SEQUENCE LISTING

<110> Fate Therapeutics, Inc.

<120> CD3 RECONSTITUTION IN ENGINEERED iPSC AND IMMUNE EFFECTOR CELLS

<130> 056932-518001WO

<150> US 62/832,622
<151> 2019-04-11

<160> 45

<170> PatentIn version 3.5

<210> 1
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> a construct expressing constant region of TCR-beta (TRBC)

<400> 1

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
1 5 10 15

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
20 25 30

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
35 40 45

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
50 55 60

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
65 70 75 80

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
85 90 95

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
100 105 110

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
        115                 120                 125

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140

<210>  2
<211>  176
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  a construct expressing constant region of TCR-beta(TRBC1)

<400>  2

Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
1               5                   10                  15

Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
            20                  25                  30

Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
        35                  40                  45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
    50                  55                  60

Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
65                  70                  75                  80

Asn His Phe Arg Cys Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Gln
                85                  90                  95

Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
            100                 105                 110

Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
        115                 120                 125

Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val Leu Ser Ala
    130                 135                 140

```
Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
145                 150                 155                 160


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


<210>  3
<211>  178
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  TRBC2

<400>  3

Asp Leu Lys Asn Val Phe Pro Pro Lys Val Ala Val Phe Glu Pro Ser
1               5                   10                  15


Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
            20                  25                  30


Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
        35                  40                  45


Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
    50                  55                  60


Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
65                  70                  75                  80


Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
                85                  90                  95


Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
            100                 105                 110


Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala
        115                 120                 125


Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala
    130                 135                 140
```

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
145 150 155 160

Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser
165 170 175

Arg Gly

<210> 4
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary signal peptide for the construct encoding TCR-beta constant region (tgTRBC) - CD8asp

<400> 4

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

His Ala

<210> 5
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary signal peptide for the construct encoding TCR-beta constant region (tgTRBC) - IgKsp

<400> 5

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

Val Ile Met Ser Arg
20

<210> 6

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

<220>
<223> Exemplary linker peptide for the construct encoding TCR-beta constant region (tgTRBC) - FLAG

<400> 6

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 7
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> 340 a.a. CD64 domain-based construction

<400> 7

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

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys

```
        115                 120                 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
    130                 135                 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145                 150                 155                 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
                165                 170                 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
            180                 185                 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
        195                 200                 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
    210                 215                 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225                 230                 235                 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
                245                 250                 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
            260                 265                 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
        275                 280                 285

Val Trp Phe His Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu
    290                 295                 300

Phe Ala Val Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg
305                 310                 315                 320

Ser Ser Thr Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp
                325                 330                 335
```

Pro Gln Asp Lys
            340

<210>  8
<211>  336
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  336 a.a. CD64 exon-based construction

<400>  8

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

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
            20                  25                  30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
        35                  40                  45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
    50                  55                  60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65                  70                  75                  80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
                85                  90                  95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
            100                 105                 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
        115                 120                 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
    130                 135                 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile

```
145                 150                 155                 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
                165                 170                 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
            180                 185                 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
        195                 200                 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
    210                 215                 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225                 230                 235                 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
                245                 250                 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
            260                 265                 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Phe Phe Pro Pro Gly
        275                 280                 285

Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp
    290                 295                 300

Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg
305                 310                 315                 320

Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
                325                 330                 335
```

<210> 9
<211> 335
<212> PRT
<213> Artificial Sequence

<220>

<223> 335 a.a. CD64 exon-based construction

<400> 9

```
Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln
1               5                  10                  15


Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
            20                  25                  30


Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
        35                  40                  45


Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
    50                  55                  60


Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65                  70                  75                  80


Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
                85                  90                  95


Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
            100                 105                 110


Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
        115                 120                 125


Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
    130                 135                 140


Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145                 150                 155                 160


Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
                165                 170                 175


Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
            180                 185                 190


Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
```

```
        195                 200                 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
    210                 215                 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225                 230                 235                 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
                245                 250                 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
            260                 265                 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Phe Phe Pro Pro Gly Tyr
        275                 280                 285

Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr
    290                 295                 300

Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp
305                 310                 315                 320

Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
                325                 330                 335
```

