SEQUENCE LISTING

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<120> TCRS SPECIFIC FOR MINOR HISTOCOMPATIBILITY
(H) ANTIGEN HA-1 AND USES THEREOF

<130> 360056.455WO

<140> PCT
<141> 2017-09-22

<150> US 62/399,291
<151> 2016-09-23

<160> 127

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta chain variable region
with signal peptide

<400> 1
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110
Ser Ser Ser Thr Gly Gly His Asn Glu Gln Phe Phe Gly Pro Gly Thr
115 120 125
Arg Leu Thr Val Leu

130

<210> 2
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain variable region
with signal peptide

<400> 2
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15
Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30
Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45
Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
50 55 60
His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65 70 75 80
Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
85 90 95
Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Lys
100 105 110
Arg Asp Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr
115 120 125
Lys Leu Ser Val Ile Pro
130

<210> 3
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain variable region
with signal peptide

<400> 3
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85   90   95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100   105   110
Ser Ser Leu Val Lys Gly Glu Lys Leu Phe Gly Ser Gly Thr Gln Leu
        115   120   125
Ser Val Leu
    130

<210> 4
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 alpha chain variable region
      with signal peptide

<400> 4
Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
 1   5   10   15
Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
            20   25   30
Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
        35   40   45
Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
    50   55   60
Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65   70   75   80
Leu Asn Ala Ser Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala
                85   90   95
Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ile Gly
            100   105   110
Leu Gly Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys
        115   120   125
Val Leu Ala
    130

<210> 5
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain variable region
      with signal peptide

<400> 5
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1   5   10   15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr

```
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Thr Thr Leu Asp Glu Gln Tyr Val Gly Pro Gly Thr Arg
        115                 120                 125
Leu Thr Val Thr
    130
```

<210> 6
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain variable region
with signal peptide

<400> 6

```
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
 1               5                  10                  15
Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
            20                  25                  30
Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
        35                  40                  45
Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
    50                  55                  60
His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65                  70                  75                  80
Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
                85                  90                  95
Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asn
            100                 105                 110
Ser Gly Asn Thr Pro Leu Val Phe Gly Lys Gly Thr Arg Leu Ser Val
        115                 120                 125
Ile Ala
    130
```

<210> 7
<211> 132
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic sequence TCR10 beta chain variable region
with signal peptide

<400> 7
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1   5   10   15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20   25   30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35   40   45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50   55   60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65   70   75   80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85   90   95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100   105   110
Ser Ser Met Leu Thr Asn Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
        115   120   125
Leu Thr Val Thr
    130

<210> 8
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain variable region
with signal peptide

<400> 8
Met Lys Lys His Leu Thr Thr Phe Leu Val Ile Leu Trp Leu Tyr Phe
 1   5   10   15
Tyr Arg Gly Asn Gly Lys Asn Gln Val Glu Gln Ser Pro Gln Ser Leu
            20   25   30
Ile Ile Leu Glu Gly Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val
        35   40   45
Ser Pro Phe Ser Asn Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly
    50   55   60
Pro Val Ser Leu Thr Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn
65   70   75   80
Gly Arg Tyr Thr Ala Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu
                85   90   95
His Ile Thr Ala Ser Gln Leu Ser Asp Ser Ala Ser Tyr Ile Cys Val
            100   105   110
Val Asp Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr
        115   120   125
His Leu Ile Ile Gln Pro
    130

<210> 9
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta chain variable region
with signal peptide

<400> 9
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110
Ser Ser Leu Val Val Gly Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg
115 120 125
Leu Thr Val Leu
130

<210> 10
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain variable region
with signal peptide

<400> 10
Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15
Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
20 25 30
Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
35 40 45
Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
50 55 60
Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65 70 75 80
Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile

```
                85                  90                  95
Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val His
            100                 105                 110
Leu Leu Asn Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr
        115                 120                 125
Val Arg Ala
    130
```

<210> 11
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain variable region
with signal peptide

<400> 11

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Val Ser Gly Asn Thr Ile Tyr Phe Gly Glu Gly Ser Trp
        115                 120                 125
Leu Thr Val Val
    130
```

<210> 12
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain variable region
with signal peptide

<400> 12

```
Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
 1               5                  10                  15
Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
            20                  25                  30
```

```
Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
        35                  40                  45
Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
    50                  55                  60
Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65                  70                  75                  80
Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
                85                  90                  95
Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg
            100                 105                 110
Gly Gly Thr Thr Ser Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr
        115                 120                 125
Arg Leu Lys Val Leu Ala
    130

<210> 13
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1 beta chain CDR3

<400> 13
Cys Ala Ser Ser Ser Thr Gly Gly His Asn Glu Gln Phe Phe
 1               5                   10

<210> 14
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2 beta chain CDR3

<400> 14
Cys Ala Ser Ser Leu Val Lys Gly Glu Lys Leu Phe
 1               5                   10

<210> 15
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain CDR3

<400> 15
Cys Ala Ser Ser Leu Thr Thr Leu Asp Glu Gln Tyr Val
 1               5                   10
```

<210> 16
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta chain CDR3

<400> 16
Cys Ala Ser Ser Met Leu Thr Asn Tyr Glu Gln Tyr Phe
 1   5   10

<210> 17
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta chain CDR3

<400> 17
Cys Ala Ser Ser Leu Val Val Gly Asn Glu Gln Phe Phe
 1   5   10

<210> 18
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,5,10,13,16 beta chain constant
      region (Cys modified)

<400> 18
Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1   5   10   15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
            20   25   30
Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35   40   45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
    50   55   60
Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65   70   75   80
Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
                85   90   95
Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
            100   105   110
Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
        115   120   125
Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser

```
    130                 135                 140
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145                 150                 155                 160
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
                165                 170                 175
Ser
```

<210> 19
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain constant region (Cys modified)

<400> 19

```
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140
```

<210> 20
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain constant
region (Cys modified)

<400> 20

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

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

<210> 21
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain constant region (Cys modified)

<400> 21
Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
65                  70                  75                  80
Ser


<210> 22
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain constant
```

region (Cys modified)

<400> 22
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1   5   10   15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20   25   30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35   40   45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50   55   60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65   70   75   80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85   90   95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100   105   110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115   120   125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130   135   140

<210> 23
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain constant
region (Cys modified)

<400> 23
Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1   5   10   15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
            20   25   30
Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35   40   45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
    50   55   60
Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65   70   75   80
Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
                85   90   95
Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
            100   105   110
Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
        115   120   125
Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
    130   135   140
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala

145 150 155 160
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175

<210> 24
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 alpha chain constant region (Cys modified)

<400> 24
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
35 40 45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 25
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain constant region

<400> 25
Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30
Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45
Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
50 55 60
Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu

65 70 75 80
Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95
Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110
Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125
Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser
130 135 140
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145 150 155 160
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175
Phe

<210> 26
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain constant region

<400> 26
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 27
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta chain (full length)

(Cys modified)

<400> 27
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1   5   10   15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20   25   30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35   40   45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50   55   60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65   70   75   80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85   90   95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100   105   110
Ser Ser Ser Thr Gly Gly His Asn Glu Gln Phe Phe Gly Pro Gly Thr
        115   120   125
Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
    130   135   140
Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145   150   155   160
Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu
                165   170   175
Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
            180   185   190
Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
        195   200   205
Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
    210   215   220
Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
225   230   235   240
Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
                245   250   255
Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln
            260   265   270
Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
        275   280   285
Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
    290   295   300
Val Lys Arg Lys Asp Ser
305   310

<210> 28
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain (full length)

(Cys modified) with signal peptide

<400> 28
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
 1   5   10   15
Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
            20   25   30
Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
        35   40   45
Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val
    50   55   60
His Leu Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg
65   70   75   80
Leu Arg Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile
                85   90   95
Thr Ala Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Lys
            100   105   110
Arg Asp Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr
        115   120   125
Lys Leu Ser Val Ile Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr
    130   135   140
Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145   150   155   160
Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
                165   170   175
Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys
            180   185   190
Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
        195   200   205
Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
    210   215   220
Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225   230   235   240
Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
                245   250   255
Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
            260   265   270
Trp Ser Ser
        275

<210> 29
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain (full length)
(Cys modified) with signal peptide

<400> 29
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala

```
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Val Lys Gly Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln
        115                 120                 125
Leu Ser Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala
    130                 135                 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145                 150                 155                 160
Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp
305
```

<210> 30
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 alpha chain (full length)
(Cys modified) with signal peptide

<400> 30
Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp

```
 1               5                  10                  15
Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
            20                  25                  30
Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
        35                  40                  45
Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
    50                  55                  60
Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65                  70                  75                  80
Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
                85                  90                  95
Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ile
            100                 105                 110
Gly Leu Gly Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu
        115                 120                 125
Lys Val Leu Ala 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 Cys 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> 31
<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain (full length)
(Cys modified) with signal peptide

<400> 31

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
```

```
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Thr Thr Leu Asp Glu Gln Tyr Val Gly Pro Gly Thr Arg
        115                 120                 125
Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
    130                 135                 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145                 150                 155                 160
Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Ser
305
```

<210> 32
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain (full length)
(Cys modified) with signal peptide

<400> 32

```
Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
 1               5                  10                  15
Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
            20                  25                  30
Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
```

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

<210> 33
<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta chain (full length)
(Cys modified) with signal peptide

<400> 33

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
```

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

<210> 34
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain (full length)
(Cys modified) with signal peptide

<400> 34

```
Met Lys Lys His Leu Thr Thr Phe Leu Val Ile Leu Trp Leu Tyr Phe
 1               5                  10                  15
Tyr Arg Gly Asn Gly Lys Asn Gln Val Glu Gln Ser Pro Gln Ser Leu
            20                  25                  30
Ile Ile Leu Glu Gly Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val
        35                  40                  45
Ser Pro Phe Ser Asn Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly
    50                  55                  60
Pro Val Ser Leu Thr Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn
65                  70                  75                  80
Gly Arg Tyr Thr Ala Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu
```

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

<210> 35
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta chain (full length)
(Cys modified) with signal peptide

<400> 35

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Val Val Gly Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg
```

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

<210> 36
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain (full length)
(Cys modified) with signal peptide

<400> 36

```
Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
 1               5                  10                  15
Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
            20                  25                  30
Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
        35                  40                  45
Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
    50                  55                  60
Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65                  70                  75                  80
Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
                85                  90                  95
Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val His
            100                 105                 110
Leu Leu Asn Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr
```

```
        115                 120                 125
Val Arg Ala Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
    130                 135                 140
Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
145                 150                 155                 160
Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
                165                 170                 175
Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
            180                 185                 190
Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
        195                 200                 205
Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
    210                 215                 220
Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
225                 230                 235                 240
Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe 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> 37
<211> 309
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain
(full length) (Cys modified) with signal peptide

<400> 37

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

```
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Phe
305
```

<210> 38
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain
(full length) (Cys modified) with signal peptide

<400> 38

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

```
                165                 170                 175
Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
            180                 185                 190
Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
        195                 200                 205
Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
    210                 215                 220
Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225                 230                 235                 240
Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
                245                 250                 255
Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
            260                 265                 270
Trp Ser Ser
        275
```

<210> 39
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta chain
(codon optimized, Cys modified)

<400> 39

