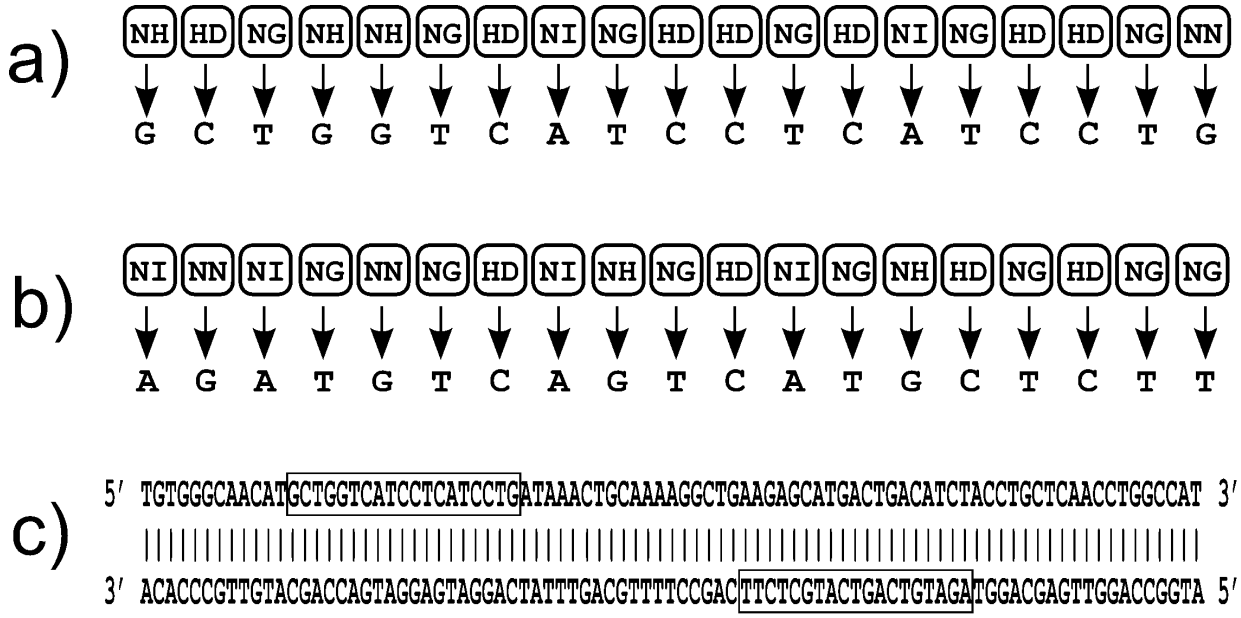

a)
NH HD NG NH NH NG HD NI NG HD HD NG HD NI NG HD HD NG NN
G C T G G T C A T C C T C A T C C T G
b)
NI NN NI NG NN NG HD NI NH NG HD NI NG NH HD NG HD NG NG
A G A T G T C A G T C A T G C T C T T
c)
5′ TGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCAT 3′
3′ ACACCCGTTGTACGACCAGTAGGAGTAGGACTATTTGACGTTTTCCGACTTCTCGTACTGACTGTAGATGGACGAGTTGGACCGGTA 5′

FIG. 1


100
80
60
40
20
0
% CCR5-negative
2x5µg plasmid DNA
2x10µg plasmid DNA
mock (pUC)
Mco-TALEN
Uco-TALEN

