SEQUENCE LISTING

<110> UCL Business PLC

<120> Signalling system

<130> P105610PCT

<150> GB1415347.2
<151> 2014-08-29

<160> 29

<170> PatentIn version 3.5

<210> 1
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> TetR binding domain

<400> 1

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Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1               5                   10                  15


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


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


Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
    50                  55                  60


Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65                  70                  75                  80


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


Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
            100                 105                 110
```

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His
130 135

<210> 2
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> TiP binding domain

<400> 2

Met Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Gly
1 5 10 15

Ser

<210> 3
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified CD4 endodomain linker

<400> 3

Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly
1 5 10 15

Leu Gly Ile Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala
20 25 30

Glu Arg Met Ala Gln Ile Lys Arg Val Val Ser Glu Lys Lys Thr Ala
35 40 45

Gln Ala Pro His Arg Phe Gln Lys Thr Cys Ser Pro Ile
50 55 60

<210> 4
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, long nanotag

<400> 4

Asp Val Glu Ala Trp Leu Asp Glu Arg Val Pro Leu Val Glu Thr
1 5 10 15

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, short nanotag

<400> 5

Asp Val Glu Ala Trp Leu Gly Ala Arg
1 5

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, streptag

<400> 6

Trp Arg His Pro Gln Phe Gly Gly
1 5

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, streptagII

<400> 7

Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 8
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, SBP-tag

<400> 8

Met Asp Glu Lys Thr Thr Gly Trp Arg Gly Gly His Val Val Glu Gly
1 5 10 15

Leu Ala Gly Glu Leu Glu Gln Leu Arg Ala Arg Leu Glu His His Pro
20 25 30

Gln Gly Gln Arg Glu Pro
35

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, ccstreptag

<400> 9

Cys His Pro Gln Gly Pro Pro Cys
1 5

<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Biotin mimicking peptide, flankedccstreptag

<400> 10

Ala Glu Cys His Pro Gln Gly Pro Pro Cys Ile Glu Gly Arg Lys

1 5 10 15

<210> 11
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Core streptavidin sequence

<400> 11

Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe
1 5 10 15

Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser
20 25 30

Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp
35 40 45

Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val
50 55 60

Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser
65 70 75 80

Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu
85 90 95

Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val
100 105 110

Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser
115 120 125

<210> 12
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide

<400> 12

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Gly
20

<210> 13
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide

<400> 13

Met Ser Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 14
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide

<400> 14

Met Ala Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys
20

<210> 15
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer sequence, hinge-CH2CH3 of human IgG1

<400> 15

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


Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30


Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
```

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp
225 230

<210> 16
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer sequence, human CD8 stalk

<400> 16

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
35 40 45

<210> 17
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer sequence, human IgG1 hinge

<400> 17

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

Lys Asp Pro Lys
20

<210> 18
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer sequence, CD2 ectodomain

<400> 18

```
Lys Glu Ile Thr Asn Ala Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp
1               5                  10                  15


Ile Asn Leu Asp Ile Pro Ser Phe Gln Met Ser Asp Asp Ile Asp Asp
            20                  25                  30


Ile Lys Trp Glu Lys Thr Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg
        35                  40                  45


Lys Glu Lys Glu Thr Phe Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys
    50                  55                  60


Asn Gly Thr Leu Lys Ile Lys His Leu Lys Thr Asp Asp Gln Asp Ile
65                  70                  75                  80


Tyr Lys Val Ser Ile Tyr Asp Thr Lys Gly Lys Asn Val Leu Glu Lys
                85                  90                  95


Ile Phe Asp Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser
            100                 105                 110


Trp Thr Cys Ile Asn Thr Thr Leu Thr Cys Glu Val Met Asn Gly Thr
        115                 120                 125


Asp Pro Glu Leu Asn Leu Tyr Gln Asp Gly Lys His Leu Lys Leu Ser
    130                 135                 140


Gln Arg Val Ile Thr His Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe
145                 150                 155                 160


Lys Cys Thr Ala Gly Asn Lys Val Ser Lys Glu Ser Ser Val Glu Pro
```