```
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat      60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc     120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag     180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg     240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg     300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcagcacagg cggccacaac     360
gagcagttct ttggccctgg cacccggctg accgtgctgg aagatctgaa gaacgtgttc     420
cccccagagg tggccgtgtt cgagccttct gaggccgaga tcagccacac ccagaaagcc     480
accctcgtgt gtctggccac cggcttctac cccgaccacg tggaactgtc ttggtgggtc     540
aacggcaaag aggtgcactc cggcgtgtgc accgatcccc agcctctgaa agaacagccc     600
gccctgaacg acagccggta ctgcctgagc agcagactga gagtgtccgc caccttctgg     660
cagaaccccc ggaaccactt cagatgccag gtgcagttct acggcctgag cgagaacgac     720
gagtggaccc aggacagagc caagcccgtg acccagatcg tgtctgccga agcctggggc     780
agagccgatt gcggctttac cagcgagagc taccagcagg gcgtgctgag cgccaccatc     840
ctgtacgaga tcctgctggg caaggccacc ctgtacgccg tgctggtgtc tgccctggtg     900
ctgatggcca tggtcaagcg gaaggacagc                                      930
```

<210> 40
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain
(codon optimized; Cys modified)

<400> 40
atggaaacac tgctgggcgt gtccctcgtg atcctgtggc tgcagctggc cagagtgaac 60
agccagcagg gggaagagga tccccaggcc ctgagcattc aggaaggcga gaacgccacc 120
atgaactgca gctacaagac cagcatcaac aacctgcagt ggtacagaca gaacagcggc 180
agaggcctgg tgcacctgat cctgatcaga agcaacgaga gagagaagca cagcggacgg 240
ctgagagtga ccctggacac ctccaagaag tccagctccc tgctgatcac cgccagcaga 300
gccgccgata ccgccagcta cttctgtgcc accaagcggg attctggcgc cggatcctac 360
cagctgacct tcggcaaggg caccaagctg agcgtgatcc ccaacatcca gaaccccgac 420
cccgccgtgt atcagctgag agacagcaag agcagcgaca agagcgtgtg cctgttcacc 480
gacttcgaca gccagaccaa cgtgtcccag agcaaggaca gcgacgtgta catcaccgat 540
aagtgcgtgc tggacatgcg gagcatggac ttcaagagca acagcgccgt ggcctggtcc 600
aacaagagcg acttcgcctg cgccaacgcc ttcaacaaca gcatcatccc cgaggacacc 660
tttttcccca gccccgagag cagctgcgac gtgaaactgg tggagaagtc cttcgagaca 720
gacaccaatc tgaactttca gaacctgagc gtgatcggct tccggatcct gctgctgaaa 780
gtggccggct tcaatctgct gatgaccctg cggctgtgga gcagctga 828

<210> 41
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain
(codon optimized; Cys modified)

<400> 41
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcctcgtgaa gggcgagaag 360
ctgttcttcg gcagcggcac ccagctgagc gtgctggaag atctgaacaa ggtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgcc tggccaccgg ctttttcccc gaccacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgcg gctttaccag cgtgtcctat cagcagggcg tgctgagcgc caccatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg 900
atggccatgg tcaagcggaa ggactttggc 930

<210> 42
<211> 820
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 alpha chain

(codon optimized; Cys modified)

<400> 42
atggaaacac tgctgggcct gctgatcctg tggctgcagc tgcagtgggt gtccagcaag 60
caggaagtga cacagatccc tgccgccctg tctgtgcccg agggcgaaaa tctggtgctg 120
aactgcagct tcaccgacag cgccatctac aacctgcagt ggttcagaca ggaccccggc 180
aagggcctga caagcctgct gctgattcag agcagccaga gagagcagac cagcggcaga 240
ctgaacgcca gcctggataa gagcagcggc cgcagcaccc tgtatatcgc cgcttctcag 300
cctggcgact ctgccacata tctgtgcgcc gtgatcggcc tgggcggcac ctacaagtac 360
atctttggca ccggcaccag actgaaagtg ctggccaaca tccagaaccc cgaccccgcc 420
gtgtaccagc tgagagacag caagtccagc gacaagagcg tgtgtctgtt caccgacttc 480
gacagccaga ccaacgtgtc ccagagcaag gacagcgacg tgtacatcac cgataagtgc 540
gtgctggaca tgcggagcat ggacttcaag agcaacagcg ccgtggcctg gtccaacaag 600
agcgacttcg cctgcgccaa cgccttcaac aacagcatca tccccgagga caccttttc 660
cccagccccg agagcagctg cgacgtgaaa ctggtggaga agtccttcga gacagacacc 720
aatctgaact ttcagaacct gagcgtgatc ggcttccgga tcctgctgct gaaagtggcc 780
ggcttcaatc tgctgatgac cctgcggctg tggagcagcg 820

<210> 43
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain
(codon optimized; Cys modified)

<400> 43
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gggacagcgc catgtatctg tgtgccagct ccctgaccac cctggacgag 360
cagtatgtgg gcccaggcac cagactgacc gtgaccgagg acctgaagaa cgtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgtc tggccaccgg cttctacccc gatcacgtgg agctgtcttg gtgggtgaac 540
ggcaaagagg tgcacagcgg cgtctgcacc gacccccagc ccctgaaaga gcagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc cggctgagag tgagcgccac cttctggcag 660
aacccccgga accacttccg gtgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtga gcgccgaggc ctggggcaga 780
gccgactgcg gcttcaccag cgagagctac cagcagggcg tgctgtccgc cacaatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtccgc cctggtgctg 900
atggccatgg tgaagcggaa ggacagccgg ggc 933

<210> 44
<211> 816
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence TCR5 alpha chain
(codon optimized; Cys modified)

<400> 44
atggaaaccc tgctgggcgt gtccctcgtg atcctgtggc tgcagctggc cagagtgaac 60
agccagcagg gcgaagaaga tccccaggcc ctgagcatcc aggaaggcga gaacgccaca 120
atgaactgca gctacaagac cagcatcaac aacctgcagt ggtacagaca gaacagcggc 180
agaggcctgg tgcacctgat cctgatcaga agcaacgaga gagagaagca ctccggcaga 240
ctgagagtga ccctggacac cagcaagaag tccagcagcc tgctgatcac cgccagcaga 300
gccgccgata ccgccagcta cttctgcgcc accaactccg gcaacacccc cctggtgttt 360
ggcaagggca cccggctgag cgtgatcgcc aacatccaga accccgaccc cgccgtgtac 420
cagctgagag acagcaagag cagcgacaag agcgtgtgcc tgttcaccga cttcgacagc 480
cagaccaacg tgtcccagag caaggacagc gacgtgtaca tcaccgataa gtgcgtgctg 540
gacatgcgga gcatggactt caagagcaac agcgccgtgg cctggtccaa caagagcgac 600
ttcgcctgcg ccaacgcctt caacaacagc atcatccccg aggacacctt tttccccagc 660
cccgagagca gctgcgacgt gaaactggtg gagaagtcct tcgagacaga caccaatctg 720
aactttcaga acctgagcgt gatcggcttc cggatcctgc tgctgaaagt ggccggcttc 780
aatctgctga tgaccctgcg gctgtggagc agctga 816

<210> 45
<211> 933
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta chain
(codon optimized; Cys modified)

<400> 45
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gcgatagcgc catgtacctg tgcgccagct ccatgctgac caactacgag 360
cagtacttcg gccctggcac ccggctgacc gtgaccgagg atctgaagaa cgtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgtc tggccaccgg cttctacccc gaccacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgcg gctttaccag cgagagctac cagcagggcg tgctgagcgc caccatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg 900
atggccatgg tcaagcggaa ggacagcaga ggc 933

<210> 46
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain
(codon optimized; Cys modified)

<400> 46
atgaagaagc acctgaccac ctttctcgtg atcctgtggc tgtacttcta ccggggcaac 60
ggcaagaacc aggtggaaca gagcccccag agcctgatca tcctggaagg caagaattgc 120
accctgcagt gcaactacac cgtgtccccc ttcagcaacc tgcggtggta caagcaggac 180
accggcagag gccctgtgtc cctgaccatc atgaccttca gcgagaacac caagagcaac 240
ggccggtaca ccgccaccct ggatgccgat acaaagcaga gcagcctgca catcaccgcc 300
agccagctga gcgattccgc cagctacatc tgcgtggtgg attctggcgg cggagccgat 360
ggcctgacat ttggcaaggg cacccacctg atcattcagc cctacatcca gaaccccgac 420
cccgccgtgt accagctgag agacagcaag tccagcgaca agagcgtgtg cctgttcacc 480
gacttcgaca gccagaccaa cgtgtcccag agcaaggaca gcgacgtgta catcaccgat 540
aagtgcgtgc tggacatgcg gagcatggac ttcaagagca acagcgccgt ggcctggtcc 600
aacaagagcg acttcgcctg cgccaacgcc ttcaacaaca gcatcatccc cgaggacacc 660
tttttcccca gccccgagag cagctgcgac gtgaaactgg tggagaagtc cttcgagaca 720
gacaccaatc tgaactttca gaacctgagc gtgatcggct tccggatcct gctgctgaaa 780
gtggccggct tcaatctgct gatgaccctg cggctgtgga gcagctga 828

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

<220>
<223> Synthetic sequence TCR16 beta chain
(codon optimized; Cys modified)

<400> 47
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcctggtcgt gggcaacgag 360
cagtttttcg gccctggcac cagactgacc gtgctggaag atctgaagaa cgtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgtc tggccaccgg cttctacccc gaccacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgcg gctttaccag cgagagctac cagcagggcg tgctgagcgc caccatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg 900
atggccatgg tcaagcggaa ggacagcaga ggc 933

<210> 48
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain
(codon optimized; Cys modified)

<400> 48
atggaaacac tgctgggcct gctgatcctg tggctgcagc tgcagtgggt gtccagcaag 60
caggaagtga cacagatccc tgccgccctg tctgtgcccg agggcgaaaa tctggtgctg 120
aactgcagct tcaccgacag cgccatctac aacctgcagt ggttcagaca ggaccccggc 180
aagggcctga caagcctgct gctgattcag agcagccaga gagagcagac cagcggcaga 240
ctgaacgcca gcctggataa gagcagcggc cgcagcaccc tgtatatcgc cgcttctcag 300
cctggcgact ctgccacata tctgtgcgcc gtgcatctgc tgaacgacta caagctgagc 360
ttcggagccg gcaccaccgt gacagtgcgg gccaacatcc agaaccccga ccctgccgtg 420
taccagctga gagacagcaa gtccagcgac aagagcgtgt gcctgttcac cgacttcgac 480
agccagacca acgtgtccca gagcaaggac agcgacgtgt acatcaccga taagtgcgtg 540
ctggacatgc ggagcatgga cttcaagagc aacagcgccg tggcctggtc caacaagagc 600
gacttcgcct gcgccaacgc cttcaacaac agcatcatcc ccgaggacac ctttttcccc 660
agccccgaga gcagctgcga cgtgaaactg gtggagaagt ccttcgagac agacaccaat 720
ctgaactttc agaacctgag cgtgatcggc ttccggatcc tgctgctgaa agtggccggc 780
ttcaatctgc tgatgaccct gcggctgtgg agcagctga 819

<210> 49
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR24 beta chain (wild type)

<400> 49
atgggtcctg ggcttctcca ctggatggcc ctttgtctcc ttggaacagg tcatggggat 60
gccatggtca tccagaaccc aagataccag gttacccagt ttggaaagcc agtgaccctg 120
agttgttctc agactttgaa ccataacgtc atgtactggt accagcagaa gtcaagtcag 180
gccccaaagc tgctgttcca ctactatgac aaagatttta acaatgaagc agacaccct 240
gataacttcc aatccaggag gccgaacact tctttctgct ttcttgacat ccgctcacca 300
ggcctggggg acgcagccat gtacctgtgt gccaccagca agacacggat agctcaagag 360
acccagtact tcgggccagg cacgcggctc ctggtgctcg aggacctgaa aaacgtgttc 420
ccacccgagg tcgctgtgtt tgagccatca gaagcagaga tctcccacac ccaaaaggcc 480
acactggtgt gcctggccac aggcttctac cccgaccacg tggagctgag ctggtgggtg 540
aatgggaagg aggtgcacag tggggtcagc acagacccgc agcccctcaa ggagcagccc 600
gccctcaatg actccagata ctgcctgagc agccgcctga gggtctcggc caccttctgg 660
cagaaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgac 720
gagtggaccc aggatagggc caaacctgtc acccagatcg tcagcgccga ggcctggggt 780
agagcagact gtggcttcac ctccgagtct taccagcaag gggtcctgtc tgccaccatc 840
ctctatgaga tcttgctagg gaaggccacc ttgtatgccg tgctggtcag tgccctcgtg 900
ctgatggcca tggtcaagag aaaggattcc agaggctag 939

<210> 50
<211> 825
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR24 alpha chain (wild type)

<400> 50
atgctcctgg agcttatccc actgctgggg atacattttg tcctgagaac tgccagagcc 60
cagtcagtga cccagcctga catccacatc actgtctctg aaggagcctc actggagttg 120
agatgtaact attcctatgg ggcaacacct tatctcttct ggtatgtcca gtcccccggc 180
caaggcctcc agctgctcct gaagtacttt tcaggagaca ctctggttca aggcattaaa 240
ggctttgagg ctgaatttaa gaggagtcaa tcttccttca acctgaggaa accctctgtg 300
cattggagtg atgctgctga gtacttctgt gctgtgggtt ataacaccaa tgcaggcaaa 360
tcaacctttg gggatgggac tacgctcact gtgaagccaa atatccagaa ccctgaccct 420
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 480
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 540
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 600
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 660
ttccccagcc cagaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat 720
acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg 780
gccgggttta atctgctcat gacgctgcgg ctgtggtcca gctga 825

<210> 51
<211> 929
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain
(codon optimized; Cys modified)

<400> 51
atgggcacaa gcctgctgtg ttggatggcc ctgtgtctgc tgggagccga tcatgccgat 60
acgggagtgt cccaggatcc tcggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ctatcagcga gcacaaccgg ctgtactggt acagacagac actcggccag 180
ggacctgagt tcctgaccta cttccagaac gaggcccagc tggaaaagag cagactgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagaga 300
accgagcagg gcgacagcgc catgtatctg tgtgccagct ctctggtgtc cggcaacacc 360
atctacttcg gcgaaggcag ctggctgaca gtggttaaga tctgaacaag gtgttccccc 420
cagaggtggc cgtgttcgag ccttctgagg ccgagatcag ccacacccag aaagccaccc 480
tcgtgtgcct ggccaccggc tttttccccg accacgtgga actgtcttgg tgggtcaacg 540
gcaaagaggt gcactccggc gtgtgcaccg atccccagcc tctgaaagaa cagcccgccc 600
tgaacgacag ccggtactgc ctgagcagca gactgagagt gtccgccacc ttctggcaga 660
acccccggaa ccacttcaga tgccaggtgc agttctacgg cctgagcgag aacgacgagt 720
ggacccagga cagagccaag cccgtgaccc agatcgtgtc tgccgaagcc tggggcagag 780
ccgattgcgg ctttaccagc gtgtcctatc agcagggcgt gctgagcgcc accatcctgt 840
acgagatcct gctgggcaag gccaccctgt acgccgtgct ggtgtctgcc ctggtgctga 900
tggccatggt caagcggaag gactttggc 929

<210> 52
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain
(codon optimized; Cys modified)

<400> 52
atggaaacac tgctgggcct gctgatcctg tggctgcaac tgcaatgggt gtccagcaag 60
caagaagtga cacagatccc tgccgctctg tctgtgcctg agggcgaaaa cctggtgctg 120
aactgcagct tcaccgacag cgccatctac aacctgcagt ggttcagaca ggaccccggc 180
aagggactga caagcctgct gctgattcag agcagccaga gagagcagac cagcggcaga 240
ctgaatgcca gcctggataa gtcctccggc agaagcaccc tgtatatcgc cgcttctcag 300
cctggcgata gcgccacata tctgtgtgcc gttagaggcg gcaccacctc cggcacctac 360
aagtacatct ttggcaccgg caccagactg aaggtgctgg ccaatatcca gaaccccgac 420
cccgccgtgt accagctgag agacagcaag tccagcgaca agagcgtgtg tctgttcacc 480
gacttcgaca gccagaccaa cgtgtcccag agcaaggaca gcgacgtgta catcaccgat 540
aagtgcgtgc tggacatgcg gagcatggac ttcaagagca acagcgccgt ggcctggtcc 600
aacaagagcg acttcgcctg cgccaacgcc ttcaacaaca gcatcatccc cgaggacacc 660
tttttcccca gccccgagag cagctgcgac gtgaaactgg tggagaagtc cttcgagaca 720
gacaccaatc tgaactttca gaacctgagc gtgatcggct tccggatcct gctgctgaaa 780
gtggccggct tcaatctgct gatgaccctg cggctgtgga gcagctga 828

<210> 53
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta-P2A-alpha
(Cys modified) with signal peptide

<400> 53
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
20 25 30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110
Ser Ser Ser Thr Gly Gly His Asn Glu Gln Phe Phe Gly Pro Gly Thr
115 120 125
Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
130 135 140
Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145 150 155 160

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Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu
                165                 170                 175
Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp
            180                 185                 190
Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
        195                 200                 205
Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
    210                 215                 220
Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
225                 230                 235                 240
Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
                245                 250                 255
Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln
            260                 265                 270
Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
        275                 280                 285
Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
    290                 295                 300
Val Lys Arg Lys Asp Ser Arg Gly 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 Glu
                325                 330                 335
Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu Ala Arg
            340                 345                 350
Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln
        355                 360                 365
Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn
    370                 375                 380
Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu
385                 390                 395                 400
Ile Leu Ile Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg
                405                 410                 415
Val Thr Leu Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala
            420                 425                 430
Ser Arg Ala Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Lys Arg Asp
        435                 440                 445
Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr Lys Leu
    450                 455                 460
Ser Val Ile Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
465                 470                 475                 480
Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
                485                 490                 495
Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
            500                 505                 510
Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
        515                 520                 525
Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
    530                 535                 540
Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
545                 550                 555                 560
Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr
```

```
                565                 570                 575
Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu
            580                 585                 590
Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
        595                 600                 605
Ser
```

