SEQUENCE LISTING

<110> LYELL IMMUNOPHARMA, INC.

<120> ROR1 TARGETING CHIMERIC ANTIGEN RECEPTOR

<130> 4385.042PC04

<150> US 63/153,878
<151> 2021-02-25

<150> US 63/263,229
<151> 2021-10-28

<150> US 63/309,393
<151> 2022-02-11

<160> 64

<170> PatentIn version 3.5

<210> 1
<211> 331
<212> PRT
<213> artificial sequence

<220>
<223> wild type human c-Jun protein

<400> 1

```
Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
1               5                  10                  15


Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
            20                  25                  30


Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
        35                  40                  45


Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
    50                  55                  60


Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
65                  70                  75                  80


Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
                85                  90                  95
```

```
Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
            100                 105                 110

Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
        115                 120                 125

Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
    130                 135                 140

Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
145                 150                 155                 160

Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
                165                 170                 175

Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
            180                 185                 190

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
        195                 200                 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
    210                 215                 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225                 230                 235                 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
                245                 250                 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
            260                 265                 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
        275                 280                 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
    290                 295                 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
```

3
305 310 315 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe
325 330

<210> 2
<211> 3257
<212> DNA
<213> artificial sequence

<220>
<223> wild type human c-Jun gene

<400> 2
gctcagagtt gcactgagtg tggctgaagc agcgaggcgg gagtggaggt gcgcggagtc 60

aggcagacag acagacacag ccagccagcc aggtcggcag tatagtccga actgcaaatc 120

ttattttctt ttcaccttct ctctaactgc ccagagctag cgcctgtggc tcccgggctg 180

gtgtttcggg agtgtccaga gagcctggtc tccagccgcc cccgggagga gagccctgct 240

gcccaggcgc tgttgacagc ggcggaaagc agcggtaccc acgcgcccgc cgggggaagt 300

cggcgagcgg ctgcagcagc aaagaacttt cccggctggg aggaccggag acaagtggca 360

gagtcccgga gccaactttt gcaagccttt cctgcgtctt aggcttctcc acggcggtaa 420

agaccagaag gcggcggaga gccacgcaag agaagaagga cgtgcgctca gcttcgctcg 480

caccggttgt tgaacttggg cgagcgcgag ccgcggctgc cgggcgcccc ctccccctag 540

cagcggagga ggggacaagt cgtcggagtc cgggcggcca agacccgccg ccggccggcc 600

actgcagggt ccgcactgat ccgctccgcg gggagagccg ctgctctggg aagtgagttc 660

gcctgcggac tccgaggaac cgctgcgcac gaagagcgct cagtgagtga ccgcgacttt 720

tcaaagccgg gtagcgcgcg cgagtcgaca agtaagagtg cgggaggcat cttaattaac 780

cctgcgctcc ctggagcgag ctggtgagga gggcgcagcg gggacgacag ccagcgggtg 840

cgtgcgctct tagagaaact ttccctgtca aaggctccgg ggggcgcggg tgtcccccgc 900

ttgccacagc cctgttgcgg ccccgaaact tgtgcgcgca gcccaaacta acctcacgtg 960

aagtgacgga ctgttctatg actgcaaaga tggaaacgac cttctatgac gatgccctca 1020

acgcctcgtt cctcccgtcc gagagcggac cttatggcta cagtaacccc aagatcctga 1080

aacagagcat gaccctgaac ctggccgacc cagtggggag cctgaagccg cacctccgcg 1140

ccaagaactc ggacctcctc acctcgcccg acgtggggct gctcaagctg gcgtcgcccg 1200

agctggagcg cctgataatc cagtccagca acgggcacat caccaccacg ccgaccccca 1260

cccagttcct gtgccccaag aacgtgacag atgagcagga gggcttcgcc gagggcttcg 1320

tgcgcgccct ggccgaactg cacagccaga acacgctgcc cagcgtcacg tcggcggcgc 1380

agccggtcaa cggggcaggc atggtggctc ccgcggtagc ctcggtggca gggggcagcg 1440

gcagcggcgg cttcagcgcc agcctgcaca gcgagccgcc ggtctacgca aacctcagca 1500

acttcaaccc aggcgcgctg agcagcggcg gcggggcgcc ctcctacggc gcggccggcc 1560

tggcctttcc cgcgcaaccc cagcagcagc agcagccgcc gcaccacctg ccccagcaga 1620

tgcccgtgca gcacccgcgg ctgcaggccc tgaaggagga gcctcagaca gtgcccgaga 1680

tgcccggcga gacaccgccc ctgtccccca tcgacatgga gtcccaggag cggatcaagg 1740

cggagaggaa gcgcatgagg aaccgcatcg ctgcctccaa gtgccgaaaa aggaagctgg 1800

agagaatcgc ccggctggag gaaaaagtga aaaccttgaa agctcagaac tcggagctgg 1860

cgtccacggc caacatgctc agggaacagg tggcacagct taaacagaaa gtcatgaacc 1920

acgttaacag tgggtgccaa ctcatgctaa cgcagcagtt gcaaacattt tgaagagaga 1980

ccgtcggggg ctgaggggca acgaagaaaa aaaataacac agagagacag acttgagaac 2040

ttgacaagtt gcgacggaga gaaaaaagaa gtgtccgaga actaaagcca agggtatcca 2100

agttggactg ggttgcgtcc tgacggcgcc cccagtgtgc acgagtggga aggacttggc 2160

gcgccctccc ttggcgtgga gccagggagc ggccgcctgc gggctgcccc gctttgcgga 2220

cgggctgtcc ccgcgcgaac ggaacgttgg acttttcgtt aacattgacc aagaactgca 2280

tggacctaac attcgatctc attcagtatt aaaggggggа gggggagggg gttacaaact 2340

gcaatagaga ctgtagattg cttctgtagt actccttaag aacacaaagc gggggggaggg 2400

ttggggaggg gcggcaggag ggaggtttgt gagagcgagg ctgagcctac agatgaactc 2460

tttctggcct gccttcgtta actgtgtatg tacatatata tatttttaa tttgatgaaa 2520

