
450 455 460

Leu Leu Val Ser Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
465 470 475 480

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
485 490 495

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
500 505 510

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
515 520 525

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
530 535 540

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Ser
545 550 555 560

Asp Val Pro Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
565 570 575

Thr Asn Leu Asn Phe Gln Asn Leu Leu Val Ile Val Leu Arg Ile Leu
580 585 590

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
595 600 605

Ser Ser
610