FIG. 2

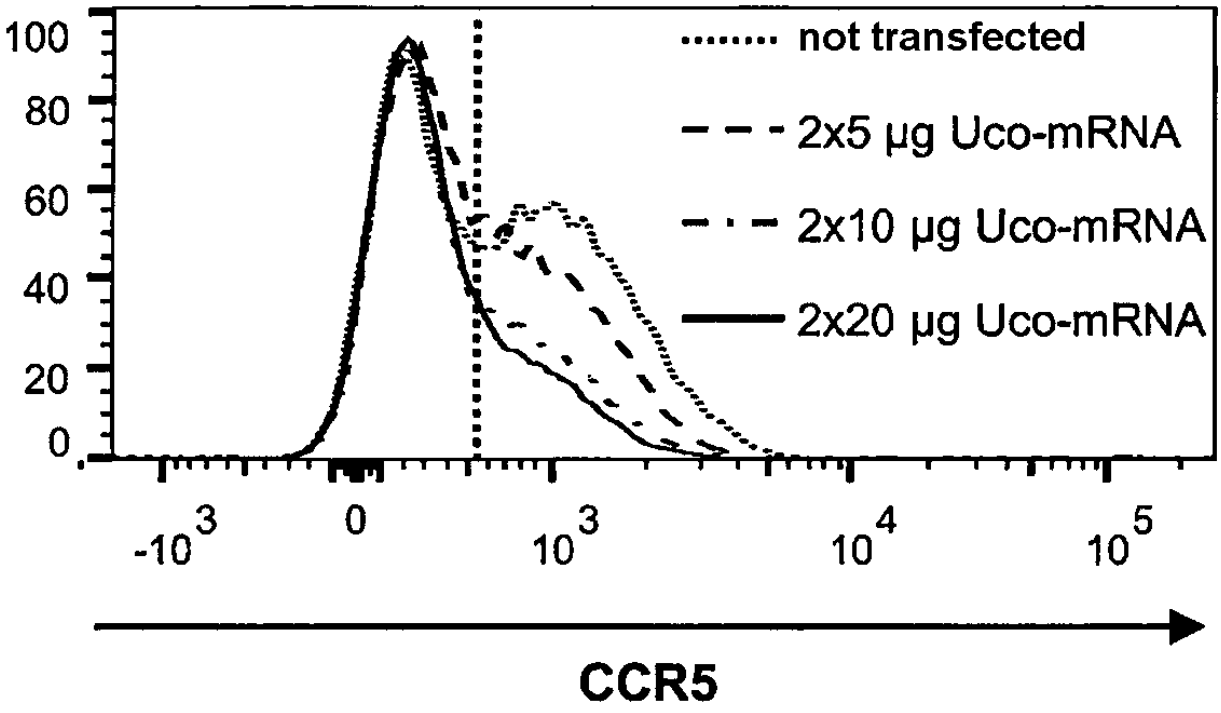

100
80
60
40
20
0
not transfected
2x5 µg Uco-mRNA
2x10 µg Uco-mRNA
2x20 µg Uco-mRNA
-10^3
0
10^3
10^4
10^5
CCR5