gctgattact gtcaataaac agcttcatgc ctttgtaagt tatttcttgt ttgtttgttt 2580

gggtatcctg cccagtgttg tttgtaaata agagatttgg agcactctga gtttaccatt 2640

tgtaataaag tatataattt ttttatgttt tgtttctgaa aattccagaa aggatattta 2700

agaaaatаca ataaactatt ggaaagtact cccctaacct cttttctgca tcatctgtag 2760

atactagcta tctaggtgga gttgaaagag ttaagaatgt cgattaaaat cactctcagt 2820

gcttcttact attaagcagt aaaaactgtt ctctattaga ctttagaaat aaatgtacct 2880

gatgtacctg atgctatggt caggttatac tcctcctccc ccagctatct atatggaatt 2940

gcttaccaaa ggatagtgcg atgtttcagg aggctggagg aaggggggtt gcagtggaga 3000

gggacagccc actgagaagt caaacatttc aaagtttgga ttgtatcaag tggcatgtgc 3060

tgtgaccatt tataatgtta gtagaaattt tacaataggt gcttattctc aaagcaggaa 3120

ttggtggcag attttacaaa agatgtatcc ttccaatttg gaatcttctc tttgacaatt 3180

cctagataaa aagatggcct ttgcttatga atatttataa cagcattctt gtcacaataa 3240

atgtattcaa ataccaa 3257

<210> 3
<211> 338
<212> PRT
<213> artificial sequence

<220>
<223> epidermal growth factor receptor protein opt (EGFRopt)

<400> 3

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

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile

100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
290 295 300

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
305 310 315 320

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg
325 330 335

Arg Arg

<210> 4

<400> 4
000

<210> 5
<211> 353
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot: P01876, IGHA1_HUMAN, immunoglobulin heavy constant alpha 1

<400> 5

Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
1 5 10 15

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
20 25 30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
35 40 45

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

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
65 70 75 80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
85 90 95

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
100 105 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser

```
        115                 120                 125

Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
    130                 135                 140

Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
145                 150                 155                 160

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

Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
            180                 185                 190

Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
        195                 200                 205

Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
    210                 215                 220

Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
225                 230                 235                 240

Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
                245                 250                 255

Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
            260                 265                 270

Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
        275                 280                 285

Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
    290                 295                 300

Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
305                 310                 315                 320

Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
                325                 330                 335
```

Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
340 345 350

Tyr

<210> 6
<211> 340
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01877, IGHA2_HUMAN, immunoglobulin heavy constant alpha 2

<400> 6

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

Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe
20 25 30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Asn Val
35 40 45

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

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
65 70 75 80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser Gln Asp
85 90 95

Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Pro Cys Cys His Pro
100 105 110

Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser
115 120 125

Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly
130 135 140

```
Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly
145                 150                 155                 160

Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu
                165                 170                 175

Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr Cys Thr
            180                 185                 190

Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile Thr Lys
        195                 200                 205

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

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
225                 230                 235                 240

Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln
                245                 250                 255

Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro
            260                 265                 270

Ser Gln Gly Thr Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg Val Ala
        275                 280                 285

Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val Gly His
    290                 295                 300

Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Met Ala
305                 310                 315                 320

Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu Ala Asp
                325                 330                 335

Gly Thr Cys Tyr
            340
```

