

pctgb2014052464-seq1
SEQUENCE LISTING

<110> Immunocore Ltd
<120> T cell receptors
<130> P57437WO
<160> 22
<170> PatentIn version 3.5
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<213> Epstein Barr Virus
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Cys Leu Gly Gly Leu Leu Thr Met Val
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<212> PRT
<213> Homo sapiens
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Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Ser Ala Phe Gln Tyr
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Phe Met Trp Tyr Arg Gln Tyr Ser Arg Lys Gly Pro Glu Leu Leu Met
35 40 45

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

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

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

Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

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<213> Homo sapiens
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Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His Ala Thr Leu
20 25 30

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

Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro Lys Asp Arg
50 55 60

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

Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Leu
85 90 95

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

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
115 120 125

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

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
145 150 155 160

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
165 170 175

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
180 185 190

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Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
195 200 205

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
210 215 220

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

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<213> Artificial sequence

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<400> 4

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

Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Ser Ala Phe Gln Tyr
20 25 30

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

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

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

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

Ser Gly Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val

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Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
 195 200 205

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<400> 5

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

Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His Ala Thr Leu
 20 25 30

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

Phe Gln Asn Asn Gly Val Val Asp Asp Ser Gln Leu Pro Lys Asp Arg
 50 55 60

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

Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Leu
 85 90 95

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

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 115 120 125

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

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 145 150 155 160

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
 165 170 175

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg Leu
 180 185 190

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Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg Cys
195 200 205

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
210 215 220

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

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Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Ser Ala Phe Gln Tyr
20 25 30

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

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

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Glu Ala His
85 90 95

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

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val

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165

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Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
 195 200 205

<210> 7

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<213> Artificial sequence

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<223> T cell receptor alpha chain variable domain

<400> 7

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

Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Ser Ala Phe Gln Tyr
 20 25 30

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

Tyr Leu Pro Gly Gly Gly Asn Lys Glu Asp Gly Arg Phe Thr Ala Gln
 50 55 60

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Asp Ala Tyr
 85 90 95

Gly His Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
 100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
 130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 180 185 190

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

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

Tyr Gln Phe Gln Asp Gly Asn Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Glu Ala His
85 90 95

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

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

<210> 9

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<211> 207
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 <213> Artificial sequence

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<400> 9

Gln Lys Glu Val Glu Gln Asp Pro Gly Pro Leu Ser Val Pro Glu Gly
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Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Pro His Met Ala Tyr
 20 25 30

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

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

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Asp Ala Tyr
 85 90 95

Gly His Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
 100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
 130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
 195 200 205

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<400> 10

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

<210> 11

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<400> 11

Gln Lys Glu Val Glu Gln Asp Pro Gly Pro Leu Ser Val Pro Glu Gly
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Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Pro His Met Ala Tyr
20 25 30

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

Tyr Gln Phe Gln Asp Gly Asn Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Asp Ala Tyr
85 90 95

Gly His Tyr Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr
100 105 110

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

<210> 12

<211> 207

<212> PRT

<213> Artificial sequence

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<223> T cell receptor alpha chain variable domain

<400> 12

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

Ala Ile Val Ser Leu Asn Cys Thr Tyr Ser Asn Pro His Met Ala Tyr
20 25 30

Phe Met Trp Tyr Arg Gln Tyr Ser Arg Lys Gly Pro Glu Leu Leu Met
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Tyr Gln Phe Gln Asp Gly Asn Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

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

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Met Ser Ala Glu Ala His
85 90 95

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

Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
115 120 125

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
130 135 140

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
145 150 155 160

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

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
180 185 190

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser
195 200 205

<210> 13
<211> 242
<212> PRT
<213> Artificial sequence

<220>
<223> T cell receptor beta chain variable domain

<400> 13

Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile Glu Lys Arg
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Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His Ala Thr Leu
20 25 30

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

Phe Val Val Ala Ala Ser Val Asp Asp Ser Gln Leu Pro Lys Asp Arg
50 55 60

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

Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Leu
85 90 95

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

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
115 120 125

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

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
145 150 155 160

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
165 170 175

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg Leu
180 185 190

Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg Cys
195 200 205

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
210 215 220

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
225 230 235 240

Ala Asp

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aggtttacag cacaggtcga taaatccagc aagtatatct ccttgttcat cagagactca 240
cagcccagtg attcagccac ctacctctgt gcaatgagcg cggaagcaaa ttccgggtat 300

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gcactcaact tcggcaaagg cacctcgctg ttggtcacac cccatatcca gaaccctgac	360
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gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac	480
aaatgtgtgc tagacatgag gtctatggac ttcaagagca acagtgtgtg ggcctggagc	540
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc	600
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<220>
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gccctcaatg actccagata cgctctgagc agccgcctga gggctctggc caccttctgg	600
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<210> 16
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<220>
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X at position 2 = I or Q

<400> 16

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 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 130 135 140
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe
 145 150 155 160
 Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 165 170 175
 Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn
 180 185 190
 Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn
 195 200 205
 Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 210 215 220
 Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe
 225 230 235 240
 Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 245 250 255
 Gly Ser Glu Ala Gly Val Ala Gln Ser Pro Arg Tyr Lys Ile Ile Glu
 260 265 270
 Lys Arg Gln Ser Val Ala Phe Trp Cys Asn Pro Ile Ser Gly His Ala

275

Thr Leu Tyr Trp Tyr Gln Gln Ile Leu Gly Gln Gly Pro Lys Leu Leu
290 295 300

Ile Gln Phe Val Val Ala Ala Ser Val Asp Asp Ser Gln Leu Pro Lys
305 310 315 320

Asp Arg Phe Ser Ala Glu Arg Leu Lys Gly Val Asp Ser Thr Leu Lys
325 330 335

Ile Gln Pro Ala Lys Leu Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
340 345 350

Ser Leu Gly Gly Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
355 360 365

Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe
370 375 380

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
385 390 395 400

Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp
405 410 415

Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro
420 425 430

Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser
435 440 445

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe
450 455 460

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
465 470 475 480

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
485 490 495

Gly Arg Ala Asp
500

<210> 17
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<212> PRT
<213> Epstein Barr Virus

<400> 17

Ser Leu Gly Gly Leu Leu Thr Met Val
1 5

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<210> 18
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 <212> PRT
 <213> Epstein Barr Virus

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Cys Leu Gly Gly Leu Ile Thr Met Val
 1 5

<210> 19
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 <223> Primer

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<400> 22
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