<210> 10
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplifying sequence encoding 340 a.a. CD64 domain-based construction

<400> 10
cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa 60

gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag 120

gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg 180

tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt 240

gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata 300

cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa 360

ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt 420

tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg 480

aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac 540

acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca 600

tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg 660

ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg 720

cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg 780

ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg 840

gagcttcaag tgcttggcct ccagttacca actcctgtct ggtttcatta ccaagtctct 900

ttctgcttgg tgatggtact ccttttttgca gtggacacag gactatattt ctctgtgaag 960

acaaacattc gaagctcaac aagagactgg aaggaccata aatttaaatg gagaaaggac 1020

cctcaagaca aa 1032

<210> 11
<211> 1020
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> exemplifying sequence encoding 336 a.a. CD64 exon-based construction

<400> 11
cttggagaca acatgtggtt cttgacaact ctgctccttt gggttccagt tgatgggcaa 60

gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag 120

gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg 180

tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt 240

gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata 300

cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa 360

ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt 420

tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg 480

aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac 540

acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca 600

tctgtgacat ccccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg 660

ctcttgcaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg 720

cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg 780

ttatactggt gcgaggctgc cacagaggat ggaaatgtcc ttaagcgcag ccctgagttg 840

gagcttcaag tgcttggttt gttctttcca cctgggtacc aagtctcttt ctgcttggtg 900

atggtactcc tttttgcagt ggacacagga ctatatttct ctgtgaagac aaacattcga 960

agctcaacaa gagactggaa ggaccataaa tttaaatgga gaaaggaccc tcaagacaaa 1020

<210> 12
<211> 1005
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> exemplifying sequence encoding 335 a.a. CD64 exon-based construction

<400> 12
atgtggttct tgacaactct gctcctttgg gttccagttg atgggcaagt ggacaccaca 60

aaggcagtga tcactttgca gcctccatgg gtcagcgtgt tccaagagga aaccgtaacc 120

ttgcactgtg aggtgctcca tctgcctggg agcagctcta cacagtggtt tctcaatggc 180

acagccactc agacctcgac ccccagctac agaatcacct ctgccagtgt caatgacagt 240

ggtgaataca ggtgccagag aggtctctca gggcgaagtg accccataca gctggaaatc 300

cacagaggct ggctactact gcaggtctcc agcagagtct tcacggaagg agaacctctg 360

gccttgaggt gtcatgcgtg gaaggataag ctggtgtaca atgtgcttta ctatcgaaat 420

ggcaaagcct ttaagttttt ccactggaac tctaacctca ccattctgaa aaccaacata 480

agtcacaatg gcacctacca ttgctcaggc atgggaaagc atcgctacac atcagcagga 540

atatctgtca ctgtgaaaga gctatttcca gctccagtgc tgaatgcatc tgtgacatcc 600

ccactcctgg aggggaatct ggtcaccctg agctgtgaaa caaagttgct cttgcagagg 660

cctggtttgc agctttactt ctccttctac atgggcagca agaccctgcg aggcaggaac 720

acatcctctg aataccaaat actaactgct agaagagaag actctgggtt atactggtgc 780

gaggctgcca cagaggatgg aaatgtcctt aagcgcagcc ctgagttgga gcttcaagtg 840

cttggcttct ttccacctgg gtaccaagtc tctttctgct tggtgatggt actccttttt 900

gcagtggaca caggactata tttctctgtg aagacaaaca ttcgaagctc aacaagagac 960

tggaaggacc ataaatttaa atggagaaag gaccctcaag acaaa 1005

<210> 13
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> 153 a.a. CD28 co-stim + CD3-zeta-ITAM

<400> 13

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

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

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

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

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

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

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

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

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

Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 14
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 219 a.a. CD28 hinge + CD28 TM + CD28 co-stim + CD3-zeta-ITAM