<210> 7
<211> 398
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01665, GCAM_MOUSE, immunoglobulin gamma 2A chain C region

<400> 7

Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp
1 5 10 15

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

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
50 55 60

Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr
65 70 75 80

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
85 90 95

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
100 105 110

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

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
130 135 140

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
145 150 155 160

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
165 170 175

```
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
            180                 185                 190

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
        195                 200                 205

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
    210                 215                 220

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
225                 230                 235                 240

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

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
            260                 265                 270

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
        275                 280                 285

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
    290                 295                 300

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
305                 310                 315                 320

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

Glu Ala Gln Asp Gly Glu Leu Asp Gly Leu Trp Thr Thr Ile Thr Ile
            340                 345                 350

Phe Ile Ser Leu Phe Leu Leu Ser Val Cys Tyr Ser Ala Ser Val Thr
        355                 360                 365

Leu Phe Lys Val Lys Trp Ile Phe Ser Ser Val Val Glu Leu Lys Gln
    370                 375                 380

Thr Ile Ser Pro Asp Tyr Arg Asn Met Ile Gly Gln Gly Ala
```

385 390 395

<210> 8
<211> 330
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01857, IGHG1_HUMAN, immunoglobulin heavy constant gamma 1

<400> 8

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

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

```
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 9
<211> 326
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01859, IGHG2_HUMAN, immunoglobulin heavy constant gamma 2

<400> 9

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
```

210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 10
<211> 377
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01860, IGHG3_HUMAN, immunoglobulin heavy constant gamma 3

<400> 10

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

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

```
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

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

```
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340                 345                 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375
```

<210> 11
<211> 327
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01861, IGHG4, immunoglobulin heavy constant gamma 4

<400> 11

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                   10                  15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
```

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
```

```
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285


Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
    290                 295                 300


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320


Leu Ser Leu Ser Leu Gly Lys
                325
```

<210> 12
<211> 384
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01880, IGHD_HUMAN, immunoglobulin heavy constant delta

<400> 12

```
Ala Pro Thr Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys Arg
1               5                   10                  15


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


Tyr His Pro Thr Ser Val Thr Val Thr Trp Tyr Met Gly Thr Gln Ser
        35                  40                  45


Gln Pro Gln Arg Thr Phe Pro Glu Ile Gln Arg Arg Asp Ser Tyr Tyr
    50                  55                  60


Met Thr Ser Ser Gln Leu Ser Thr Pro Leu Gln Gln Trp Arg Gln Gly
65                  70                  75                  80


Glu Tyr Lys Cys Val Val Gln His Thr Ala Ser Lys Ser Lys Lys Glu
                85                  90                  95


Ile Phe Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro
            100                 105                 110
```

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

Pro Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys
    130                 135                 140

Glu Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu
145                 150                 155                 160

Cys Pro Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala
                165                 170                 175

Val Gln Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val
            180                 185                 190

Val Gly Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala Gly
        195                 200                 205

Lys Val Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser
    210                 215                 220

Asn Gly Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu
225                 230                 235                 240

Trp Asn Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser Leu
                245                 250                 255

Pro Pro Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro
            260                 265                 270

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

Ala Ser Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile
    290                 295                 300

Leu Leu Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe
305                 310                 315                 320

Ala Pro Ala Arg Pro Pro Pro Gln Pro Arg Ser Thr Thr Phe Trp Ala
                325                 330                 335
```

```
Trp Ser Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr
            340                 345                 350

Tyr Thr Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala
        355                 360                 365

Ser Arg Ser Leu Glu Val Ser Tyr Val Thr Asp His Gly Pro Met Lys
    370                 375                 380
```

<210> 13
<211> 428
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01854, IGHE_HUMAN, immunoglobulin heavy constant chain epsilon

<400> 13

```
Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys
1               5                   10                  15

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

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

Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly
    50                  55                  60

His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys
65                  70                  75                  80

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

Val Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro
            100                 105                 110

Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro
```

```
        115                 120                 125

Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr
    130                 135                 140

Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu
145                 150                 155                 160

Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser
                165                 170                 175

Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr
            180                 185                 190

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

Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro
    210                 215                 220

Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu
225                 230                 235                 240

Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser
                245                 250                 255

Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys
            260                 265                 270

Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr
        275                 280                 285

Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro
    290                 295                 300

His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro
305                 310                 315                 320

Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly
                325                 330                 335
```

```
Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro
            340                 345                 350

Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp
        355                 360                 365

Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe
    370                 375                 380

Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys
385                 390                 395                 400

Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln
                405                 410                 415

Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
            420                 425
```