<210> 54
<211> 604
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta-P2A-alpha
(Cys modified) with signal peptide

<400> 54

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Val Lys Gly Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln
        115                 120                 125
Leu Ser Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala
    130                 135                 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145                 150                 155                 160
Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln
```

```
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Phe Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
305                 310                 315                 320
Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu
                325                 330                 335
Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln
            340                 345                 350
Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn
        355                 360                 365
Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln
    370                 375                 380
Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile
385                 390                 395                 400
Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu
                405                 410                 415
Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro
            420                 425                 430
Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ile Gly Leu Gly Gly Thr
        435                 440                 445
Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys Val Leu Ala Asn
    450                 455                 460
Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
465                 470                 475                 480
Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
                485                 490                 495
Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
            500                 505                 510
Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
        515                 520                 525
Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
    530                 535                 540
Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
545                 550                 555                 560
Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
                565                 570                 575
Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
            580                 585                 590
Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
        595                 600
```

<210> 55
<211> 604
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta-P2A-alpha

(Cys modified) with signal peptide

<400> 55

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Leu Thr Thr Leu Asp Glu Gln Tyr Val Gly Pro Gly Thr Arg
        115                 120                 125
Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
    130                 135                 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145                 150                 155                 160
Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Ser Arg Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu
305                 310                 315                 320
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr
                325                 330                 335
Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu Ala Arg Val
            340                 345                 350
Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu
        355                 360                 365
Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn
    370                 375                 380
```

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

<210> 56
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta-P2A-alpha
(Cys modified) with signal peptide

<400> 56

```
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1               5                  10                  15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20                  25                  30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35                  40                  45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50                  55                  60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65                  70                  75                  80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85                  90                  95
```

```
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100                 105                 110
Ser Ser Met Leu Thr Asn Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
        115                 120                 125
Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
    130                 135                 140
Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145                 150                 155                 160
Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
                165                 170                 175
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
            180                 185                 190
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
        195                 200                 205
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Ser Arg Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu
305                 310                 315                 320
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Lys Lys
                325                 330                 335
His Leu Thr Thr Phe Leu Val Ile Leu Trp Leu Tyr Phe Tyr Arg Gly
            340                 345                 350
Asn Gly Lys Asn Gln Val Glu Gln Ser Pro Gln Ser Leu Ile Ile Leu
        355                 360                 365
Glu Gly Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val Ser Pro Phe
    370                 375                 380
Ser Asn Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly Pro Val Ser
385                 390                 395                 400
Leu Thr Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn Gly Arg Tyr
                405                 410                 415
Thr Ala Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu His Ile Thr
            420                 425                 430
Ala Ser Gln Leu Ser Asp Ser Ala Ser Tyr Ile Cys Val Val Asp Ser
        435                 440                 445
Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu Ile
    450                 455                 460
Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
465                 470                 475                 480
Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
                485                 490                 495
Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
```

```
            500                 505                 510
Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
        515                 520                 525
Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
    530                 535                 540
Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
545                 550                 555                 560
Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
                565                 570                 575
Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
            580                 585                 590
Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
        595                 600                 605
```

<210> 57
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta-P2A-alpha
(Cys modified) with signal peptide

<400> 57

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

```
    210                 215                 220
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225                 230                 235                 240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
                245                 250                 255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
            260                 265                 270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
        275                 280                 285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
    290                 295                 300
Lys Arg Lys Asp Ser Arg Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu
305                 310                 315                 320
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr
                325                 330                 335
Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser
            340                 345                 350
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
        355                 360                 365
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
    370                 375                 380
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
385                 390                 395                 400
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
                405                 410                 415
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
            420                 425                 430
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val His Leu Leu Asn
        435                 440                 445
Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr Val Arg Ala
    450                 455                 460
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
465                 470                 475                 480
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
                485                 490                 495
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
            500                 505                 510
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
        515                 520                 525
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
    530                 535                 540
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
545                 550                 555                 560
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
                565                 570                 575
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
            580                 585                 590
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
        595                 600                 605
```

<210> 58

<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence Consensus sequence of the TCR
beta-P2A-alpha

<400> 58
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1   5   10   15
Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
            20   25   30
Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
        35   40   45
Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
    50   55   60
Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65   70   75   80
Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
                85   90   95
Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
            100   105   110
Ser Ser Leu Val Gly Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr
        115   120   125
Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe
    130   135   140
Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
145   150   155   160
Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp
                165   170   175
Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro
            180   185   190
Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
        195   200   205
Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
    210   215   220
Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
225   230   235   240
Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
                245   250   255
Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln 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 Ala Leu Val Leu Met Ala Met Val Lys Arg
    290   295   300
Lys Asp Ser Arg Gly Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
305   310   315   320
Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu
                325   330   335

```
Gly Leu Val Ile Leu Trp Leu Gln Leu Arg Val Asn Ser Lys Gln Gln
            340                 345                 350
Pro Gln Ala Leu Ser Ile Glu Gly Glu Asn Thr Leu Asn Cys Ser Tyr
        355                 360                 365
Thr Ser Ile Asn Leu Gln Trp Tyr Arg Gln Asp Ser Gly Arg Gly Leu
    370                 375                 380
Val Ser Leu Leu Leu Ile Ser Ser Glu Arg Glu Lys Thr Ser Gly Arg
385                 390                 395                 400
Leu Ala Thr Leu Asp Ser Ser Lys Ser Ser Leu Ile Thr Ala Ser Gln
                405                 410                 415
Gly Asp Ser Ala Ser Tyr Leu Cys Ala Val Ser Gly Gly Gly Tyr Leu
            420                 425                 430
Thr Phe Gly Lys Gly Thr Arg Leu Ser Val Leu Ala Asn Ile Gln Asn
        435                 440                 445
Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys
    450                 455                 460
Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln
465                 470                 475                 480
Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met
                485                 490                 495
Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys
            500                 505                 510
Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu
        515                 520                 525
Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val
    530                 535                 540
Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser
545                 550                 555                 560
Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
                565                 570                 575
Leu Met Thr Leu Arg Leu Trp Ser Ser
            580                 585
```

