

SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> T Cell Receptor Like Antibodies

<130> RIC/FP7336001

<150> SG 10201701883R

<151> 2017-08-03

<160> 77

<170> PatentIn version 3.5

<210> 1

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> P1C1

<400> 1

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Asp
20 25 30

Tyr Glu Thr His Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
85 90 95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Ile Leu Ser

100

105

110

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190

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

Lys Thr Val Ala Pro Ala Glu Cys Ser
 210 215

<210> 2
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<220>
 <223> P1C1_gl; P1C1_dm; 2E3; 1E11

<400> 2

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Asp
 20 25 30

Tyr Glu Thr His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu

35

40

45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
85 90 95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Ile Leu Ser
100 105 110

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

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

Lys Thr Val Ala Pro Ala Glu Cys Ser
210 215

<210> 3

<211> 217

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<213> Artificial Sequence

<220>

<223> 1G7; P1C1_tm

<400> 3

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

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

Tyr Glu Thr His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
85 90 95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Ile Leu Ser
100 105 110

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

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

Lys Thr Val Ala Pro Ala Glu Cys Ser
210 215

<210> 4
<211> 214
<212> PRT
<213> Artificial Sequence

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<223> P1H4

<400> 4

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Thr Phe Gly Gly Ala Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
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<400> 5

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Asn
85 90 95

Leu Ser Asp Thr Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

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

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
130 135 140

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

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
165 170 175

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
180 185 190

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

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 6

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<223> P1A8

<400> 6

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Asn Ser Gly Thr Ser Val Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly
100 105 110

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser

180

185

190

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

Lys Thr Val Ala Pro Ala Glu Cys Ser
 210 215

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<220>
 <223> P2B4

<400> 7

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

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

Met Ile Tyr Asp Val Ser Ser Arg Pro Ser Gly Val Ser Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80

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

Ser Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu

115

120

125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
 145 150 155 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205

Thr Val Ala Pro Ala Glu Cys Ser
 210 215

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

<220>
 <223> P1C1

<400> 8

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

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

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser

50

55

60

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

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

Cys Ala Arg Glu Asn Phe Gly Ala Phe Asp His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 9

<211> 118

<212> PRT

<213> Artificial Sequence

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<223> P1C1_g1; 1G7

<400> 9

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

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

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

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

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

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

85

90

95

Cys Ala Arg Glu Asn Phe Gly Ala Phe Asp His Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 10

<211> 118

<212> PRT

<213> Artificial Sequence

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<223> 2E3

<400> 10

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

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

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

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

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

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

Cys Ala Arg Glu Asn Phe Gly Ala Phe Asp His Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser

115

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<211> 118
<212> PRT
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<220>
<223> 1E11

<400> 11

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

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

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

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

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

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

Cys Ala Arg Glu Asn Phe Gly Ser Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

<223> P1C1_dm; P1C1_tm

<400> 12

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

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

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

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

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

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

Cys Ala Arg Glu Asn Phe Gly Ser Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 13

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> P1H4

<400> 13

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

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

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

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

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

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

Ala Arg Glu Gly Ala Asp Gly Ile Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 14
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> P1B11

<400> 14

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 15
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<220>
<223> P1A8

<400> 15

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

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

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

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

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

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

Cys Ala Arg Glu Asn Phe Gly Ala Phe Asp His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 16
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<213> Artificial Sequence

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<223> P2B4

<400> 16

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

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

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

Gly Trp Met Ser Pro Asp Ser Gly Ala Thr Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Val Arg Asp Thr Tyr Gly His Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 17
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<223> P1C1; P1C1_g1; P1C1_dm; 2E3; 1E11 LC-CDR1

<400> 17

Thr Gly Ser Ser Ser Asn Ile Gly Ala Asp Tyr Glu Thr His
1 5 10

<210> 18
<211> 7
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<220>
<223> P1C1; P1C1_g1; P1C1_dm; 2E3; 1E11 LC-CDR2

<400> 18

Gly Asn Thr Asn Arg Pro Ser
1 5

<210> 19
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<223> P1C1; P1C1_g1; P1C1_dm; 2E3; 1E11 LC-CDR3