FIG. 3a

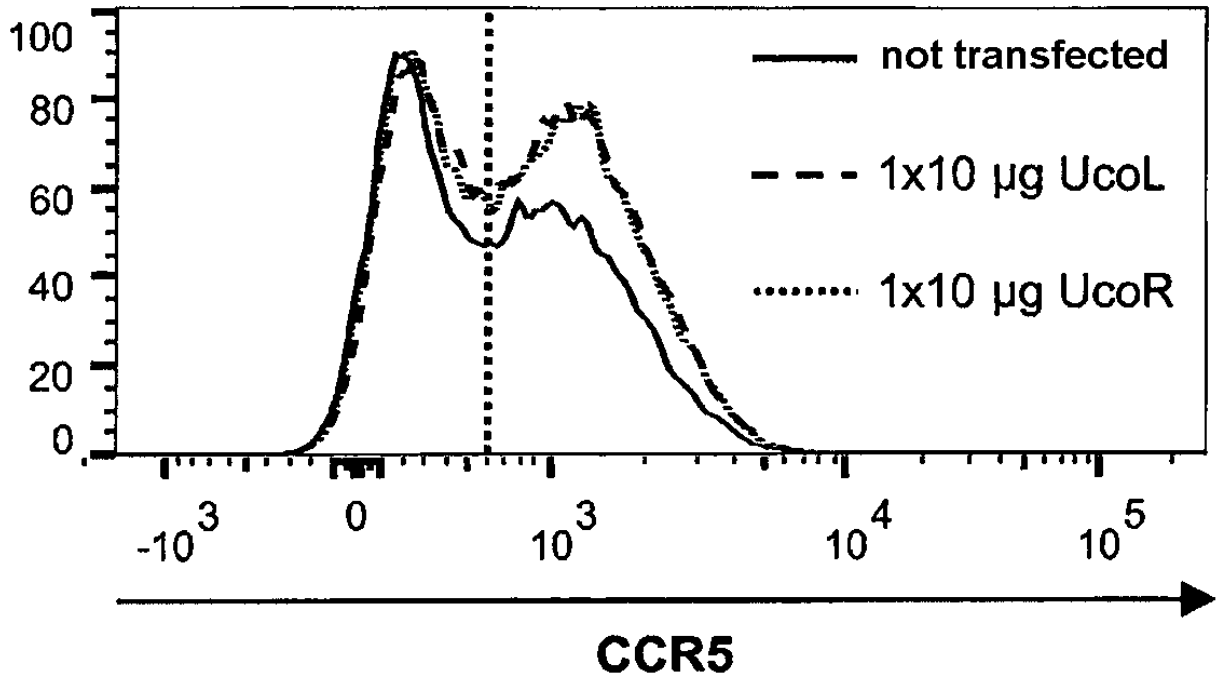

100
80
60
40
20
0
not transfected
1x10 µg UcoL
1x10 µg UcoR
-10^3
0
10^3
10^4
10^5
CCR5

FIG. 3b

```
WT  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#1  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#2  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#3  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#4  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#5  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#6  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#7  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#8  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#9  TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAAA-------GGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#10 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTAA----------GGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#11 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAA----------CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#12 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATAAAC----------GCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#13 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAA----------ACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#14 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCAGATG----------ACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#15 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATGCATG----------ACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
#16 TTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCA----------GATAAACT--GCCATCTCTGACCTG
#17 TTGGTTTTGTGGGCAACANNCTGGTCGTCATCATG----------ACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTG
```

FIG. 3c

SEQUENCE LISTING

<110> Universitätsklinikum Hamburg-Eppendorf (UKE)

<120> TAL-Effektornuklease zum gezielten Knockout des HIV-Korezeptors CCR5

<130> PAT 1473 PCT

<150> DE102014106327.9
<151> 2014-05-07

<160> 18

<170> BiSSAP 1.3

<210> 1
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<212> DNA
<213> Homo sapiens