<210> 14
<211> 453
<212> PRT
<213> artificial sequence

<220>
<223> Uniprot P01871, IGHM_HUMAN, immunoglobulin heavy constant mu

<400> 14

```
Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1               5                   10                  15

Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
            20                  25                  30

Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
        35                  40                  45

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

Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
65                  70                  75                  80
```

```
Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
                85                  90                  95

Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
            100                 105                 110

Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
        115                 120                 125

Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile
    130                 135                 140

Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr
145                 150                 155                 160

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

Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln
            180                 185                 190

Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln
        195                 200                 205

Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val
    210                 215                 220

Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr
225                 230                 235                 240

Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr
                245                 250                 255

Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn
            260                 265                 270

Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala
        275                 280                 285

Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr
```

290 295 300

Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg
305 310 315 320

Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro
325 330 335

Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu
340 345 350

Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg
355 360 365

Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro
370 375 380

Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val
385 390 395 400

Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala
405 410 415

His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser
420 425 430

Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr
435 440 445

Ala Gly Thr Cys Tyr
450

<210> 15
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> Spacer 1

<400> 15

Lys Pro Cys Pro Pro Cys Lys Cys Pro

1 5

<210> 16
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> linker

<400> 16

Gly Gly Gly Ser Gly
1 5

<210> 17
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> human Ig kappa signal peptide

<400> 17

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly
20

<210> 18
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> GM-CSF signal peptide

<400> 18

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
20

<210> 19

<211> 24
<212> PRT
<213> artificial sequence

<220>
<223> EGFR signal peptide

<400> 19

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala
20

<210> 20
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> human CD33 signal peptide

<400> 20

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

<210> 21
<211> 2
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(1)
<223> Wherein Gly may be repeated by an integer from 1 to 100.

<220>
<221> misc_feature
<222> (1)..(2)
<223> Wherein the sequence may be repeated by an integer from 1 to 100.

<400> 21

Gly Ser
1

<210> 22
<211> 2
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (0)..(1)
<223> Wherein Ser may be repeated by an integer from 1 to 100.

<220>
<221> misc_feature
<222> (1)..(1)
<223> Wherein Gly may be repeated by an integer from 1 to 4.

<220>
<221> misc_feature
<222> (1)..(2)
<223> Wherein The sequence may be repeated by an integer from 1 to 50.

<400> 22

Gly Ser
1

<210> 23
<211> 1
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(1)
<223> Wherein Gly can be repeated between 1 to 100.

<400> 23

Gly
1

<210> 24
<211> 2

<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(2)
<223> Wherein Gly Ala may be repeated between 1 and 100.

<400> 24

Gly Ala
1

<210> 25
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 25

Gly Gly Gly Gly
1

<210> 26
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 26

Gly Gly Gly Ser Gly
1 5

<210> 27
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(5)
<223> Wherein the sequence can be repeated between an integer of 1 and 100

<400> 27

Gly Gly Gly Ser Gly
1 5

<210> 28
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(5)
<223> Wherein the sequence can be repeated between an integer of 1 and 100.

<400> 28

Gly Gly Gly Gly Ser
1 5

<210> 29
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(4)
<223> Wherein the sequence can be repeated between an integer of 1 and 100

<400> 29

Gly Gly Gly Ser
1

<210> 30
<211> 3
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(3)
<223> Wherein the sequence can be repeated between an integer of 1 and 100

<400> 30

Gly Gly Ser
1

<210> 31
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 31

Gly Ser Gly Ser Gly Ser
1 5

<210> 32
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 32

Gly Gly Ser Gly Gly
1 5

<210> 33
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 33

Ser Gly Gly Ser Gly Gly Ser
1   5

<210> 34
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 34

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

<210> 35
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 35

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

<210> 36
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 36

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

<210> 37
<211> 19

<212> PRT
<213> artificial sequence

<220>
<223> P2A

<400> 37

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 38
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> T2A

<400> 38

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

Gly Pro

<210> 39
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> F2A

<400> 39

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 40
<211> 20

<212> PRT
<213> artificial sequence

<220>
<223> E2A

<400> 40

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> 41
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Furin Cleavage Site

<400> 41

Arg Ala Lys Arg
1

<210> 42
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<220>
<221> misc_feature
<222> (1)..(5)
<223> Wherein the sequence can be repeated by a positive integer equal to, or greater than 1