<400> 19

Gln Ser Tyr Asp Ser Asn Leu Ser Ala Trp Val
1 5 10

<210> 20
<211> 14
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<223> 1G7; P1C1_tm LC-CDR1

<400> 20

Ala Gly Ser Tyr Ser Asn Ile Gly Asp Asp Tyr Glu Thr His
1 5 10

<210> 21

<211> 11

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<223> P1H4 LC-CDR1

<400> 21

Arg Ala Ser Gln Ser Ile Gly Thr Asp Leu Ala
1 5 10

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> P1H4 LC-CDR2

<400> 22

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 23

<211> 9

<212> PRT

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<223> P1H4 LC-CDR3

<400> 23

Gln Gln Arg Ser Asn Trp Pro Pro Thr

1 5

<210> 24
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<223> P1B11 LC-CDR1

<400> 24

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
1 5 10

<210> 25
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<223> P1B11 LC-CDR2

<400> 25

Gly Asn Asn Asn Arg Pro Ser
1 5

<210> 26
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<223> P1B11 LC-CDR3

<400> 26

Gln Ser Tyr Asp Ser Asn Leu Ser Asp Thr Trp Val
1 5 10

<210> 27
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<223> P1A8 LC-CDR1

<400> 27

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val Asn
1 5 10

<210> 28

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<223> P1A8 LC-CDR3

<400> 28

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

<210> 29

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<223> P2B4 LC1-CDR1

<400> 29

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 30

<211> 7

<212> PRT

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<223> P2B4 LC-CDR2

<400> 30

Asp Val Ser Ser Arg Pro Ser
1 5

<210> 31
<211> 10
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<220>
<223> P2B4 LC-CDR3

<400> 31

Ser Ser Tyr Thr Val Phe Ser Thr Leu Val
1 5 10

<210> 32
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<223> P1C1; P1C1_g1; 1G7; P1A8 HC-CDR1

<400> 32

Ser Gly Gly Tyr Tyr Trp Ser
1 5

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<400> 33

Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 34
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<400> 34

Glu Asn Phe Gly Ala Phe Asp His
1 5

<210> 35

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<223> 2E3 HC-CDR1

<400> 35

Ser Gly Gly Tyr Tyr Trp Ala
1 5

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<211> 8

<212> PRT

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<223> 1E11 HC-CDR3

<400> 36

Glu Asn Phe Gly Ser Tyr Asp Tyr
1 5

<210> 37

<211> 5

<212> PRT

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<223> P1H4 HC-CDR1

<400> 37

Gly Tyr Tyr Met His
1 5

<210> 38

<211> 17
<212> PRT
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<223> P1H4 HC-CDR2

<400> 38

Trp	Ile	Asn	Pro	Asn	Ser	Ala	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 39
<211> 11
<212> PRT
<213> Artificial Sequence

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<223> P1H4 HC-CDR3

<400> 39

Glu	Gly	Ala	Asp	Gly	Ile	Tyr	Tyr	Phe	Asp	Tyr
1				5				10		

<210> 40
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<400> 40

Ser	Gly	Gly	Tyr	Tyr	Trp	Ser
1				5		

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<223> P1B11 HC-CDR2

<400> 41

Tyr Ile Tyr Tyr Ser Gly Thr Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 42

<211> 8

<212> PRT

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<223> P1B11 HC-CDR3

<400> 42

Glu Asn Phe Gly Ala Phe Asp Tyr
1 5

<210> 43

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> P2B4 HC-CDR1

<400> 43

Asp Tyr Tyr Ile His
1 5

<210> 44

<211> 17

<212> PRT

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<223> P2B4 HC-CDR2

<400> 44

Trp Met Ser Pro Asp Ser Gly Ala Thr Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 45
<211> 7
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<223> P2B4 HC-CDR3

<400> 45

Asp Thr Tyr Gly His Asp Tyr
1 5

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<223> Xaa = T or A

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<223> Xaa = S or Y

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<223> Xaa = A or D

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<223> Xaa = G or D

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<222> (12)..(12)
<223> Xaa = D or E