<210> 59
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta-P2A-alpha
(codon optimized; Cys modified)

<400> 59

```
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat      60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc     120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag     180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg     240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg     300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcagcacagg cggccacaac     360
gagcagttct ttggccctgg cacccggctg accgtgctgg aagatctgaa gaacgtgttc     420
cccccagagg tggccgtgtt cgagccttct gaggccgaga tcagccacac ccagaaagcc     480
```

```
accctcgtgt gtctggccac cggcttctac cccgaccacg tggaactgtc ttggtgggtc     540
aacggcaaag aggtgcactc cggcgtgtgc accgatcccc agcctctgaa agaacagccc     600
gccctgaacg acagccggta ctgcctgagc agcagactga gagtgtccgc caccttctgg     660
cagaaccccc ggaaccactt cagatgccag gtgcagttct acggcctgag cgagaacgac     720
gagtggaccc aggacagagc caagcccgtg acccagatcg tgtctgccga agcctggggc     780
agagccgatt gcggctttac cagcgagagc taccagcagg gcgtgctgag cgccaccatc     840
ctgtacgaga tcctgctggg caaggccacc ctgtacgccg tgctggtgtc tgccctggtg     900
ctgatggcca tggtcaagcg gaaggacagc agaggcggaa gcggcgccac caacttcagc     960
ctgctgaaac aggccggcga cgtggaagag aaccctggcc ctatggaaac actgctgggc    1020
gtgtccctcg tgatcctgtg gctgcagctg gccagagtga acagccagca gggggaagag    1080
gatccccagg ccctgagcat tcaggaaggc gagaacgcca ccatgaactg cagctacaag    1140
accagcatca acaacctgca gtggtacaga cagaacagcg gcagaggcct ggtgcacctg    1200
atcctgatca gaagcaacga gagagagaag cacagcggac ggctgagagt gaccctggac    1260
acctccaaga agtccagctc cctgctgatc accgccagca gagccgccga taccgccagc    1320
tacttctgtg ccaccaagcg ggattctggc gccggatcct accagctgac cttcggcaag    1380
ggcaccaagc tgagcgtgat ccccaacatc cagaaccccg accccgccgt gtatcagctg    1440
agagacagca agagcagcga caagagcgtg tgcctgttca ccgacttcga cagccagacc    1500
aacgtgtccc agagcaagga cagcgacgtg tacatcaccg ataagtgcgt gctggacatg    1560
cggagcatgg acttcaagag caacagcgcc gtggcctggt ccaacaagag cgacttcgcc    1620
tgcgccaacg ccttcaacaa cagcatcatc cccgaggaca ccttttccc cagccccgag     1680
agcagctgcg acgtgaaact ggtggagaag tccttcgaga cagacaccaa tctgaacttt    1740
cagaacctga gcgtgatcgg cttccggatc ctgctgctga aagtggccgg cttcaatctg    1800
ctgatgaccc tgcggctgtg gagcagctga                                     1830

<210> 60
<211> 1813
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta-P2A-alpha
      (codon optimized; Cys modified)

<400> 60
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat      60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc     120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag     180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg     240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg     300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcctcgtgaa gggcgagaag     360
ctgttcttcg gcagcggcac ccagctgagc gtgctggaag atctgaacaa ggtgttcccc     420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc     480
ctcgtgtgcc tggccaccgg ctttttcccc gaccacgtgg aactgtcttg gtgggtcaac     540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc     600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag     660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag     720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga     780
gccgattgcg gctttaccag cgtgtcctat cagcagggcg tgctgagcgc caccatcctg     840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg     900
atggccatgg tcaagcggaa ggactttggc agcggcgcca ccaacttcag cctgctgaaa     960
caggccggcg acgtggaaga gaaccctggc cctaatctga actttcagaa cctgagcgtg    1020
```

atcggcttcc ggatcctgct gctgaaagtg gccggcttca atctgctgat gaccctgcgg 1080
ctgtggagca gcgatggaaa cactgctggg cctgctgatc ctgtggctgc agctgcagtg 1140
ggtgtccagc aagcaggaag tgacacagat ccctgccgcc ctgtctgtgc ccgagggcga 1200
aaatctggtg ctgaactgca gcttcaccga cagcgccatc tacaacctgc agtggttcag 1260
acaggacccc ggcaagggcc tgacaagcct gctgctgatt cagagcagcc agagagagca 1320
gaccagcggc agactgaacg ccagcctgga taagagcagc ggccgcagca ccctgtatat 1380
cgccgcttct cagcctggcg actctgccac atatctgtgc gccgtgatcg gcctgggcgg 1440
cacctacaag tacatctttg gcaccggcac cagactgaaa gtgctggcca acatccagaa 1500
ccccgacccc gccgtgtacc agctgagaga cagcaagtcc agcgacaaga gcgtgtgtct 1560
gttcaccgac ttcgacagcc agaccaacgt gtcccagagc aaggacagcg acgtgtacat 1620
caccgataag tgcgtgctgg acatgcggag catggacttc aagagcaaca gcgccgtggc 1680
ctggtccaac aagagcgact tcgcctgcgc caacgccttc aacaacagca tcatccccga 1740
ggacaccttt ttccccagcc ccgagagcag ctgcgacgtg aaactggtgg agaagtcctt 1800
cgagacagac acc 1813

<210> 61
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta-P2A-alpha
(codon optimized; Cys modified)

<400> 61
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gggacagcgc catgtatctg tgtgccagct ccctgaccac cctggacgag 360
cagtatgtgg gcccaggcac cagactgacc gtgaccgagg acctgaagaa cgtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgtc tggccaccgg cttctacccc gatcacgtgg agctgtcttg gtgggtgaac 540
ggcaaagagg tgcacagcgg cgtctgcacc gacccccagc ccctgaaaga gcagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc cggctgagag tgagcgccac cttctggcag 660
aacccccgga accacttccg gtgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtga gcgccgaggc ctggggcaga 780
gccgactgcg gcttcaccag cgagagctac cagcagggcg tgctgtccgc cacaatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtccgc cctggtgctg 900
atggccatgg tgaagcggaa ggacagccgg ggcggcagcg gcgccaccaa cttcagcctg 960
ctgaagcagg ccggcgacgt ggaggaaaac cctggcccca tggaaaccct gctgggcgtg 1020
tccctcgtga tcctgtggct gcagctggcc agagtgaaca gccagcaggg cgaagaagat 1080
ccccaggccc tgagcatcca ggaaggcgag aacgccacaa tgaactgcag ctacaagacc 1140
agcatcaaca acctgcagtg gtacagacag aacagcggca gaggcctggt gcacctgatc 1200
ctgatcagaa gcaacgagag agagaagcac tccggcagac tgagagtgac cctggacacc 1260
agcaagaagt ccagcagcct gctgatcacc gccagcagag ccgccgatac cgccagctac 1320
ttctgcgcca ccaactccgg caacaccccc ctggtgtttg gcaagggcac ccggctgagc 1380
gtgatcgcca acatccagaa ccccgacccc gccgtgtacc agctgagaga cagcaagagc 1440
agcgacaaga gcgtgtgcct gttcaccgac ttcgacagcc agaccaacgt gtcccagagc 1500
aaggacagcg acgtgtacat caccgataag tgcgtgctgg acatgcggag catggacttc 1560

```
aagagcaaca gcgccgtggc ctggtccaac aagagcgact tcgcctgcgc caacgccttc    1620
aacaacagca tcatccccga ggacaccttt ttccccagcc ccgagagcag ctgcgacgtg    1680
aaactggtgg agaagtcctt cgagacagac accaatctga actttcagaa cctgagcgtg    1740
atcggcttcc ggatcctgct gctgaaagtg gccggcttca atctgctgat gaccctgcgg    1800
ctgtggagca gctga                                                    1815
```

<210> 62
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta P2A-alpha
(codon optimized; Cys modified)