<400> 42

Gly Gly Gly Gly Ser
1 5

<210> 43
<211> 20
<212> PRT

<213> artificial sequence

<220>
<223> Linker

<400> 43

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

Gly Gly Gly Ser
20

<210> 44
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> R12 VH

<400> 44

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

Ser Leu Thr Leu Ser Cys Lys Ala Ser Gly Phe Asp Phe Ser Ala Tyr
20 25 30

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

Ala Thr Ile Tyr Pro Ser Ser Gly Lys Thr Tyr Tyr Ala Thr Trp Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Gln Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Thr Ala Ala Asp Arg Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Asp Ser Tyr Ala Asp Asp Gly Ala Leu Phe Asn Ile Trp Gly
100 105 110

Pro Gly Thr Leu Val Thr Ile Ser Ser

115 120

<210> 45
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> R12 VH CDR1

<400> 45

Ala Tyr Tyr Met Ser
1 5

<210> 46
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> R12 VH CDR2

<400> 46

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

Gly

<210> 47
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> R12 VH CDR3

<400> 47

Asp Ser Tyr Ala Asp Asp Gly Ala Leu Phe Asn Ile
1 5 10

<210> 48
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> R12 VL

<400> 48

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

Pro Ala Lys Ile Thr Cys Thr Leu Ser Ser Ala His Lys Thr Asp Thr
20 25 30

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

Gln Val Gln Ser Asp Gly Ser Tyr Thr Lys Arg Pro Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Ile Ile Pro
65 70 75 80

Ser Val Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Asp Tyr
85 90 95

Ile Gly Gly Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Thr Gly
100 105 110

<210> 49
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> R12 VL CDR1

<400> 49

Thr Leu Ser Ser Ala His Lys Thr Asp Thr Ile Asp
1 5 10

<210> 50
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> R12 VL CDR2

<400> 50

Gly Ser Tyr Thr Lys Arg Pro
1 5

<210> 51
<211> 9
<212> PRT
<213> artificial sequence

<220>
<223> R12 VL CDR3

<400> 51

Gly Ala Asp Tyr Ile Gly Gly Tyr Val
1 5

<210> 52
<211> 248
<212> PRT
<213> artificial sequence

<220>
<223> R12 scFv

<400> 52

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

Ser Leu Thr Leu Ser Cys Lys Ala Ser Gly Phe Asp Phe Ser Ala Tyr
20 25 30

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

Ala Thr Ile Tyr Pro Ser Ser Gly Lys Thr Tyr Tyr Ala Thr Trp Val
50 55 60

Asn Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Gln Asn Thr Val Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Thr Ala Ala Asp Arg Ala Thr Tyr Phe Cys
85 90 95

```
Ala Arg Asp Ser Tyr Ala Asp Asp Gly Ala Leu Phe Asn Ile Trp Gly
            100                 105                 110

Pro Gly Thr Leu Val Thr Ile Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro
    130                 135                 140

Ser Val Ser Ala Ala Leu Gly Ser Pro Ala Lys Ile Thr Cys Thr Leu
145                 150                 155                 160

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

Gly Glu Ala Pro Arg Tyr Leu Met Gln Val Gln Ser Asp Gly Ser Tyr
            180                 185                 190

Thr Lys Arg Pro Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly
        195                 200                 205

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

Asp Tyr Tyr Cys Gly Ala Asp Tyr Ile Gly Gly Tyr Val Phe Gly Gly
225                 230                 235                 240

Gly Thr Gln Leu Thr Val Thr Gly
                245
```

<210> 53
<211> 42
<212> PRT
<213> artificial sequence

<220>
<223> 4-1BB costimulatory domain

<400> 53

```
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
35 40

<210> 54
<211> 28
<212> PRT
<213> artificial sequence

<220>
<223> CD28 transmembrane domain

<400> 54

Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
1 5 10 15

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 55
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> CD3zeta activating domain

<400> 55

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> 56
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> p2A

<400> 56

Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
1 5 10 15

Val Glu Glu Asn Pro Gly Pro
20

<210> 57
<211> 1198
<212> PRT
<213> artificial sequence

<220>
<223> c-jun-anti-ROR1 CAR

<400> 57

Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
1 5 10 15

Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
20 25 30

Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
35 40 45

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
50 55 60

```
Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
65                  70                  75                  80

Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
                85                  90                  95

Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
            100                 105                 110

Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
        115                 120                 125

Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
    130                 135                 140

Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
145                 150                 155                 160

Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
                165                 170                 175

Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
            180                 185                 190