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<222> (13)..(13)
<223> Xaa = V or T

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<222> (14)..(14)
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<400> 46

Xaa Gly Ser Xaa Ser Asn Ile Gly Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10

<210> 47
<211> 7
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<222> (3)..(3)
<223> Xaa = N or T

<400> 47

Gly Asn Xaa Asn Arg Pro Ser
1 5

<210> 48
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<222> (6)..(6)
<223> Xaa = N or S

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<223> Xaa = Absent or D

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<222> (10)..(10)
<223> Xaa = A or T

<400> 48

Gln Ser Tyr Asp Ser Xaa Leu Ser Xaa Xaa Trp Val
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<210> 49
<211> 7
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<220>
<223> Sequence family HC-CDR1-1 family consensus

<220>
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<222> (7)..(7)
<223> Xaa = S or A

<400> 49

Ser Gly Gly Tyr Tyr Trp Xaa
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<210> 50
<211> 5
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<213> Artificial Sequence

<220>
<223> Sequence family HC-CDR1-2 family consensus

<220>
<221> MISC_FEATURE

<222> (1)..(1)
<223> Xaa = G or D

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = M or I

<400> 50

Xaa Tyr Tyr Xaa His
1 5

<210> 51
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence family HC-CDR2-1 family consensus

<220>
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<222> (7)..(7)
<223> Xaa = S or T

<400> 51

Tyr Ile Tyr Tyr Ser Gly Xaa Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
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<210> 52
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<213> Artificial Sequence

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<223> Sequence family HC-CDR2-2 family consensus

<220>
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<222> (2)..(2)
<223> Xaa = I or M

<220>
<221> MISC_FEATURE

<222> (3)..(3)
<223> Xaa = N or S

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = N or D

<220>
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<222> (7)..(7)
<223> Xaa = A or G

<220>
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<222> (8)..(8)
<223> Xaa = G or A

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = N or Y

<400> 52

Trp	Xaa	Xaa	Pro	Xaa	Ser	Xaa	Xaa	Thr	Xaa	Tyr	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 53
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<213> Artificial Sequence

<220>
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<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = A or S

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

<223> Xaa = F or Y

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa = H or Y

<400> 53

Glu Asn Phe Gly Xaa Xaa Asp Xaa
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<210> 54

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> P1C1

<400> 54

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cttccaggaa cggcccccaa actcctcatt tatggtaaca ccaatcggcc ctcagggggtc      180
cctcaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc      240
caggctgagg atgaggctga ttattattgc cagtcctatg acagcaatct gagtgtttgg      300
gtgttcggcg gagggaccaa gctgaccatc ctaagtcagc ccaaggctgc cccctcggtc      360
actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc      420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc      480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc      540
agctacctga gcctgacgcc tgagcagtg aagtcccaca aaagctacag ctgccagggtc      600
acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgttc a              651
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<210> 55

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> P1C1_g1; P1C1_dm; 2E3; 1E11

<400> 55

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cttccaggaa cggcccccaa actcctcatt tatggtaaca ccaatcggcc ctcaggggtc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
caggctgagg atgaggctga ttattattgc cagtcctatg acagcaatct gagtgtttgg	300
gtgttcggcg gagggaccaa gctgaccatc ctaagtcagc ccaaggctgc cccctcggtc	360
actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	420
ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc	480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	540
agctacctga gcctgacgcc tgagcagtg aagtcccaca aaagctacag ctgccaggtc	600
acgcatgaag ggagcaccgt ggagaagaca gtggcccctg cagaatgttc a	651

<210> 56

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> 1G7; P1C1_tm

<400> 56

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cttccaggaa cggcccccaa actcctcatt tatggtaaca ccaatcggcc ctcaggggtc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
caggctgagg atgaggctga ttattattgc cagtcctatg acagcaatct gagtgtttgg	300
gtgttcggcg gagggaccaa gctgaccatc ctaagtcagc ccaaggctgc cccctcggtc	360
actctgttcc caccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc	420

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc	480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	540
agctacctga gcctgacgcc tgagcagtgg aagtcccaca aaagctacag ctgccaggtc	600
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<210> 57
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P1H4