<400> 14

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
1 5 10 15

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

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
35 40 45

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
50 55 60

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
65 70 75 80

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
85 90 95

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
100 105 110

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
115 120 125

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

```
    130                 135                 140

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
145                 150                 155                 160

Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
                165                 170                 175

Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
            180                 185                 190

His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe
        195                 200                 205

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    210                 215


<210>  15
<211>  263
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  263 a.a NKG2D TM + 2B4 + CD3-zeta

<400>  15

Ser Asn Leu Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg
1               5                   10                  15

Ile Gly Met Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp
            20                  25                  30

Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe
        35                  40                  45

Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His
    50                  55                  60

Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met
65                  70                  75                  80
```

```
Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr
                85                  90                  95

Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg
            100                 105                 110

Asn His Ser Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys
        115                 120                 125

Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu
    130                 135                 140

Glu Asn Phe Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
145                 150                 155                 160

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                165                 170                 175

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            180                 185                 190

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        195                 200                 205

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    210                 215                 220

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
225                 230                 235                 240

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                245                 250                 255

Met Gln Ala Leu Pro Pro Arg
            260
```

<210> 16
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223>  308 a.a CD8 hinge + NKG2D TM + 2B4 + CD3-zeta

<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 Ser Asn Leu
        35                  40                  45


Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg Ile Gly Met
    50                  55                  60


Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp Arg Arg Lys
65                  70                  75                  80


Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe Leu Thr Ile
                85                  90                  95


Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His Glu Gln Glu
            100                 105                 110


Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met Ile Gln Ser
        115                 120                 125


Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr Leu Tyr Ser
    130                 135                 140


Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg Asn His Ser
145                 150                 155                 160


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


Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu Glu Asn Phe
            180                 185                 190
```

```
Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        195                 200                 205

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    210                 215                 220

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
225                 230                 235                 240

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                245                 250                 255

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            260                 265                 270

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        275                 280                 285

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    290                 295                 300

Leu Pro Pro Arg
305
```

<210> 17
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> construct mimicking trans-presentation of IL15 (design 3)

<400> 17

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

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
            20                  25                  30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
        35                  40                  45
```

```
Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
    50                  55                  60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65                  70                  75                  80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
                85                  90                  95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
            100                 105                 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
        115                 120                 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
    130                 135                 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
                165                 170                 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
            180                 185                 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
        195                 200                 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
    210                 215                 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225                 230                 235                 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr
                245                 250                 255
```

```
Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser
            260                 265                 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala
        275                 280                 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser
    290                 295                 300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly
305                 310                 315                 320

Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala
                325                 330                 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
            340                 345                 350

Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val
        355                 360                 365

Ser Leu Leu Ala Cys Tyr Leu Lys Ser Arg Gln
    370                 375
```

<210> 18
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> an exemplary nucleic acid sequence encoding construct mimicking trans-presentation of IL15 (design 3)

<400> 18

```
atggactgga cctggattct gttcctggtc gcggctgcaa cgcgagtcca tagcggtatc       60

catgttttta ttcttgggtg tttttctgct gggctgccta agaccgaggc caactgggta      120

aatgtcatca gtgacctcaa gaaaatagaa gaccttatac aaagcatgca cattgatgct      180

actctctaca ctgagtcaga tgtacatccc tcatgcaaag tgacggccat gaaatgtttc      240

ctcctcgaac ttcaagtcat atctctggaa agtggcgacg cgtccatcca cgacacggtc      300

gaaaacctga taatactcgc taataatagt ctctcttcaa atggtaacgt aaccgagtca      360
```

ggttgcaaag agtgcgaaga gttggaagaa aaaaacataa aggagttcct gcaaagtttc 420

gtgcacattg tgcagatgtt cattaatacc tctagcggcg gaggatcagg tggcggtgga 480

agcggaggtg gaggctccgg tggaggaggt agtggcggag gttctcttca aataacttgt 540

cctccaccga tgtccgtaga acatgcggat atttgggtaa aatcctatag cttgtacagc 600

cgagagcggt atatctgcaa cagcggcttc aagcggaagg ccggcacaag cagcctgacc 660

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccctag cctgaagtgc 720

atcagagatc ccgccctggt gcatcagcgg cctgcccctc caagcacagt gacaacagct 780

ggcgtgaccc cccagcctga gagcctgagc ccttctggaa aagagcctgc cgccagcagc 840

cccagcagca acaatactgc cgccaccaca gccgccatcg tgcctggatc tcagctgatg 900

cccagcaaga gccctagcac cggcaccacc gagatcagca gccacgagtc tagccacggc 960

accccatctc agaccaccgc caagaactgg gagctgacag ccagcgcctc tcaccagcct 1020

ccaggcgtgt accctcaggg ccacagcgat accacagtgg ccatcagcac ctccaccgtg 1080

ctgctgtgtg gactgagcgc cgtgtcactg ctggcctgct acctgaagtc cagacagtga 1140

<210> 19
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> fused IL15/mb-Sushi construct (design 4)