165 170 175

Val Ser Cys Pro Glu Lys Gly Leu Asp
180 185

<210> 19
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer sequence, CD34 ectodomain

<400> 19

Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro Thr Gln Gly
1 5 10 15

Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu Thr Thr Thr
20 25 30

Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser Gln His Gly
35 40 45

Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys Phe Thr Ser
50 55 60

Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser Ser Val Gln
65 70 75 80

Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro Ala Asn Val
85 90 95

Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro Gly Asn Val
100 105 110

Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser Pro Thr Lys
115 120 125

Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys Ala Glu Ile
130 135 140

```
Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly Ile Cys Leu
145                 150                 155                 160


Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys Asp Arg Gly
                165                 170                 175


Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala Asp Ala Asp
            180                 185                 190


Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser Glu Val Arg
        195                 200                 205


Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu Ile Ser Ser
    210                 215                 220


Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys Lys Leu Gly
225                 230                 235                 240


Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln Ser Tyr Ser
                245                 250                 255


Gln Lys Thr
```

<210> 20
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> signalling component, CD3 Z endodomain

<400> 20

```
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1               5                   10                  15


Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20                  25                  30


Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
```

35 40 45

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

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 21
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> signalling component, CD28 and CD3 Zeta endodomains

<400> 21

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
1 5 10 15

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
20 25 30

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
35 40 45

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
50 55 60

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
65 70 75 80

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
85 90 95

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
100 105 110

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
115 120 125

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
130 135 140

His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 22
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> signalling component, CD28, OX40 and CD3 Zeta endodomains

<400> 22

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
1 5 10 15

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
20 25 30

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp
35 40 45

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu
50 55 60

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

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
85 90 95

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp

100 105 110

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
115 120 125

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
130 135 140

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
145 150 155 160

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
165 170 175

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
180 185

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> self-cleaving site, 2a self-cleaving peptide

<400> 23

Arg Ala Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
1 5 10 15

Asn Pro Gly Pro
20

<210> 24
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> self-cleaving site, 2a self-cleaving peptide

<400> 24

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser

1 5 10 15

Asn Pro Gly Pro
20

<210> 25
<211> 652
<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric antigen receptor (CAR) sequence

<400> 25

Met Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Gly
1 5 10 15

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
20 25 30

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
35 40 45

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
50 55 60

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
65 70 75 80

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
85 90 95

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
100 105 110

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
115 120 125

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
130 135 140

```
Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
145                 150                 155                 160


Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175


Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
            180                 185                 190


Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205


Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
    210                 215                 220


Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240


Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
                245                 250                 255


Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
            260                 265                 270


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285


Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
    290                 295                 300


Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
305                 310                 315                 320


Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
                325                 330                 335


Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
            340                 345                 350
```

```
Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
        355                 360                 365


Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
    370                 375                 380


Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
385                 390                 395                 400


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
                405                 410                 415


Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            420                 425                 430


Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        435                 440                 445


Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
    450                 455                 460


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
465                 470                 475                 480


Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                485                 490                 495


Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            500                 505                 510


Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
        515                 520                 525


Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
    530                 535                 540


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
545                 550                 555                 560
```

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
                565                 570                 575


Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
            580                 585                 590


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
        595                 600                 605


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
    610                 615                 620


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
625                 630                 635                 640


Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Met
                645                 650


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

<220>
<223>  chimeric antigen receptor (CAR) sequence

<400>  26

Ser Gly Gly Gly Gly Ser Met Ser Arg Leu Asp Lys Ser Lys Val Ile
1               5                   10                  15


Asn Ser Ala Leu Glu Leu Leu Asn Glu Val Gly Ile Glu Gly Leu Thr
            20                  25                  30


Thr Arg Lys Leu Ala Gln Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr
        35                  40                  45


Trp His Val Lys Asn Lys Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu
    50                  55                  60