<400> 62

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atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat      60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc     120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag     180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg     240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg     300
accgagcagg gcgatagcgc catgtacctg tgcgccagct ccatgctgac caactacgag     360
cagtacttcg gccctggcac ccggctgacc gtgaccgagg atctgaagaa cgtgttcccc     420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc     480
ctcgtgtgtc tggccaccgg cttctacccc gaccacgtgg aactgtcttg gtgggtcaac     540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc     600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag     660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag     720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga     780
gccgattgcg gctttaccag cgagagctac cagcagggcg tgctgagcgc caccatcctg     840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg     900
atggccatgg tcaagcggaa ggacagcaga ggcggaagcg gcgccaccaa cttcagcctg     960
ctgaaacagg ccggcgacgt ggaagagaac cctggcccca tgaagaagca cctgaccacc    1020
tttctcgtga tcctgtggct gtacttctac cggggcaacg gcaagaacca ggtggaacag    1080
agcccccaga gcctgatcat cctggaaggc aagaattgca ccctgcagtg caactacacc    1140
gtgtcccccct tcagcaacct gcggtggtac aagcaggaca ccggcagagg ccctgtgtcc    1200
ctgaccatca tgaccttcag cgagaacacc aagagcaacg gccggtacac cgccaccctg    1260
gatgccgata caaagcagag cagcctgcac atcaccgcca gccagctgag cgattccgcc    1320
agctacatct gcgtggtgga ttctggcggc ggagccgatg gcctgacatt tggcaagggc    1380
acccacctga tcattcagcc ctacatccag aaccccgacc ccgccgtgta ccagctgaga    1440
gacagcaagt ccagcgacaa gagcgtgtgc ctgttcaccg acttcgacag ccagaccaac    1500
gtgtcccaga gcaaggacag cgacgtgtac atcaccgata agtgcgtgct ggacatgcgg    1560
agcatggact tcaagagcaa cagcgccgtg gcctggtcca acaagagcga cttcgcctgc    1620
gccaacgcct tcaacaacag catcatcccc gaggacacct ttttccccag ccccgagagc    1680
agctgcgacg tgaaactggt ggagaagtcc ttcgagacag acaccaatct gaactttcag    1740
aacctgagcg tgatcggctt ccggatcctg ctgctgaaag tggccggctt caatctgctg    1800
atgaccctgc ggctgtggag cagctga                                       1827
```

<210> 63
<211> 1818
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta-P2A-alpha
(codon optimized; Cys modified)

<400> 63
atgggcacct ccctgctgtg ttggatggcc ctgtgtctgc tgggagccga ccatgccgat 60
acaggggtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc 120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acaggcagac cctgggccag 180
ggccccgagt tcctgaccta ctttcagaac gaggcccagc tggaaaagtc ccggctgctg 240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg 300
accgagcagg gcgatagcgc catgtacctg tgtgccagca gcctggtcgt gggcaacgag 360
cagtttttcg gccctggcac cagactgacc gtgctggaag atctgaagaa cgtgttcccc 420
ccagaggtgg ccgtgttcga gccttctgag gccgagatca gccacaccca gaaagccacc 480
ctcgtgtgtc tggccaccgg cttctacccc gaccacgtgg aactgtcttg gtgggtcaac 540
ggcaaagagg tgcactccgg cgtgtgcacc gatccccagc ctctgaaaga acagcccgcc 600
ctgaacgaca gccggtactg cctgagcagc agactgagag tgtccgccac cttctggcag 660
aacccccgga accacttcag atgccaggtg cagttctacg gcctgagcga gaacgacgag 720
tggacccagg acagagccaa gcccgtgacc cagatcgtgt ctgccgaagc ctggggcaga 780
gccgattgcg gctttaccag cgagagctac cagcagggcg tgctgagcgc caccatcctg 840
tacgagatcc tgctgggcaa ggccaccctg tacgccgtgc tggtgtctgc cctggtgctg 900
atggccatgg tcaagcggaa ggacagcaga ggcggaagcg gcgccaccaa cttcagcctg 960
ctgaaacagg ccggcgacgt ggaagagaac cctggcccta tggaaacact gctgggcctg 1020
ctgatcctgt ggctgcagct gcagtgggtg tccagcaagc aggaagtgac acagatccct 1080
gccgccctgt ctgtgcccga gggcgaaaat ctggtgctga actgcagctt caccgacagc 1140
gccatctaca acctgcagtg gttcagacag gaccccggca agggcctgac aagcctgctg 1200
ctgattcaga gcagccagag agagcagacc agcggcagac tgaacgccag cctggataag 1260
agcagcggcc gcagcaccct gtatatcgcc gcttctcagc ctggcgactc tgccacatat 1320
ctgtgcgccg tgcatctgct gaacgactac aagctgagct tcggagccgg caccaccgtg 1380
acagtgcggg ccaacatcca gaaccccgac cctgccgtgt accagctgag agacagcaag 1440
tccagcgaca agagcgtgtg cctgttcacc gacttcgaca gccagaccaa cgtgtcccag 1500
agcaaggaca gcgacgtgta catcaccgat aagtgcgtgc tggacatgcg gagcatggac 1560
ttcaagagca acagcgccgt ggcctggtcc aacaagagcg acttcgcctg cgccaacgcc 1620
ttcaacaaca gcatcatccc cgaggacacc tttttcccca gccccgagag cagctgcgac 1680
gtgaaactgg tggagaagtc cttcgagaca gacaccaatc tgaactttca gaacctgagc 1740
gtgatcggct tccggatcct gctgctgaaa gtggccggct tcaatctgct gatgaccctg 1800
cggctgtgga gcagctga 1818

<210> 64
<211> 1135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence HMHA1 (wt)

<400> 64
Met Phe Ser Arg Lys Lys Arg Glu Leu Met Lys Thr Pro Ser Ile Ser
1 5 10 15
Lys Lys Asn Arg Ala Gly Ser Pro Ser Pro Gln Pro Ser Gly Glu Leu

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            20                  25                  30
Pro Arg Lys Asp Gly Ala Asp Ala Val Phe Pro Gly Pro Ser Leu Glu
        35                  40                  45
Pro Pro Ala Gly Ser Ser Gly Val Lys Ala Thr Gly Thr Leu Lys Arg
    50                  55                  60
Pro Thr Ser Leu Ser Arg His Ala Ser Ala Ala Gly Phe Pro Leu Ser
65                  70                  75                  80
Gly Ala Ala Ser Trp Thr Leu Gly Arg Ser His Arg Ser Pro Leu Thr
                85                  90                  95
Ala Ala Ser Pro Gly Glu Leu Pro Thr Glu Gly Ala Gly Pro Asp Val
            100                 105                 110
Val Glu Asp Ile Ser His Leu Leu Ala Asp Val Ala Arg Phe Ala Glu
        115                 120                 125
Gly Leu Glu Lys Leu Lys Glu Cys Val Leu Arg Asp Asp Leu Leu Glu
    130                 135                 140
Ala Arg Arg Pro Arg Ala His Glu Cys Leu Gly Glu Ala Leu Arg Val
145                 150                 155                 160
Met His Gln Ile Ile Ser Lys Tyr Pro Leu Leu Asn Thr Val Glu Thr
                165                 170                 175
Leu Thr Ala Ala Gly Thr Leu Ile Ala Lys Val Lys Ala Phe His Tyr
            180                 185                 190
Glu Ser Asn Asn Asp Leu Glu Lys Gln Glu Phe Glu Lys Ala Leu Glu
        195                 200                 205
Thr Ile Ala Val Ala Phe Ser Ser Thr Val Ser Glu Phe Leu Met Gly
    210                 215                 220
Glu Val Asp Ser Ser Thr Leu Leu Ala Val Pro Pro Gly Asp Ser Ser
225                 230                 235                 240
Gln Ser Met Glu Ser Leu Tyr Gly Pro Gly Ser Glu Gly Thr Pro Pro
                245                 250                 255
Ser Leu Glu Asp Cys Asp Ala Gly Cys Leu Pro Ala Glu Glu Val Asp
            260                 265                 270
Val Leu Leu Gln Arg Cys Glu Gly Gly Val Asp Ala Ala Leu Leu Tyr
        275                 280                 285
Ala Lys Asn Met Ala Lys Tyr Met Lys Asp Leu Ile Ser Tyr Leu Glu
    290                 295                 300
Lys Arg Thr Thr Leu Glu Met Glu Phe Ala Lys Gly Leu Gln Lys Ile
305                 310                 315                 320
Ala His Asn Cys Arg Gln Ser Val Met Gln Glu Pro His Met Pro Leu
                325                 330                 335
Leu Ser Ile Tyr Ser Leu Ala Leu Glu Gln Asp Leu Glu Phe Gly His
            340                 345                 350
Ser Met Val Gln Ala Val Gly Thr Leu Gln Thr Gln Thr Phe Met Gln
        355                 360                 365
Pro Leu Thr Leu Arg Arg Leu Glu His Glu Lys Arg Arg Lys Glu Ile
    370                 375                 380
Lys Glu Ala Trp His Arg Gln Arg Lys Leu Gln Glu Ala Glu Ser Asn
385                 390                 395                 400
Leu Arg Lys Ala Lys Gln Gly Tyr Val Gln Arg Cys Glu Asp His Asp
                405                 410                 415
Lys Ala Arg Phe Leu Val Ala Lys Ala Glu Glu Glu Gln Ala Gly Ser
            420                 425                 430
```

```
Ala Pro Gly Ala Gly Ser Thr Ala Thr Lys Thr Leu Asp Lys Arg Arg
        435                 440                 445
Arg Leu Glu Glu Glu Ala Lys Asn Lys Ala Glu Glu Ala Met Ala Thr
    450                 455                 460
Tyr Arg Thr Cys Val Ala Asp Ala Lys Thr Gln Lys Gln Glu Leu Glu
465                 470                 475                 480
Asp Thr Lys Val Thr Ala Leu Arg Gln Ile Gln Glu Val Ile Arg Gln
                485                 490                 495
Ser Asp Gln Thr Ile Lys Ser Ala Thr Ile Ser Tyr Tyr Gln Met Met
            500                 505                 510
His Met Gln Thr Ala Pro Leu Pro Val His Phe Gln Met Leu Cys Glu
        515                 520                 525
Ser Ser Lys Leu Tyr Asp Pro Gly Gln Gln Tyr Ala Ser His Val Arg
    530                 535                 540
Gln Leu Gln Arg Asp Gln Glu Pro Asp Val His Tyr Asp Phe Glu Pro
545                 550                 555                 560
His Val Ser Ala Asn Ala Trp Ser Pro Val Met Arg Ala Arg Lys Ser
                565                 570                 575
Ser Phe Asn Val Ser Asp Val Ala Arg Pro Glu Ala Ala Gly Ser Pro
            580                 585                 590
Pro Glu Glu Gly Gly Cys Thr Glu Gly Thr Pro Ala Lys Asp His Arg
        595                 600                 605
Ala Gly Arg Gly His Gln Val His Lys Ser Trp Pro Leu Ser Ile Ser
    610                 615                 620
Asp Ser Asp Ser Gly Leu Asp Pro Gly Pro Gly Ala Gly Asp Phe Lys
625                 630                 635                 640
Lys Phe Glu Arg Thr Ser Ser Ser Gly Thr Met Ser Ser Thr Glu Glu
                645                 650                 655
Leu Val Asp Pro Asp Gly Gly Ala Gly Ala Ser Ala Phe Glu Gln Ala
            660                 665                 670
Asp Leu Asn Gly Met Thr Pro Glu Leu Pro Val Ala Val Pro Ser Gly
        675                 680                 685
Pro Phe Arg His Glu Gly Leu Ser Lys Ala Ala Arg Thr His Arg Leu
    690                 695                 700
Arg Lys Leu Arg Thr Pro Ala Lys Cys Arg Glu Cys Asn Ser Tyr Val
705                 710                 715                 720
Tyr Phe Gln Gly Ala Glu Cys Glu Glu Cys Cys Leu Ala Cys His Lys
                725                 730                 735
Lys Cys Leu Glu Thr Leu Ala Ile Gln Cys Gly His Lys Lys Leu Gln
            740                 745                 750
Gly Arg Leu Gln Leu Phe Gly Gln Asp Phe Ser His Ala Ala Arg Ser
        755                 760                 765
Ala Pro Asp Gly Val Pro Phe Ile Val Lys Lys Cys Val Cys Glu Ile
    770                 775                 780
Glu Arg Arg Ala Leu Arg Thr Lys Gly Ile Tyr Arg Val Asn Gly Val
785                 790                 795                 800
Lys Thr Arg Val Glu Lys Leu Cys Gln Ala Phe Glu Asn Gly Lys Glu
                805                 810                 815
Leu Val Glu Leu Ser Gln Ala Ser Pro His Asp Ile Ser Asn Val Leu
            820                 825                 830
Lys Leu Tyr Leu Arg Gln Leu Pro Glu Pro Leu Ile Ser Phe Arg Leu
```

```
        835                 840                 845
Tyr His Glu Leu Val Gly Leu Ala Lys Asp Ser Leu Lys Ala Glu Ala
    850                 855                 860
Glu Ala Lys Ala Ala Ser Arg Gly Arg Gln Asp Gly Ser Glu Ser Glu
865                 870                 875                 880
Ala Val Ala Val Ala Leu Ala Gly Arg Leu Arg Glu Leu Leu Arg Asp
                885                 890                 895
Leu Pro Pro Glu Asn Arg Ala Ser Leu Gln Tyr Leu Leu Arg His Leu
            900                 905                 910
Arg Arg Ile Val Glu Val Glu Gln Asp Asn Lys Met Thr Pro Gly Asn
        915                 920                 925
Leu Gly Ile Val Phe Gly Pro Thr Leu Leu Arg Pro Arg Pro Thr Glu
    930                 935                 940
Ala Thr Val Ser Leu Ser Ser Leu Val Asp Tyr Pro His Gln Ala Arg
945                 950                 955                 960
Val Ile Glu Thr Leu Ile Val His Tyr Gly Leu Val Phe Glu Glu Glu
                965                 970                 975
Pro Glu Glu Thr Pro Gly Gly Gln Asp Glu Ser Ser Asn Gln Arg Ala
            980                 985                 990
Glu Val Val Val Gln Val Pro Tyr Leu Glu Ala Gly Glu Ala Val Val
        995                 1000                1005
Tyr Pro Leu Gln Glu Ala Ala Ala Asp Gly Cys Arg Glu Ser Arg Val
    1010                1015                1020
Val Ser Asn Asp Ser Asp Ser Asp Leu Glu Glu Ala Ser Glu Leu Leu
1025                1030                1035                1040
Ser Ser Ser Glu Ala Ser Ala Leu Gly His Leu Ser Phe Leu Glu Gln
                1045                1050                1055
Gln Gln Ser Glu Ala Ser Leu Glu Val Ala Ser Gly Ser His Ser Gly
            1060                1065                1070
Ser Glu Glu Gln Leu Glu Ala Thr Ala Arg Glu Asp Gly Asp Gly Asp
        1075                1080                1085
Glu Asp Gly Pro Ala Gln Gln Leu Ser Gly Phe Asn Thr Asn Gln Ser
    1090                1095                1100
Asn Asn Val Leu Gln Ala Pro Leu Pro Pro Met Arg Leu Arg Gly Gly
1105                1110                1115                1120
Arg Met Thr Leu Gly Ser Cys Arg Glu Arg Gln Pro Glu Phe Val
                1125                1130                1135

<210> 65
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence HA-1 non-immunogenic peptide wild type

<400> 65
Val Leu Arg Asp Asp Leu Leu Glu Ala
 1               5

<210> 66
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<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence HA-1H antigen polymorphism

<400> 66
Val Leu His Asp Asp Leu Leu Glu Ala
 1   5

<210> 67
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence Inducible Caspase9 (codon optimized)

<400> 67
atgctggaag gcgtgcaggt ggaaaccatc agccctggcg acggcagaac cttccctaag 60
aggggccaga cctgcgtggt gcactacacc ggaatgctgg aagatggcaa gaaggtggac 120
agcagccggg accggaacaa gcccttcaag ttcatgctgg gcaagcagga agtgatccgg 180
ggctgggaag agggcgtggc ccagatgtct gtgggccaga gagccaagct gaccatctcc 240
cccgattacg cctacggcgc cacaggccac cctggcatca ttcctccaca cgccacactg 300
gtgttcgacg tggaactgct gaagctggaa agcggcggag gcagcggagt ggatggcttt 360
ggagatgtgg gcgccctgga aagcctgaga ggcaatgccg acctggccta catcctgagc 420
atggaacctt gcggccactg cctgattatc aacaacgtga acttctgcag agagagcggc 480
ctgcggacca gaaccggcag caacatcgac tgcgagaagc tgcggcggag attcagcagc 540
ctgcacttca tggtggaagt gaagggcgac ctgaccgcca agaaaatggt gctggccctg 600
ctggaactgg cccagcagga tcatggcgct ctggactgct gtgtggtcgt gatcctgagc 660
cacggctgcc aggccagcca tctgcagttc cctggcgccg tgtatggcac cgatggctgt 720
cctgtgtccg tggaaaagat cgtgaacatc ttcaacggca ccagctgccc cagcctgggc 780
ggaaagccca agctgttctt tattcaagcc tgcggaggcg agcagaagga ccacggattt 840
gaggtggcct ccaccagccc cgaggatgag agccctggaa gcaaccctga gcccgacgcc 900
accccatttc aggaaggcct gagaaccttc gaccagctgg acgccatcag ctccctgccc 960
acccccagcg atatcttcgt gtcctacagc accttccccg gctttgtgtc ctggcgggat 1020
cccaagtccg gctcttggta cgtggaaacc ctggacgaca tcttcgagca gtgggcccat 1080
agcgaggacc tgcagagcct gctgctgaga gtggccaatg ccgtgtccgt gaagggcatc 1140
tacaagcaga tgcctggctg cttcaacttc ctgcggaaga agctgttttt caagaccagc 1200
gccagc 1206

<210> 68
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence RQR (codon optimized)

<400> 68

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gcctgcccct acagcaaccc tagcctgtgt tctggcggcg gaggcagcga actgcctacc      60
cagggcacct tcagcaacgt gtccaccaat gtgtctggcg gaggcggctc tgcctgccct     120
tactccaatc catccctgtg cagcggaggg ggcggaagc                            159

<210> 69
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence RQR

<400> 69
Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser Gly Gly Gly Gly Ser
 1               5                  10                  15
Glu Leu Pro Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser
            20                  25                  30
Gly Gly Gly Gly Ser Ala Cys Pro Tyr Ser Asn Pro Ser Leu Cys Ser
        35                  40                  45
Gly Gly Gly Gly Ser
    50

<210> 70
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor alpha chain
      with signal peptide

<400> 70
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1               5                  10                  15
His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
            20                  25                  30
Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
        35                  40                  45
Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
    50                  55                  60
Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65                  70                  75                  80
Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
                85                  90                  95
Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
            100                 105                 110
Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
        115                 120                 125
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
    130                 135                 140
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
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145                 150                 155                 160
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
                165                 170                 175
Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
            180                 185                 190
Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
        195                 200                 205
Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
    210                 215                 220
Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225                 230                 235
```