<400> 19

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

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
50 55 60

```
Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65                  70                  75                  80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
                85                  90                  95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
            100                 105                 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
        115                 120                 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
    130                 135                 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
                165                 170                 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
            180                 185                 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
        195                 200                 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
    210                 215                 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225                 230                 235                 240

Ile Arg
```

<210> 20
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> an exemplary nucleic acid sequence encoding fused IL15/mb-Sushi construct (design 4)

<400> 20
atggactgga cctggattct gttcctggtc gcggctgcaa cgcgagtcca tagcggtatc 60

catgttttta ttcttgggtg tttttctgct gggctgccta agaccgaggc caactgggta 120

aatgtcatca gtgacctcaa gaaaatagaa gaccttatac aaagcatgca cattgatgct 180

actctctaca ctgagtcaga tgtacatccc tcatgcaaag tgacggccat gaaatgtttc 240

ctcctcgaac ttcaagtcat atctctggaa agtggcgacg cgtccatcca cgacacggtc 300

gaaaacctga taatactcgc taataatagt ctctcttcaa atggtaacgt aaccgagtca 360

ggttgcaaag agtgcgaaga gttggaagaa aaaaacataa aggagttcct gcaaagtttc 420

gtgcacattg tgcagatgtt cattaatacc tctagcggcg gaggatcagg tggcggtgga 480

agcggaggtg gaggctccgg tggaggaggt agtggcggag gttctcttca aataacttgt 540

cctccaccga tgtccgtaga acatgcggat atttgggtaa aatcctatag cttgtacagc 600

cgagagcggt atatctgcaa cagcggcttc aagcggaagg ccggcacaag cagcctgacc 660

gagtgcgtgc tgaacaaggc caccaacgtg gcccactgga ccacccctag cctgaagtgc 720

atcaga 726

<210> 21
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> protein construct further modified from SEQ ID NO. 17

<400> 21

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

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
35 40 45

```
Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
    50                  55                  60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
65                  70                  75                  80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
                85                  90                  95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
            100                 105                 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
        115                 120                 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
    130                 135                 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
                165                 170                 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp
            180                 185                 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser
        195                 200                 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu
    210                 215                 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
225                 230                 235                 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr
                245                 250                 255
```

```
Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser
            260                 265                 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala
        275                 280                 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser
    290                 295                 300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly
305                 310                 315                 320

Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala
                325                 330                 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr
            340                 345                 350

Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val
        355                 360                 365

Ser Leu Leu Ala Cys Tyr Leu
    370                 375
```

<210> 22
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> non-limiting exemplary signal peptide for the construct encoding tgpTCR-alpha

<400> 22

```
Met Ala Gly Thr Trp Leu Leu Leu Leu Leu Ala Leu Gly Cys Pro Ala
1               5                   10                  15

Leu Pro Thr Gly Val Gly Gly
            20
```

<210> 23

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

<220>
<223> exemplary sequence of a construct encoding tgpTCR-alpha (tgpTCR-alpha with TM)