<400> 57	
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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc	180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct	240
gaagattttg cagtttatta ctgtcagcag cgtagtaact ggccctccac tttcggcgga	300
gcgaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcc	360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg	540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc	600
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<210> 58
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P1B11

<400> 58

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cttccaggaa cagcccccaa actcctcatt tatggtaaca acaatcgacc ctcaggggtc	180
cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc	240
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gtcactctgt tcccgcctc ctctgaggag cttcaagcca acaaggccac actggtgtgt	420
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agcagctacc tgagcctgac gcctgagcag tggaagtccc acaaaaagcta cagctgccag	600
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<210> 59
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P1A8

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cttccaggaa cagcccccaa actcctcatc tatggaaaca acaatcggcc ctcaggggtc	180
cctgaccgat tctctggctc caactctggc acctcagtct ccctggccat cactgggctc	240
cagcctgagg atgaggctga ttactactgc cagtcctacg acagcagcct gagtgcctgg	300
gtgttcggcg gagggacgaa gctggccgtc ctaggtcagc ccaaggctgc cccctcggtc	360
actctgttcc cgccctcctc tgaggagctc caagccaaca aggccacact agtgtgtctg	420
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aaggcgggag tggagaccac caaacctcc aaacagagca acaacaagta cgcggccagc	540

agctacctga gcctgacgcc tgagcagtgg aagtcccaca aaagctacag ctgccaggtc	600
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<210> 60
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P2B4

<400> 60	
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caggcaggca aagcccccaa actcatgatt tatgatgtca gtagtcggcc ctcagggggtt	180
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gcgggagtgg agaccaccaa accctccaaa cagagcaaca acaagtacgc ggccagcagc	540
tacctgagcc tgacgcctga gcagtggaag tcccacagaa gctacagctg ccaggtcacg	600
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<210> 61
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P1C1

<400> 61	
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cagcgcccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcacctac	180
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tccctgaaac tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa	300
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<210> 62
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P1C1_g1; 1G7

<400> 62	
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cagcaccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcacctac	180
tacaacccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc	240
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<210> 63
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2E3

<400> 63	
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cagcaccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcacctac	180
tacaacccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc	240
tccctgaaac tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa	300

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

<220>
<223> 1E11

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tacaacccgt ccctcaagag tcgagttacc atatcagtag acacgtctaa gaaccagttc 240
tcctgaaac tgagctctgt gactgccgcg gacacggccg tgtattactg tgcgagagaa 300
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<210> 65
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<220>
<223> P1C1_dm; P1C1_tm

<400> 65
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<210> 66
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<223> P1H4

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<210> 67

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> P1B11

<400> 67

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tccctgaaag tgagctctgt gactgccgcg gacacggccg ttattactg tgcgagagaa	300
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<210> 68

<211> 354

<212> DNA

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<220>

<223> P1A8

<400> 68

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<210> 69
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<210> 70
 <211> 393
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 <213> Homo sapiens

<400> 70

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Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu
			20					25					30		

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
100 105 110

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

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
165 170 175

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

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
195 200 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
210 215 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225 230 235 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
275 280 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
370 375 380

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<210> 71

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> p53 peptide

<400> 71

Arg Met Pro Glu Ala Ala Pro Pro Val
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<210> 72

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> p53 peptide

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Ser Thr Pro Pro Pro Gly Thr Arg Val
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<210> 73

<211> 9

<212> PRT

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<400> 73

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<212> PRT

<213> Artificial Sequence

<220>

<223> p53 peptide

<400> 74

Val Val Pro Tyr Glu Pro Pro Glu Val
1 5

<210> 75

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> p53 peptide

<400> 75

Thr Tyr Ser Pro Ala Leu Asn Lys Met Phe
1 5 10

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> p53 peptide

<400> 76

Ala Ile Tyr Lys Gln Ser Gln His Met
1 5

<210> 77
<211> 9
<212> PRT
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<220>
<223> p53 peptide

<400> 77

Glu Tyr Leu Asp Asp Arg Asn Thr Phe
1 5