<210> 71
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 1 with signal peptide

<400> 71

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

<210> 72
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 2 with signal peptide

<400> 72
Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
 1   5   10   15
His Gly Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln
            20   25   30
Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
        35   40   45
Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
    50   55   60
Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
65   70   75   80
His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala
                85   90   95
Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
            100   105   110
Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
        115   120   125
Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
    130   135   140
Thr Lys Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro
145   150   155   160
Glu Thr Gln Lys Gly Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu
                165   170   175
Val Ala Gly Val Leu Val Leu Leu Val Ser Leu Gly Val Ala Ile His
            180   185   190
Leu Cys Cys Arg Arg Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Leu
        195   200   205
Arg Leu His Pro Leu Glu Lys Cys Ser Arg Met Asp Tyr
    210   215   220

<210> 73
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 3 with signal peptide

<400> 73
Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
 1   5   10   15

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

<210> 74
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 4 with signal peptide

<400> 74

```
Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
 1               5                  10                  15
His Gly Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln
            20                  25                  30
Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
        35                  40                  45
Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
    50                  55                  60
Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
65                  70                  75                  80
```

```
His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala
                85                  90                  95
Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
            100                 105                 110
Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
        115                 120                 125
Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
    130                 135                 140
Thr Lys Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro
145                 150                 155                 160
Glu Thr Gln Lys Gly Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu
                165                 170                 175
Val Ala Gly Val Leu Val Leu Leu Val Ser Leu Gly Val Ala Ile His
            180                 185                 190
Leu Cys Cys Arg Arg Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Lys
        195                 200                 205
Phe Asn Ile Val Cys Leu Lys Ile Ser Gly Phe Thr Thr Cys Cys Cys
    210                 215                 220
Phe Gln Ile Leu Gln Ile Ser Arg Glu Tyr Gly Phe Gly Val Leu Leu
225                 230                 235                 240
Gln Lys Asp Ile Gly Gln
                245
```

<210> 75
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 5 with signal peptide

<400> 75

```
Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
 1               5                  10                  15
His Gly Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln
            20                  25                  30
Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
        35                  40                  45
Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
    50                  55                  60
Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
65                  70                  75                  80
His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala
                85                  90                  95
Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
            100                 105                 110
Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
        115                 120                 125
Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
    130                 135                 140
```

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

<210> 76
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-1 (codon-optimized)

<400> 76
ggaagtggag ctacgaattt ttctttatta aaacaagcag gagatgttga ggagaatccc 60
ggtcca 66

<210> 77
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-2 (codon-optimized)

<400> 77
agcggcgcca ccaacttcag cctgctgaaa caggccggcg acgtggaaga gaaccctggc 60
cct 63

<210> 78
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-3 (codon-optimized)

<400> 78
gaagcggcgc cacaaatttc agcctgctga agcaggccgg cgacgtggaa gagaaccctg 60
gccct 65

<210> 79
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-4 (codon-optimized)

<400> 79
ggctccggcg ccaccaactt ttcactgctg aaacaggctg gggatgtgga agaaaatccc 60
ggccca 66

<210> 80
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-5

<400> 80
ggcagcggcg ccaccaactt tagcctgctg aaacaggctg gcgacgtgga agagaacccc 60
ggacct 66

<210> 81
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence P2A-6

<400> 81
ggctctggcg ccaccaactt tagcctgctg aaacaggctg gcgacgtgga agagaacccc 60
ggacct 66

<210> 82
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence T2A

<400> 82
ggaagcggag agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctgga 60
cct 63

<210> 83
<211> 69
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic sequence E2A

<400> 83
ggaagcggac agtgtactaa ttatgctctc ttgaaattgg ctggagatgt tgagagcaac 60
cctggacct 69

<210> 84
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence F2A

<400> 84
ggaagcggag tgaaacagac tttgaatttt gaccttctca agttggcggg agacgtggag 60
tccaaccctg gacct 75

<210> 85
<211> 4713
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence iC9-HA1-TCR2-RQR-CD8

<400> 85
atgctggaag gcgtgcaggt ggaaaccatc agccctggcg acggcagaac cttccctaag 60
aggggccaga cctgcgtggt gcactacacc ggaatgctgg aagatggcaa gaaggtggac 120
agcagccggg accggaacaa gcccttcaag ttcatgctgg gcaagcagga agtgatccgg 180
ggctgggaag agggcgtggc ccagatgtct gtgggccaga gagccaagct gaccatctcc 240
cccgattacg cctacggcgc cacaggccac cctggcatca ttcctccaca cgccacactg 300
gtgttcgacg tggaactgct gaagctggaa agcggcggag gcagcggagt ggatggcttt 360
ggagatgtgg gcgccctgga aagcctgaga ggcaatgccg acctggccta catcctgagc 420
atggaacctt gcggccactg cctgattatc aacaacgtga acttctgcag agagagcggc 480
ctgcggacca gaaccggcag caacatcgac tgcgagaagc tgcggcggag attcagcagc 540
ctgcacttca tggtggaagt gaagggcgac ctgaccgcca agaaaatggt gctggccctg 600
ctggaactgg cccagcagga tcatggcgct ctggactgct gtgtggtcgt gatcctgagc 660
cacggctgcc aggccagcca tctgcagttc cctggcgccg tgtatggcac cgatggctgt 720
cctgtgtccg tggaaaagat cgtgaacatc ttcaacggca ccagctgccc cagcctgggc 780
ggaaagccca agctgttctt tattcaagcc tgcggaggcg agcagaagga ccacggattt 840
gaggtggcct ccaccagccc cgaggatgag agccctggaa gcaaccctga gcccgacgcc 900
accccatttc aggaaggcct gagaaccttc gaccagctgg acgccatcag ctccctgccc 960
acccccagcg atatcttcgt gtcctacagc accttccccg gctttgtgtc ctggcgggat 1020
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agcgaggacc tgcagagcct gctgctgaga gtggccaatg ccgtgtccgt gaagggcatc 1140
tacaagcaga tgcctggctg cttcaacttc ctgcggaaga agctgttttt caagaccagc 1200
gccagcggaa gtggagctac gaatttttct ttattaaaac aagcaggaga tgttgaggag 1260