<400> 23

Thr Pro Phe Pro Ser Leu Ala Pro Pro Ile Met Leu Leu Val Asp Gly
1 5 10 15

Lys Gln Gln Met Val Val Val Cys Leu Val Leu Asp Val Ala Pro Pro
20 25 30

Gly Leu Asp Ser Pro Ile Trp Phe Ser Ala Gly Asn Gly Ser Ala Leu
35 40 45

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

Asn Leu Ala His Leu Ser Leu Pro Ser Glu Glu Leu Ala Ser Trp Glu
65 70 75 80

Pro Leu Val Cys His Thr Gly Pro Gly Ala Glu Gly His Ser Arg Ser
85 90 95

Thr Gln Pro Met His Leu Ser Gly Glu Ala Ser Thr Ala Arg Thr Cys
100 105 110

Pro Gln Glu Pro Leu Arg Gly Gly Cys Gly Leu Leu Arg Ala Pro Glu
115 120 125

Arg Phe Leu Leu Ala Gly Thr Pro Gly Gly Ala Leu Trp Leu Gly Val
130 135 140

Leu Arg Leu Leu Leu Phe Lys Leu Leu Leu Phe Asp Leu Leu Leu Thr
145 150 155 160

Cys Ser Cys Leu Cys Asp Pro Ala Gly Pro Leu Pro Ser Pro Ala Thr
165 170 175

```
Thr Thr Arg Leu Arg Ala Leu Gly Ser His Arg Leu His Pro Ala Thr
            180                 185                 190

Glu Thr Gly Gly Arg Glu Ala Thr Ser Ser Pro Arg Pro Gln Pro Arg
        195                 200                 205

Asp Arg Arg Trp Gly Asp Thr Pro Pro Gly Arg Lys Pro Gly Ser Pro
    210                 215                 220

Val Trp Gly Glu Gly Ser Tyr Leu Ser Ser Tyr Pro Thr Cys Pro Ala
225                 230                 235                 240

Gln Ala Trp Cys Ser Arg Ser Ala Leu Arg Ala Pro Ser Ser Ser Leu
                245                 250                 255

Gly Ala Phe Phe Ala Gly Asp Leu Pro Pro Pro Leu Gln Ala Gly Ala
            260                 265                 270

Ala
```

<210> 24
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> partial length of a construct encoding tgpTCR-alpha (Truncated tgpTCR-alpha with TM)

<400> 24

```
Thr Pro Phe Pro Ser Leu Ala Pro Pro Ile Met Leu Leu Val Asp Gly
1               5                   10                  15

Lys Gln Gln Met Val Val Val Cys Leu Val Leu Asp Val Ala Pro Pro
            20                  25                  30

Gly Leu Asp Ser Pro Ile Trp Phe Ser Ala Gly Asn Gly Ser Ala Leu
        35                  40                  45

Asp Ala Phe Thr Tyr Gly Pro Ser Pro Ala Thr Asp Gly Thr Trp Thr
```

```
    50                  55                  60

Asn Leu Ala His Leu Ser Leu Pro Ser Glu Glu Leu Ala Ser Trp Glu
65                  70                  75                  80

Pro Leu Val Cys His Thr Gly Pro Gly Ala Glu Gly His Ser Arg Ser
                85                  90                  95

Thr Gln Pro Met His Leu Ser Gly Glu Ala Ser Thr Ala Arg Thr Cys
            100                 105                 110

Pro Gln Glu Pro Leu Arg Gly Gly Cys Gly Leu Leu Arg Ala Pro Glu
        115                 120                 125

Arg Phe Leu Leu Ala Gly Thr Pro Gly Gly Ala Leu Trp Leu Gly Val
    130                 135                 140

Leu Arg Leu Leu Leu Phe Lys Leu Leu Leu Phe Asp Leu Leu Leu Thr
145                 150                 155                 160

Cys Ser Cys Leu Cys Asp Pro Ala Gly Pro Leu Pro Ser Pro Ala Thr
                165                 170                 175

Thr Thr Arg Leu Arg Ala Leu Gly Ser His Arg Leu His Pro Ala Thr
            180                 185                 190

Glu Thr Gly Gly Arg Glu Ala Thr Ser Ser Pro Arg Pro Gln Pro Arg
        195                 200                 205

Asp Arg Arg Trp Gly Asp Thr Pro Pro Gly Arg Lys Pro Gly Ser Pro
    210                 215                 220

Val
225


<210>  25
<211>  104
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> exemplary sequence of a construct encoding a full or partial length of CD3-epsilon ectodomain

<400> 25

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

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

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Cys Glu Asn Cys Met Glu Met Asp
100

<210> 26
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding a full or partial length of CD3-delta ectodomain

<400> 26

Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1 5 10 15

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

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly

35 40 45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
50 55 60

Val Gln Val His Tyr Arg Met Cys Gln Ser Cys Val Glu Leu Asp Pro
65 70 75 80

Ala Thr Val Ala

<210> 27
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of a construct encoding a full or partial length of CD3-gamma ectodomain

<400> 27

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

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

Trp Phe Lys Asp Gly Lys Met Ile Gly Phe Leu Thr Glu Asp Lys Lys
35 40 45

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

Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg
65 70 75 80

Met Cys Gln Asn Cys Ile Glu Leu Asn Ala Ala Thr Ile Ser
85 90

<210> 28
<211> 22
<212> PRT

<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length of CD3-epsilon ectodomain

<400> 28

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln
20

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length of CD3-delta ectodomain

<400> 29

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

Ser Gln Val Ser Pro
20

<210> 30
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide for a construct encoding a full or partial length of CD3-gamma ectodomain

<400> 30

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
1 5 10 15

Leu Gln Gly Thr Leu Ala
20

<210> 31
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence polynucleotide encoding
tgCD3(epsilon-delta)-TRAC fusion protein

<400> 31

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30

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

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
100 105 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Phe Lys Ile Pro Ile Glu
115 120 125

Glu Leu Glu Asp Arg Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp
130 135 140

Val Glu Gly Thr Val Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp
145 150 155 160

Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly

```
                165                 170                 175

Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg
            180                 185                 190

Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        195                 200                 205

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
    210                 215                 220

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

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val
                245                 250                 255

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

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
        275                 280                 285

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
    290                 295                 300

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
305                 310                 315                 320

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
                325                 330                 335

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
            340                 345
```

<210> 32
<211> 394
<212> PRT
<213> Artificial Sequence

<220>

<223> exemplary sequence polynucleotide encoding
tgCD3(epsilon-delta)-TRAC fusion protein

<400> 32

```
Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1               5                  10                  15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20                  25                  30

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

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50                  55                  60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65                  70                  75                  80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85                  90                  95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
            100                 105                 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Gln Ser Ile Lys Gly Asn
        115                 120                 125

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

Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys
145                 150                 155                 160

Met Ile Gly Phe Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser
                165                 170                 175

Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn
            180                 185                 190
```

```
Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Gly Gly Gly Gly Ser
        195                 200                 205

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Leu Asn Lys Val Phe
    210                 215                 220

Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His
225                 230                 235                 240

Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp
                245                 250                 255

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
            260                 265                 270

Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp
        275                 280                 285

Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp
    290                 295                 300

Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu
305                 310                 315                 320

Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln
                325                 330                 335

Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser
            340                 345                 350

Val Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile
        355                 360                 365

Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val
    370                 375                 380

Leu Met Ala Met Val Lys Arg Lys Asp Phe
385                 390
```

<210>  33

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

<220>
<223> linker sequence to the polynucleotide encoding
tgCD3(epsilon-delta)-TRAC fusion protein (G4S linker)

<400> 33

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
1 5 10 15

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser
20 25

<210> 34
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence to the polynucleotide encoding
tgCD3(epsilon-delta)-TRAC fusion protein (G4S linker)

<400> 34

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 35
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence encoding a full or partial length of CD3-zeta
endodomain

<400> 35

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
1 5 10 15

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

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala

```
        35                  40                  45

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

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65                  70                  75                  80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
                85                  90                  95

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
            100                 105                 110

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
        115                 120                 125

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
    130                 135                 140

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
145                 150                 155                 160

Pro Pro Arg
```

<210> 36
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM1 sequence

<400> 36

```
Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
1               5                   10                  15

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            20                  25
```

<210> 37
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM2 sequence

<400> 37

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
1 5 10 15

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
20 25

<210> 38
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM3 sequence

<400> 38

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
1 5 10 15

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
20 25

<210> 39
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence from which any one or two CD3-zeta ITAMs may be removed

<400> 39

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

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

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


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


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


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


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


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


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


Leu His Met Gln Ala Leu Pro Pro Arg
145                 150
```

<210> 40
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence CD3 chimeric chain with 41BB signaling domain from which any one or two CD3-zeta ITAMs may be removed