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
        195                 200                 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
    210                 215                 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225                 230                 235                 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
                245                 250                 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
            260                 265                 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
```

275 280 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
290 295 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe Gly Ser Gly Ala Thr
325 330 335

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
340 345 350

Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile
355 360 365

Ser Gly Ala Tyr Gly Gln Glu Gln Leu Val Glu Ser Gly Gly Arg Leu
370 375 380

Val Thr Pro Gly Gly Ser Leu Thr Leu Ser Cys Lys Ala Ser Gly Phe
385 390 395 400

Asp Phe Ser Ala Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys
405 410 415

Gly Leu Glu Trp Ile Ala Thr Ile Tyr Pro Ser Ser Gly Lys Thr Tyr
420 425 430

Tyr Ala Thr Trp Val Asn Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala
435 440 445

Gln Asn Thr Val Asp Leu Gln Met Asn Ser Leu Thr Ala Ala Asp Arg
450 455 460

Ala Thr Tyr Phe Cys Ala Arg Asp Ser Tyr Ala Asp Asp Gly Ala Leu
465 470 475 480

Phe Asn Ile Trp Gly Pro Gly Thr Leu Val Thr Ile Ser Ser Gly Gly
485 490 495

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val
            500                 505                 510

Leu Thr Gln Ser Pro Ser Val Ser Ala Ala Leu Gly Ser Pro Ala Lys
        515                 520                 525

Ile Thr Cys Thr Leu Ser Ser Ala His Lys Thr Asp Thr Ile Asp Trp
    530                 535                 540

Tyr Gln Gln Leu Gln Gly Glu Ala Pro Arg Tyr Leu Met Gln Val Gln
545                 550                 555                 560

Ser Asp Gly Ser Tyr Thr Lys Arg Pro Gly Val Pro Asp Arg Phe Ser
                565                 570                 575

Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Ile Ile Pro Ser Val Gln
            580                 585                 590

Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Asp Tyr Ile Gly Gly
        595                 600                 605

Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Thr Gly Gly Gly Gly
    610                 615                 620

Ser Gly Lys Pro Cys Pro Pro Cys Lys Cys Pro Met Phe Trp Val Leu
625                 630                 635                 640

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
                645                 650                 655

Ala Phe Ile Ile Phe Trp Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr
            660                 665                 670

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu
        675                 680                 685

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
    690                 695                 700

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
```

```
705                 710                 715                 720

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                725                 730                 735

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            740                 745                 750

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        755                 760                 765

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    770                 775                 780

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
785                 790                 795                 800

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                805                 810                 815

Arg Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
            820                 825                 830

Glu Glu Asn Pro Gly Pro Met Leu Leu Leu Val Thr Ser Leu Leu Leu
        835                 840                 845

Cys Glu Leu Pro His Pro Ala Phe Leu Leu Ile Pro Arg Lys Val Cys
    850                 855                 860

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
865                 870                 875                 880

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
                885                 890                 895

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
            900                 905                 910

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
        915                 920                 925
```

```
Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
    930                 935                 940

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
945                 950                 955                 960

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
                965                 970                 975

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
            980                 985                 990

Asn Lys Asn Leu Cys Tyr Ala Asn  Thr Ile Asn Trp Lys  Lys Leu Phe
        995                 1000                1005

Gly Thr  Ser Gly Gln Lys Thr  Lys Ile Ile Ser Asn  Arg Gly Glu
    1010                1015                1020

Asn Ser  Cys Lys Ala Thr Gly  Gln Val Cys His Ala  Leu Cys Ser
    1025                1030                1035

Pro Glu  Gly Cys Trp Gly Pro  Glu Pro Arg Asp Cys  Val Ser Cys
    1040                1045                1050

Arg Asn  Val Ser Arg Gly Arg  Glu Cys Val Asp Lys  Cys Asn Leu
    1055                1060                1065

Leu Glu  Gly Glu Pro Arg Glu  Phe Val Glu Asn Ser  Glu Cys Ile
    1070                1075                1080

Gln Cys  His Pro Glu Cys Leu  Pro Gln Ala Met Asn  Ile Thr Cys
    1085                1090                1095

Thr Gly  Arg Gly Pro Asp Asn  Cys Ile Gln Cys Ala  His Tyr Ile
    1100                1105                1110

Asp Gly  Pro His Cys Val Lys  Thr Cys Pro Ala Gly  Val Met Gly
    1115                1120                1125

Glu Asn  Asn Thr Leu Val Trp  Lys Tyr Ala Asp Ala  Gly His Val
```