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gaccatgccg atacaggggt gtcccaggac ccccggcaca agattaccaa gcggggccag    1380
aacgtgacct tcagatgcga ccccatcagc gagcacaacc ggctgtactg gtacaggcag    1440
accctgggcc agggccccga gttcctgacc tactttcaga acgaggccca gctggaaaag    1500
tcccggctgc tgagcgacag attcagcgcc gaaagaccca agggcagctt cagcaccctg    1560
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aaggtgttcc ccccagaggt ggccgtgttc gagccttctg aggccgagat cagccacacc    1740
cagaaagcca ccctcgtgtg cctggccacc ggctttttcc ccgaccacgt ggaactgtct    1800
tggtgggtca acggcaaaga ggtgcactcc ggcgtgtgca ccgatcccca gcctctgaaa    1860
gaacagcccg ccctgaacga cagccggtac tgcctgagca gcagactgag agtgtccgcc    1920
accttctggc agaacccccg gaaccacttc agatgccagg tgcagttcta cggcctgagc    1980
gagaacgacg agtggaccca ggacagagcc aagcccgtga cccagatcgt gtctgccgaa    2040
gcctggggca gagccgattg cggctttacc agcgtgtcct atcagcaggg cgtgctgagc    2100
gccaccatcc tgtacgagat cctgctgggc aaggccaccc tgtacgccgt gctggtgtct    2160
gccctggtgc tgatggccat ggtcaagcgg aaggactttg gcagcggcgc caccaacttc    2220
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gacagcgcca tctacaacct gcagtggttc agacaggacc ccggcaaggg cctgacaagc    2460
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gacagcaagt ccagcgacaa gagcgtgtgt ctgttcaccg acttcgacag ccagaccaac    2760
gtgtcccaga gcaaggacag cgacgtgtac atcaccgata agtgcgtgct ggacatgcgg    2820
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atgaccctgc ggctgtggag cagcggaagc ggcgccacaa atttcagcct gctgaagcag    3120
gccggcgacg tggaagagaa ccctggccct atgaggccca gactgtggct gctgctggcc    3180
gctcagctga cagtgctgca cggcaatagc gtggcctgcc cctacagcaa ccctagcctg    3240
tgttctggcg gcggaggcag cgaactgcct acccagggca ccttcagcaa cgtgtccacc    3300
aatgtgtctg gcggaggcgg ctctgcctgc ccttactcca atccatccct gtgcagcgga    3360
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ggcaccattc acggcgagga agtggaacag gaaaagatcg ccgtgttccg ggacgccagc    3600
cggttcatcc tgaacctgac cagcgtgaag cccgaggact ccggcatcta tttctgcatg    3660
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aggcgggcca gactgcggtt catgaagcag ttctacaagg gctccggcgc caccaacttt    3960
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ctgctgagca accccaccag cggctgcagc tggctgttcc agcctagagg cgctgccgcc    4200
agccctacct ttctgctgta cctgagccag aacaagccca aggccgccga gggcctggac    4260
acccagagat tcagcggcaa gagactgggc gacaccttcg tgctgaccct gtccgacttc    4320
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agaagagaga acgagggcta ctacttctgc tccgccctga gcaatagcat catgtacttc 4380
agccacttcg tgcccgtgtt tctgcccgcc aagcctacaa ccacccctgc cccaagacct 4440
cccacacccg cccctacaat tgccagccag cctctgtctc tgaggcccga ggcttgtaga 4500
ccagctgctg gcggagccgt gcacaccaga ggactggact ttgcctgcga catctacatc 4560
tgggcccctc tggccggcac ttgcggagtg ctgctgctga gtctcgtgat caccctgtac 4620
tgcaaccacc ggaaccggcg gagagtgtgc aagtgcccta ggcccgtcgt gaagtccggc 4680
gacaagcctt ctctgagcgc cagatatgtc tga 4713

<210> 86
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain CDR3

<400> 86
Cys Ala Ser Ser Leu Val Ser Gly Asn Thr Ile Tyr Phe
 1   5   10

<210> 87
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1 alpha chain CDR3

<400> 87
Cys Ala Thr Lys Arg Asp Ser Gly Ala Gly Ser Tyr Gln Leu Thr
 1   5   10   15

<210> 88
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2 alpha chain CDR3

<400> 88
Cys Ala Val Ile Gly Leu Gly Gly Thr Tyr Lys Tyr Ile Phe
 1   5   10

<210> 89
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain CDR3

<400> 89
Cys Ala Thr Asn Ser Gly Asn Thr Pro Leu Val Phe
 1   5   10

<210> 90
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain CDR3

<400> 90
Cys Val Val Asp Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe
 1   5   10

<210> 91
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain CDR3

<400> 91
Cys Ala Val His Leu Leu Asn Asp Tyr Lys Leu Ser Phe
 1   5   10

<210> 92
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain CDR3

<400> 92
Cys Ala Val Arg Gly Gly Thr Thr Ser Gly Thr Tyr Lys Tyr Ile Phe
 1   5   10   15

<210> 93
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR alpha-chain primer

<400> 93
ggtgaatagg cagacagact t   21

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR beta-chain primer

<400> 94
gtggccaggc acaccagtgt 20

<210> 95
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence inducible caspase-9

<400> 95
Met Leu Glu Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg
 1   5   10   15
Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met
            20   25   30
Leu Glu Asp Gly Lys Lys Val Asp Ser Ser Arg Asp Arg Asn Lys Pro
        35   40   45
Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu
    50   55   60
Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser
65   70   75   80
Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro
                85   90   95
His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser Gly
            100   105   110
Gly Gly Ser Gly Val Asp Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
        115   120   125
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
    130   135   140
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
145   150   155   160
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
                165   170   175
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
            180   185   190
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
        195   200   205
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
    210   215   220
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys

225 230 235 240
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
245 250 255
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
260 265 270
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
275 280 285
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
290 295 300
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
305 310 315 320
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
325 330 335
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
340 345 350
Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
355 360 365
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
370 375 380
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
385 390 395 400
Ala Ser

<210> 96
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta chain variable
region (mature)

<400> 96
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
1 5 10 15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
20 25 30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
35 40 45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
50 55 60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65 70 75 80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Ser Thr Gly
85 90 95
Gly His Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
100 105 110

<210> 97
<211> 113

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain variable
region (mature)

<400> 97
Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly Glu
 1   5   10   15
Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu Gln
            20   25   30
Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu Ile
        35   40   45
Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr Leu
    50   55   60
Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg Ala
65   70   75   80
Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Lys Arg Asp Ser Gly Ala
                85   90   95
Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr Lys Leu Ser Val Ile
            100   105   110
Pro

<210> 98
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain variable
region (mature)

<400> 98
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Lys
                85   90   95
Gly Glu Lys Leu Phe Gly Ser Gly Thr Gln Leu Ser Val Leu
            100   105   110

<210> 99

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

<220>
<223> Synthetic sequence TCR2,14 alpha chain variable
region (mature)

<400> 99
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1   5   10   15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20   25   30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35   40   45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50   55   60
Ser Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln
65   70   75   80
Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ile Gly Leu Gly Gly
                85   90   95
Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys Val Leu Ala
            100   105   110

<210> 100
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain variable region
(mature)

<400> 100
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Thr Thr
                85   90   95
Leu Asp Glu Gln Tyr Val Gly Pro Gly Thr Arg Leu Thr Val Thr
            100   105   110

<210> 101
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain variable
region (mature)

<400> 101
Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly Glu
 1   5   10   15
Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu Gln
            20   25   30
Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu Ile
        35   40   45
Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr Leu
    50   55   60
Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg Ala
65   70   75   80
Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asn Ser Gly Asn Thr Pro
                85   90   95
Leu Val Phe Gly Lys Gly Thr Arg Leu Ser Val Ile Ala
            100   105

<210> 102
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta chain variable
region (mature)

<400> 102
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Met Leu Thr
                85   90   95
Asn Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Thr
            100   105   110

<210> 103
<211> 113
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain variable
region (mature)

<400> 103
Lys Asn Gln Val Glu Gln Ser Pro Gln Ser Leu Ile Ile Leu Glu Gly
 1   5   10   15
Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val Ser Pro Phe Ser Asn
            20   25   30
Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly Pro Val Ser Leu Thr
        35   40   45
Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn Gly Arg Tyr Thr Ala
    50   55   60
Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu His Ile Thr Ala Ser
65   70   75   80
Gln Leu Ser Asp Ser Ala Ser Tyr Ile Cys Val Val Asp Ser Gly Gly
                85   90   95
Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu Ile Ile Gln
            100   105   110
Pro

<210> 104
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta chain variable
region (mature)

<400> 104
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Val
                85   90   95
Gly Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
            100   105   110

<210> 105
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain variable
region (mature)

<400> 105
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1   5   10   15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20   25   30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35   40   45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50   55   60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65   70   75   80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val His Leu Leu Asn
                85   90   95
Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr Val Arg Ala
            100   105   110

<210> 106
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 beta chain variable
region (mature)

<400> 106
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Ser
                85   90   95
Gly Asn Thr Ile Tyr Phe Gly Glu Gly Ser Trp Leu Thr Val Val
            100   105   110

<210> 107
<211> 115
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain variable
region (mature)

<400> 107
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1   5   10   15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20   25   30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35   40   45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50   55   60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65   70   75   80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Gly Gly Thr
                85   90   95
Thr Ser Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys
            100   105   110
Val Leu Ala
        115

<210> 108
<211> 289
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 beta chain (full
length) (Cys modified) (mature)

<400> 108
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1   5   10   15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20   25   30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35   40   45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50   55   60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65   70   75   80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Ser Thr Gly
                85   90   95
Gly His Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu
            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 Cys Leu Ser Ser Arg Leu
            180                 185                 190
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
225                 230                 235                 240
Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
                245                 250                 255
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
            260                 265                 270
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
        275                 280                 285
Ser


<210> 109
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR1,13 alpha chain (full
      length)(Cys modified) (mature)

<400> 109
Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly Glu
 1               5                  10                  15
Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu Gln
            20                  25                  30
Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu Ile
        35                  40                  45
Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr Leu
    50                  55                  60
Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg Ala
65                  70                  75                  80
Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Lys Arg Asp Ser Gly Ala
                85                  90                  95
Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr Lys Leu Ser Val Ile
            100                 105                 110
Pro Asn 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 Cys
        195                 200                 205
Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
    210                 215                 220
Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
225                 230                 235                 240
Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
                245                 250

<210> 110
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 beta chain (full
      length) (Cys modified) (mature)

<400> 110
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1               5                  10                  15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20                  25                  30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35                  40                  45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50                  55                  60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65                  70                  75                  80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Lys
                85                  90                  95
Gly Glu Lys Leu Phe Phe Gly Ser Gly Thr Gln Leu Ser Val Leu Glu
            100                 105                 110
Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
        115                 120                 125
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
    130                 135                 140
Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
145                 150                 155                 160
Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu
                165                 170                 175
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
            180                 185                 190
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
        195                 200                 205
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
```

```
    210                 215                 220
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
225                 230                 235                 240
Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala
                245                 250                 255
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
            260                 265                 270
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
        275                 280                 285
```

<210> 111
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR2,14 alpha chain (full length)(Cys modified) (mature)

<400> 111

```
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1               5                  10                  15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20                  25                  30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35                  40                  45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50                  55                  60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65                  70                  75                  80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ile Gly Leu Gly
                85                  90                  95
Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys Val Leu
            100                 105                 110
Ala Asn 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 Cys
        195                 200                 205
Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
    210                 215                 220
Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
225                 230                 235                 240
Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
```

245 250

<210> 112
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 beta chain (full length)
(Cys modified) (mature)

<400> 112
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
1 5 10 15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
20 25 30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
35 40 45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
50 55 60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65 70 75 80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Thr Thr
85 90 95
Leu Asp Glu Gln Tyr Val Gly Pro Gly Thr Arg Leu Thr Val Thr Glu
100 105 110
Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
115 120 125
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
130 135 140
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
145 150 155 160
Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu
165 170 175
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
180 185 190
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
195 200 205
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
210 215 220
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
225 230 235 240
Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
245 250 255
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
260 265 270
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
275 280 285

<210> 113
<211> 250

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR5 alpha chain (full
length)(Cys modified) (mature)

<400> 113
Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser Ile Gln Glu Gly Glu
 1   5   10   15
Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser Ile Asn Asn Leu Gln
            20   25   30
Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val His Leu Ile Leu Ile
        35   40   45
Arg Ser Asn Glu Arg Glu Lys His Ser Gly Arg Leu Arg Val Thr Leu
    50   55   60
Asp Thr Ser Lys Lys Ser Ser Ser Leu Leu Ile Thr Ala Ser Arg Ala
65   70   75   80
Ala Asp Thr Ala Ser Tyr Phe Cys Ala Thr Asn Ser Gly Asn Thr Pro
                85   90   95
Leu Val Phe Gly Lys Gly Thr Arg Leu Ser Val Ile Ala Asn Ile Gln
            100   105   110
Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
        115   120   125
Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
    130   135   140
Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp
145   150   155   160
Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn
                165   170   175
Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
            180   185   190
Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu
        195   200   205
Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu
    210   215   220
Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
225   230   235   240
Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
                245   250

<210> 114
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 beta chain (full length)
(Cys modified) (mature)

<400> 114