<400> 40

```
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1               5                   10                  15


Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            20                  25                  30
```

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
35 40 45

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

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

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

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

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
115 120 125

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

Ala Leu His Met Gln Ala Leu Pro Pro Arg
145 150

<210> 41
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of polynucleotide encoding a full or partial length of 28BB-zeta endodomain

<400> 41

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

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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu
35 40 45

```
Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
    50                  55                  60

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
65                  70                  75                  80

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

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            100                 105                 110

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        115                 120                 125

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    130                 135                 140

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
145                 150                 155                 160

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
                165                 170                 175

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
            180                 185                 190

Pro Pro Arg
        195
```

<210> 42
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary sequence of polynucleotide encoding a full or partial length of 28BB-zeta endodomain

<400> 42

```
Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1               5                  10                  15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20                  25                  30

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

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50                  55                  60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65                  70                  75                  80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85                  90                  95

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
            100                 105                 110

Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Gln Ser Ile Lys Gly Asn
        115                 120                 125

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

Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys
145                 150                 155                 160

Met Ile Gly Phe Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser
                165                 170                 175

Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn
            180                 185                 190

Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Arg Ala Ala Ala Ile
        195                 200                 205

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
```

```
    210                 215                 220

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
225                 230                 235                 240

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
                245                 250                 255

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
            260                 265                 270

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
        275                 280                 285

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
    290                 295                 300

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
305                 310                 315                 320

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
                325                 330                 335

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            340                 345                 350

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
        355                 360                 365

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
    370                 375                 380

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
385                 390                 395                 400

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
                405                 410                 415

Ala Leu His Met Gln Ala Leu Pro Pro Arg
            420                 425
```

<210> 43
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide encoding construct tgCD3(epsilon-delta)-(28/BB)-zeta

<400> 43

```
Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1               5                   10                  15


Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20                  25                  30


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


Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50                  55                  60


Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65                  70                  75                  80


Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85                  90                  95


Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
            100                 105                 110


Lys Lys Asp Asp Ala Lys Lys Asp Gly Ser Phe Lys Ile Pro Ile Glu
        115                 120                 125


Glu Leu Glu Asp Arg Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp
    130                 135                 140


Val Glu Gly Thr Val Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp
145                 150                 155                 160


Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly
```

```
                165                 170                 175

Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg
            180                 185                 190

Met Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp
        195                 200                 205

Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu
    210                 215                 220

Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu
225                 230                 235                 240

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
                245                 250                 255

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His
            260                 265                 270

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
        275                 280                 285

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    290                 295                 300

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
305                 310                 315                 320

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                325                 330                 335

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            340                 345                 350

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        355                 360                 365

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    370                 375                 380
```

```
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
385                 390                 395                 400


Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                405                 410                 415


<210>  44
<211>  276
<212>  PRT
<213>  Homo sapiens

<400>  44

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 Ser Asp Arg Gly Ser Thr Leu Gly Arg Leu Tyr Phe Gly Arg Gly
        115                 120                 125


Thr Gln Leu Thr Val Trp Pro Asp Ile Gln Asn Pro Asp Pro Ala Val
    130                 135                 140
```

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


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


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


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


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


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


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


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


Leu Trp Ser Ser
        275


<210>  45
<211>  289
<212>  PRT
<213>  Homo sapiens

<400>  45

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


Gly Leu Met Glu Ala Asp Ile Tyr Gln Thr Pro Arg Tyr Leu Val Ile
            20                  25                  30


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

```
Asp Lys Met Tyr Trp Tyr Gln Gln Asp Pro Gly Met Glu Leu His Leu
    50                  55                  60

Ile His Tyr Ser Tyr Gly Val Asn Ser Thr Glu Lys Gly Asp Leu Ser
65                  70                  75                  80

Ser Glu Ser Thr Val Ser Arg Ile Arg Thr Glu His Phe Pro Leu Thr
                85                  90                  95

Leu Glu Ser Ala Arg Pro Ser His Thr Ser Gln Tyr Leu Cys Ala Ser
            100                 105                 110

Glu Asp Leu Asn Lys 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 Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
145                 150                 155                 160

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

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

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 Val 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

Phe
```