1130 1135 1140

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro
1145 1150 1155

Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile
1160 1165 1170

Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val Val Ala
1175 1180 1185

Leu Gly Ile Gly Leu Phe Met Arg Arg Arg
1190 1195

<210> 58
<211> 4022
<212> DNA
<213> artificial sequence

<220>
<223> DNA construct

<400> 58
tgaaagaccc cacctgtagg tttggcaagc taggatcaag gttaggaaca gagagacagc 60

agaatatggg ccaaacagga tatctgtggt aagcagttcc tgccccggct cagggccaag 120

aacagttgga acagcagaat atgggccaaa caggatatct gtggtaagca gttcctgccc 180

cggctcaggg ccaagaacag atggtcccca gatgcggtcc cgccctcagc agtttctaga 240

gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg ccttatttga 300

actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata 360

aaagagccca caacccctca ctcggcgcga tcagaacctc ttacgagtcg gctagcgccg 420

ccaccatgac agccaagatg gaaaccacat tctacgacga cgccctgaac gcctcattcc 480

tgccttctga gagcggacct tacggctaca gcaatcctaa gatcctgaaa cagagcatga 540

cccttaacct ggctgatcct gttggaagcc tgaaacctca cctgagagcc aaaaacagcg 600

acctgctcac cagccctgat gtgggcctgc tgaagctggc ctctccagag ctggaacggc 660

tgatcatcca gagcagcaac ggccacatca caaccacccc taccctaca caattcctgt 720

gccctaagaa cgtgaccgac gagcaggagg gcttcgccga aggctttgtg cgggccctgg 780

cagaactgca ctctcagaac accctgccta gcgtgacctc cgccgcccag cctgtcaacg 840

gcgccggaat ggtggcccct gccgtggctt ctgtggccgg cggcagcggc agcggcggat 900

tcagcgcctc tctgcactct gagcctcctg tctacgccaa tctgtctaat ttcaaccccg 960

gagccctgtc cagcggcggc ggagctccta gctacggcgc tgctggactg gccttccccg 1020

cccagcccca gcaacagcag cagcctccac accacctgcc ccagcagatg cccgtgcagc 1080

accctagact gcaggccctg aaggaagaac cccaaacagt gcctgagatg cctggcgaga 1140

cacctccact gagccccatc gacatggaaa gccaggagcg gatcaaggcc gagagaaaga 1200

gaatgcggaa cagaatcgcc gctagcaagt gcagaaagcg gaagctggaa agaatcgcca 1260

gactggaaga gaaggtgaag accctgaaag cccaaaatag cgagctggcc agcaccgcca 1320

acatgctgcg ggaacaggtg gcccagctga agcagaaggt gatgaaccac gtgaactctg 1380

gttgtcagct gatgctgacc cagcagctcc agaccttcgg ctccggtgca acgaacttca 1440

gcctgctgaa gcaggccgga gatgttgagg aaaatccagg tcccatggtc ttgcagactc 1500

aagtatttat atccctttg ctctggatct ctggagctta cggccaggaa cagctcgtcg 1560

aaagcggcgg cagactggtg acacctggcg gcagcctgac cctgagctgc aaggccagcg 1620

gcttcgactt cagcgcctac tacatgagct gggtccgcca ggcccctggc aagggactgg 1680

aatggatcgc caccatctac cccagcagcg gcaagaccta ctacgccacc tgggtgaacg 1740

gacggttcac catctccagc gacaacgccc agaacaccgt ggacctgcag atgaacagcc 1800

tgacagccgc cgaccgggcc acctactttt gcgctcggga cagctacgcc gacgacggcg 1860

ccctgttcaa catctggggc cctggcaccc tggtgacaat ctctagcggc ggaggcggat 1920

ctggtggcgg aggaagtggc ggcggaggat ctgagctggt gctgacccag agcccctctg 1980

tgtctgctgc cctgggaagc cctgccaaga tcacctgtac cctgagcagc gcccacaaga 2040

ccgacaccat cgactggtat cagcagctgc agggcgaggc ccccagatac ctgatgcagg 2100

tgcagagcga cggcagctac accaagaggc caggcgtgcc cgacaggttc agcggatcta 2160

gctctggcgc cgaccgctac ctgatcatcc ccagcgtgca ggccgatgac gaggccgatt 2220

actactgtgg cgccgactac atcggcggct acgtgttcgg cggaggcacc cagctgaccg 2280

tgaccggtgg cggaggttca ggcaaaccgt gccctccgtg caagtgtcct atgttctggg 2340

tgctggtggt ggtcggaggc gtgctggcct gctacagcct gctggtcacc gtggccttca 2400

tcatcttttg ggtgaaacgg ggcagaaaga aactcctgta tatattcaaa caaccattta 2460

tgagaccagt acaaactact caagaggaag atggctgtag ctgccgattt ccagaagaag 2520

aagaaggagg atgtgaactg cgggtgaagt tcagcagaag cgccgacgcc cctgcctacc 2580

agcagggcca gaatcagctg tacaacgagc tgaacctggg cagaagggaa gagtacgacg 2640

tcctggataa gcggagaggc cgggaccctg agatgggcgg caagcctcgg cggaagaacc 2700

cccaggaagg cctgtataac gaactgcaga aagacaagat ggccgaggcc tacagcgaga 2760

tcggcatgaa gggcgagcgg aggcggggca agggccacga cggcctgtat cagggcctgt 2820

ccaccgccac caaggatacc tacgacgccc tgcacatgca ggccctgccc ccaaggtccg 2880

gagccactaa cttctccctg ttgaaacaag caggggatgt cgaagagaat cccgggccaa 2940

tgcttctcct ggtgacaagc cttctgctct gtgaattacc acacccagca ttcctcctga 3000

tcccacgcaa agtgtgcaac ggaataggta ttggtgaatt taaggactca ctctccataa 3060

atgctacgaa tattaaacac ttcaaaaact gcacctccat cagtggcgat ctccacatcc 3120

tgccggtggc atttaggggt gactccttca cacatactcc tcctctggac ccacaagaac 3180

tggatattct gaaaaccgta aaggaaatca cagggttttt gctgattcaa gcttggcctg 3240

aaaacaggac ggacctccat gcctttgaga acctagaaat catacgcggc aggaccaagc 3300