```
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1               5                  10                  15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20                  25                  30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35                  40                  45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50                  55                  60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65                  70                  75                  80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Met Leu Thr
                85                  90                  95
Asn Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr Val Thr Glu
            100                 105                 110
Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
        115                 120                 125
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
    130                 135                 140
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
145                 150                 155                 160
Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu
                165                 170                 175
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
            180                 185                 190
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
        195                 200                 205
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
    210                 215                 220
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
225                 230                 235                 240
Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
                245                 250                 255
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
            260                 265                 270
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
        275                 280                 285

<210> 115
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR10 alpha chain (full
      length)(Cys modified) (mature)

<400> 115
Lys Asn Gln Val Glu Gln Ser Pro Gln Ser Leu Ile Ile Leu Glu Gly
 1               5                  10                  15
Lys Asn Cys Thr Leu Gln Cys Asn Tyr Thr Val Ser Pro Phe Ser Asn
            20                  25                  30
```

```
Leu Arg Trp Tyr Lys Gln Asp Thr Gly Arg Gly Pro Val Ser Leu Thr
        35                  40                  45
Ile Met Thr Phe Ser Glu Asn Thr Lys Ser Asn Gly Arg Tyr Thr Ala
    50                  55                  60
Thr Leu Asp Ala Asp Thr Lys Gln Ser Ser Leu His Ile Thr Ala Ser
65                  70                  75                  80
Gln Leu Ser Asp Ser Ala Ser Tyr Ile Cys Val Val Asp Ser Gly Gly
                85                  90                  95
Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly Thr His Leu Ile Ile Gln
            100                 105                 110
Pro Tyr 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 Cys
        195                 200                 205
Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
    210                 215                 220
Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
225                 230                 235                 240
Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
                245                 250
```

<210> 116
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 beta chain (full length)
(Cys modified) (mature)

<400> 116

```
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1               5                  10                  15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20                  25                  30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35                  40                  45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50                  55                  60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65                  70                  75                  80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Val
                85                  90                  95
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Gly Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu
            100                 105                 110
Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
        115                 120                 125
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
    130                 135                 140
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
145                 150                 155                 160
Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu
                165                 170                 175
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
            180                 185                 190
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
        195                 200                 205
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
    210                 215                 220
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
225                 230                 235                 240
Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
                245                 250                 255
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
            260                 265                 270
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
        275                 280                 285

<210> 117
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR16 alpha chain (full length)
      (Cys modified) (mature)

<400> 117
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1               5                  10                  15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20                  25                  30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35                  40                  45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50                  55                  60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65                  70                  75                  80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val His Leu Leu Asn
                85                  90                  95
Asp Tyr Lys Leu Ser Phe Gly Ala Gly Thr Thr Val Thr Val Arg Ala
            100                 105                 110
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
        115                 120                 125
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Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
    130                 135                 140
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
145                 150                 155                 160
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
                165                 170                 175
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
            180                 185                 190
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
        195                 200                 205
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
    210                 215                 220
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
225                 230                 235                 240
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
                245                 250

<210> 118
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequenceTCR29 beta chain (full length)
      (mature)

<400> 118
Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn
 1               5                  10                  15
Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp
            20                  25                  30
Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln
        35                  40                  45
Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser
    50                  55                  60
Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr
65                  70                  75                  80
Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Leu Val Ser
                85                  90                  95
Gly Asn Thr Ile Tyr Phe Gly Glu Gly Ser Trp Leu Thr Val Val Glu
            100                 105                 110
Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
        115                 120                 125
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
    130                 135                 140
Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
145                 150                 155                 160
Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
                165                 170                 175
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
            180                 185                 190
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Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
        195                 200                 205
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
    210                 215                 220
Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
225                 230                 235                 240
Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala
                245                 250                 255
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
            260                 265                 270
Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Phe
        275                 280                 285

<210> 119
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR29 alpha chain (full length)
      (mature)

<400> 119
Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly
 1               5                  10                  15
Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn
            20                  25                  30
Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu
        35                  40                  45
Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala
    50                  55                  60
Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser
65                  70                  75                  80
Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Gly Gly Thr
                85                  90                  95
Thr Ser Gly Thr Tyr Lys Tyr Ile Phe Gly Thr Gly Thr Arg Leu Lys
            100                 105                 110
Val Leu Ala Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
        115                 120                 125
Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
    130                 135                 140
Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
145                 150                 155                 160
Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
                165                 170                 175
Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
            180                 185                 190
Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
        195                 200                 205
Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
    210                 215                 220
```

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
225 230 235 240
Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
245 250 255

<210> 120
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor alpha chain
(mature)

<400> 120
Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly Glu
1 5 10 15
Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser Gly
20 25 30
Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr Phe
35 40 45
Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu Asp
50 55 60
Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu Thr
65 70 75 80
Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Ala
85 90 95
Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu
100 105 110
Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
115 120 125
Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
130 135 140
Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
145 150 155 160
Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
165 170 175
Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
180 185 190
Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser
195 200 205
Leu Ser Ala Arg Tyr Val
210

<210> 121
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain

isoform 1 (mature)

<400> 121
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
 1   5   10   15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20   25   30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35   40   45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50   55   60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65   70   75   80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85   90   95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100   105   110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115   120   125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130   135   140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145   150   155   160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165   170   175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Phe Tyr Lys
            180   185

<210> 122
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
isoform 2 (mature)

<400> 122
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
 1   5   10   15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20   25   30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35   40   45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50   55   60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65   70   75   80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85   90   95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser

```
            100                 105                 110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145                 150                 155                 160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165                 170                 175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Leu Arg Leu His Pro Leu
            180                 185                 190
Glu Lys Cys Ser Arg Met Asp Tyr
        195                 200

<210> 123
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
      isoform 3 (mature)

<400> 123
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
 1               5                  10                  15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20                  25                  30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35                  40                  45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50                  55                  60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65                  70                  75                  80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85                  90                  95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100                 105                 110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145                 150                 155                 160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165                 170                 175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Lys Phe Asn Ile Val Cys
            180                 185                 190
Leu Lys Ile Ser Gly Phe Thr Thr Cys Cys Cys Phe Gln Ile Leu Gln
        195                 200                 205
Ile Ser Arg Glu Tyr Gly Phe Gly Val Leu Leu Gln Lys Asp Ile Gly
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    210                 215                 220
Gln
225

<210> 124
<211> 225
<212> PRT
<213> qArtificial Sequence

<220>
<223> Synthetic sequence CD8 co-receptor beta chain
      isoform 4 (mature)

<400> 124
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
 1               5                  10                  15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
            20                  25                  30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
        35                  40                  45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
    50                  55                  60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65                  70                  75                  80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
                85                  90                  95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
            100                 105                 110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
        115                 120                 125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
    130                 135                 140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145                 150                 155                 160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
                165                 170                 175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Lys Phe Asn Ile Val Cys
            180                 185                 190
Leu Lys Ile Ser Gly Phe Thr Thr Cys Cys Cys Phe Gln Ile Leu Gln
        195                 200                 205
Ile Ser Arg Glu Tyr Gly Phe Gly Val Leu Leu Gln Lys Asp Ile Gly
    210                 215                 220
Gln
225

<210> 125
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
```

<223> Synthetic sequence CD8 co-receptor beta chain
isoform 5 (mature)

<400> 125
Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln Thr Asn Lys Met Val
1 5 10 15
Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser Asn Met Arg Ile Tyr
20 25 30
Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp Ser His His Glu Phe
35 40 45
Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile His Gly Glu Glu Val
50 55 60
Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala Ser Arg Phe Ile Leu
65 70 75 80
Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly Ile Tyr Phe Cys Met
85 90 95
Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys Gly Thr Gln Leu Ser
100 105 110
Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro Thr Lys Lys Ser Thr
115 120 125
Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro Glu Thr Gln Lys Gly
130 135 140
Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu Val Ala Gly Val Leu
145 150 155 160
Val Leu Leu Val Ser Leu Gly Val Ala Ile His Leu Cys Cys Arg Arg
165 170 175
Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Pro Gln Gly Glu Gly Ile
180 185 190
Ser Gly Thr Phe Val Pro Gln Cys Leu His Gly Tyr Tyr Ser Asn Thr
195 200 205
Thr Thr Ser Gln Lys Leu Leu Asn Pro Trp Ile Leu Lys Thr
210 215 220

<210> 126
<211> 930
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR 29 beta chain (wild-type)

<400> 126
atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat 60
actggagtct cccaggaccc cagacacaag atcacaaaga ggggacagaa tgtaactttc 120
aggtgtgatc caatttctga acacaaccgc ctttattggt accgacagac cctggggcag 180
ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc 240
agtgatcggt tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc 300
acagagcagg gggactcggc catgtatctc tgtgccagca gcttagtatc cggaaacacc 360
atatattttg gagagggaag ttggctcact gttgtagagg acctgaacaa ggtgttccca 420
cccgaggtcg ctgtgtttga gccatcagaa gcagagatct cccacaccca aaaggccaca 480
ctggtgtgcc tggccacagg cttcttcccc gaccacgtgg agctgagctg gtgggtgaat 540

gggaaggagg tgcacagtgg ggtcagcaca gacccgcagc ccctcaagga gcagcccgcc 600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tctcggccac cttctggcag 660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag 720
tggacccagg atagggccaa acccgtcacc cagatcgtca gcgccgaggc ctggggtaga 780
gcagactgtg gctttacctc ggtgtcctac cagcaagggg tcctgtctgc caccatcctc 840
tatgagatcc tgctagggaa ggccaccctg tatgctgtgc tggtcagcgc ccttgtgttg 900
atggccatgg tcaagagaaa ggatttctga 930

<210> 127
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence TCR 29 alpha chain (wild-type)

<400> 127
atggagaccc tcttgggcct gcttatcctt tggctgcagc tgcaatgggt gagcagcaaa 60
caggaggtga cgcagattcc tgcagctctg agtgtcccag aaggagaaaa cttggttctc 120
aactgcagtt tcactgatag cgctatttac aacctccagt ggtttaggca ggaccctggg 180
aaaggtctca catctctgtt gcttattcag tcaagtcaga gagagcaaac aagtggaaga 240
cttaatgcct cgctggataa atcatcagga cgtagtactt tatacattgc agcttctcag 300
cctggtgact cagccaccta cctctgtgct gtgagagggg ggactacctc aggaacctac 360
aaatacatct ttggaacagg caccaggctg aaggttttag caaatatcca gaaccctgac 420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc 480
gattttgatt ctcaaacaaa tgtgtcacaa agtaaggatt ctgatgtgta tatcacagac 540
aaaactgtgc tagacatgag gtctatggac ttcaagagca acagtgctgt ggcctggagc 600
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc 660
ttcttcccca gcccagaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca 720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa 780
gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagctga 828