Met Leu Asp Arg His His Thr His Phe Cys Pro Leu Glu Gly Glu Ser
```

65 70 75 80

Trp Gln Asp Phe Leu Arg Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu
85 90 95

Leu Ser His Arg Asp Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr
100 105 110

Glu Lys Gln Tyr Glu Thr Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln
115 120 125

Gln Gly Phe Ser Leu Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly
130 135 140

His Phe Thr Leu Gly Cys Val Leu Glu Asp Gln Glu His Gln Val Ala
145 150 155 160

Lys Glu Glu Arg Glu Thr Pro Thr Thr Asp Ser Met Pro Pro Leu Leu
165 170 175

Arg Gln Ala Ile Glu Leu Phe Asp His Gln Gly Ala Glu Pro Ala Phe
180 185 190

Leu Phe Gly Leu Glu Leu Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys
195 200 205

Cys Glu Ser Gly Ser
210

<210> 27
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence of TiP

<400> 27

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

<210> 28
<211> 87
<212> PRT
<213> Homo sapiens

<400> 28

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

Pro Thr Trp Ser Thr Pro Val Gln Pro Met Ala Leu Ile Val Leu Gly
20 25 30

Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile Phe Phe Cys
35 40 45

Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met Ser Gln Ile
50 55 60

Lys Arg Leu Leu Ser Glu Lys Lys Thr Cys Gln Cys Pro His Arg Phe
65 70 75 80

Gln Lys Thr Cys Ser Pro Ile
85

<210> 29
<211> 926
<212> PRT
<213> Artificial Sequence

<220>
<223> basic TetCAR sequence

<400> 29

Met Trp Thr Trp Asn Ala Tyr Ala Phe Ala Ala Pro Ser Gly Gly Gly
1 5 10 15

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
20 25 30

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
35 40 45

```
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
    50                  55                  60

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
65                  70                  75                  80

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
                85                  90                  95

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
            100                 105                 110

Ala Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Glu Gly Arg Gly
        115                 120                 125

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
    130                 135                 140

Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr Asp Ala
145                 150                 155                 160

Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                165                 170                 175

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Tyr
            180                 185                 190

Phe Asn Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
        195                 200                 205

Leu Ile Tyr Asp Thr Asn Arg Leu Ala Asp Gly Val Pro Ser Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Lys Asn Tyr
                245                 250                 255
```

```
Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ser Gly
            260                 265                 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        275                 280                 285

Gly Gly Ser Arg Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
    290                 295                 300

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
305                 310                 315                 320

Thr Leu Ser Asn Tyr Gly Met His Trp Ile Arg Gln Ala Pro Gly Lys
                325                 330                 335

Gly Leu Glu Trp Val Ser Ser Ile Ser Leu Asn Gly Gly Ser Thr Tyr
            340                 345                 350

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
        355                 360                 365

Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
    370                 375                 380

Ala Val Tyr Tyr Cys Ala Ala Gln Asp Ala Tyr Thr Gly Gly Tyr Phe
385                 390                 395                 400

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Met Asp Pro
                405                 410                 415

Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            420                 425                 430

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        435                 440                 445

Lys Asp Thr Leu Met Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val
    450                 455                 460
```

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
465                 470                 475                 480

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                485                 490                 495

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            500                 505                 510

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
        515                 520                 525

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
    530                 535                 540

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
545                 550                 555                 560

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
                565                 570                 575

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
            580                 585                 590

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
        595                 600                 605

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
    610                 615                 620

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
625                 630                 635                 640

Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Met Ala Leu Ile Val
                645                 650                 655

Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly Ile Phe
            660                 665                 670
```

```
Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln Ala Glu Arg Met Ala
        675                 680                 685

Gln Ile Lys Arg Val Val Ser Glu Lys Lys Thr Ala Gln Ala Pro His
    690                 695                 700

Arg Phe Gln Lys Thr Cys Ser Pro Ile Ser Gly Gly Gly Gly Ser Met
705                 710                 715                 720

Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu Leu
                725                 730                 735

Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln Lys
            740                 745                 750

Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys Arg
        755                 760                 765

Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His Thr
    770                 775                 780

His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg Asn
785                 790                 795                 800

Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly Ala
                805                 810                 815

Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr Leu
            820                 825                 830

Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu Asn
        835                 840                 845

Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys Val
    850                 855                 860

Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr Pro
865                 870                 875                 880
```

```
Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu Phe
                885                 890                 895

Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu Ile
            900                 905                 910

Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
        915                 920                 925
```