agcatggaca gttttctctt gctgtcgtga gcctgaacat aacatccttg ggattacgct 3360

ccctcaagga gataagtgat ggagatgtga taatttcagg aaacaaaaat ttgtgctatg 3420

caaatacaat aaactggaaa aaactgtttg ggacctccgg ccagaaaacc aaaattataa 3480

gcaacagagg cgaaaacagc tgcaaggcca caggccaggt ctgccatgcc ttgtgctccc 3540

ccgagggctg ctggggcccg gagcccaggg attgcgtgtc ttgccggaat gtcagccgag 3600

gcagggaatg cgtggacaag tgcaaccttc tggaaggcga gccaagggag tttgtggaga 3660

actctgagtg catacagtgc cacccagagt gcctgcctca ggccatgaac atcacctgca 3720

caggacgggg accagacaac tgtatccagt gtgcccacta cattgacggc ccccactgcg 3780

tcaagacctg cccggcagga gtcatgggag aaaacaacac cctggtctgg aagtacgcag 3840

acgccggcca tgtgtgccac ctgtgccatc caaactgcac ctacggatgc actgggccag 3900

gtcttgaagg ctgtccaacg aacgggccta agatcccgtc catcgccact gggatggtgg 3960

gggccctcct cttgctgctg gtggtggccc tggggatcgg cctcttcatg cgccgaaggt 4020

ga 4022

<210> 59
<211> 352
<212> PRT
<213> artificial sequence

<220>
<223> c-Jun after P2A cleavage

<400> 59

Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
1 5 10 15

Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
20 25 30

Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
35 40 45

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
50 55 60

Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
65 70 75 80

Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
85 90 95

Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
100 105 110

Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
115 120 125

Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
130 135 140

Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
145 150 155 160

Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe

```
                165                 170                 175

Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
            180                 185                 190

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
        195                 200                 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
    210                 215                 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225                 230                 235                 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
                245                 250                 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
            260                 265                 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
        275                 280                 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
    290                 295                 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
305                 310                 315                 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe Gly Ser Gly Ala Thr
                325                 330                 335

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
            340                 345                 350
```

<210> 60
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> hIgK after P2A cleavage

<400> 60

Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile
1 5 10 15

Ser Gly Ala Tyr Gly
20

<210> 61
<211> 133
<212> PRT
<213> artificial sequence

<220>
<223> CD3z after P2A cleavage

<400> 61

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

Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
115 120 125

Glu Asn Pro Gly Pro

130

<210> 62
<211> 23
<212> PRT
<213> artificial sequence

<220>
<223> GMCSFR-alpha-SP after P2A cleavage

<400> 62

Pro Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His
1 5 10 15

Pro Ala Phe Leu Leu Ile Pro
20

<210> 63
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> Linker

<400> 63

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

Gly Ser

<210> 64
<211> 386
<212> DNA
<213> artificial sequence

<220>
<223> MND promotor

<400> 64
tgaaagaccc cacctgtagg tttggcaagc taggatcaag gttaggaaca gagagacagc 60

agaatatggg ccaaacagga tatctgtggt aagcagttcc tgccccggct cagggccaag 120

aacagttgga acagcagaat atgggccaaa caggatatct gtggtaagca gttcctgccc 180

cggctcaggg ccaagaacag atggtcccca gatgcggtcc cgccctcagc agtttctaga 240

gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg ccttatttga 300

actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata 360

aaagagccca caacccctca ctcggc 386