<400> 1
gctggtcatc ctcatcctg 19

<210> 2
<211> 19
<212> DNA
<213> Homo sapiens

<400> 2
agatgtcagt catgctctt 19

<210> 3
<211> 1071
<212> PRT
<213> Artificial Sequence

<220>
<223> CCR5-Uco-L

<400> 3

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

```
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
    210                 215                 220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
        275                 280                 285
Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
305                 310                 315                 320
Ile Ala Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
    370                 375                 380
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
            420                 425                 430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
        435                 440                 445
Leu Thr Pro Glu Gln Val Val Ala Ile Val Ser Asn Gly Gly Gly Lys
    450                 455                 460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
465                 470                 475                 480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
                485                 490                 495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
        515                 520                 525
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
545                 550                 555                 560
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
            580                 585                 590
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620
Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
                645                 650                 655
Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
    690                 695                 700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
705                 710                 715                 720
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
                725                 730                 735
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            740                 745                 750
```

```
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
        755                 760                 765
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    770                 775                 780
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
785                 790                 795                 800
Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg
                805                 810                 815
Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu
            820                 825                 830
Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu
        835                 840                 845
Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu
    850                 855                 860
Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu
865                 870                 875                 880
Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His
                885                 890                 895
Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg
            900                 905                 910
Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr
        915                 920                 925
Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr
    930                 935                 940
Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala
945                 950                 955                 960
Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln
                965                 970                 975
Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn
            980                 985                 990
Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu
        995                 1000                1005
Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg
    1010                1015                1020
Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu
1025                1030                1035                1040
Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu
                1045                1050                1055
Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser
            1060                1065                1070

<210> 4
<211> 1071
<212> PRT
<213> Artificial Sequence

<220>
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<400> 4
Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
1                   5                  10                  15
Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
            20                  25                  30
Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
        35                  40                  45
Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
    50                  55                  60
Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65                  70                  75                  80
Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
                85                  90                  95
Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
            100                 105                 110
Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
        115                 120                 125
Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
    130                 135                 140
```

```
Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val
145                 150                 155                 160
Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
                165                 170                 175
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys
            180                 185                 190
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
        195                 200                 205
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly
    210                 215                 220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225                 230                 235                 240
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
                245                 250                 255
Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
            260                 265                 270
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
        275                 280                 285
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
    290                 295                 300
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
305                 310                 315                 320
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
                325                 330                 335
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
            340                 345                 350
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
        355                 360                 365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
    370                 375                 380
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
385                 390                 395                 400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
                405                 410                 415
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
            420                 425                 430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
        435                 440                 445
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn His Gly Gly Lys
    450                 455                 460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
465                 470                 475                 480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
                485                 490                 495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His
        515                 520                 525
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
545                 550                 555                 560
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
            580                 585                 590
Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620
Val Ala Ile Ala Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
                645                 650                 655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685
```

```
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
    690                 695                 700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
705                 710                 715                 720
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
                725                 730                 735
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            740                 745                 750
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
        755                 760                 765
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
    770                 775                 780
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
785                 790                 795                 800
Gly Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg
                805                 810                 815
Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu
            820                 825                 830
Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu
        835                 840                 845
Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu
    850                 855                 860
Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu
865                 870                 875                 880
Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His
                885                 890                 895
Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg
            900                 905                 910
Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr
        915                 920                 925
Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr
    930                 935                 940
Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala
945                 950                 955                 960
Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln
                965                 970                 975
Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn
            980                 985                 990
Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu
        995                 1000                1005
Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg
    1010                1015                1020
Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu
1025                1030                1035                1040
Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu
                1045                1050                1055
Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser
            1060                1065                1070

<210> 5
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> TALEN repeat

<220>
<221> SITE
<222> 4
<223> Xaa = Any amino acid, or E, Q, D or A

<220>
<221> SITE
<222> 10
<223> Xaa = Any amino acid, or A or V

<220>
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<221> SITE
<222> 12..13
<223> Repeat variable diresidue (RVD)

<220>
<221> SITE
<222> 32
<223> Xaa = Any amino acid, or A or D

<400> 5
Leu Thr Pro Xaa Gln Val Val Ala Ile Xaa Ser Xaa Xaa Gly Gly Lys
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Xaa
20 25 30
His Gly

<210> 6
<211> 34
<212> PRT
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<220>
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<220>
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<222> 12..13
<223> Repeat variable diresidue (RVD)

<400> 6
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys
1 5 10 15
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30
His Gly

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

<220>
<223> TALEN Repeat

<220>
<221> SITE
<222> 12..13
<223> Repeat variable diresidue (RVD)

<400> 7
Leu Thr Pro Gln Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys
1 5 10 15
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
20 25 30
His Gly

<210> 8
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> TALEN Repeat

<220>

<221> SITE
<222> 12..13
<223> Repeat variable diresidue (RVD)

<400> 8
Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys
1   5   10   15
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
            20   25   30
His Gly

<210> 9
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> TALEN Repeat

<220>
<221> SITE
<222> 12..13
<223> Repeat variable diresidue (RVD)

<400> 9
Leu Thr Pro Ala Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys
1   5   10   15
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
            20   25   30
His Gly

<210> 10
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> TALEN Repeat

<220>
<221> SITE
<222> 12..13
<223> Repeat variable diresidue (RVD)

<400> 10
Leu Thr Pro Glu Gln Val Val Ala Ile Val Ser Xaa Xaa Gly Gly Lys
1   5   10   15
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            20   25   30
His Gly

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<211> 1059
<212> DNA
<213> Homo sapiens

<220>
<223> hCCR5 DNA

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ttcatctttg gttttgtggg caacatgctg gtcatcctca tcctgataaa ctgcaaaagg 180

ctgaagagca tgactgacat ctacctgctc aacctggcca tctctgacct gtttttcctt 240

cttactgtcc ccttctgggc tcactatgct gccgcccagt gggactttgg aaatacaatg 300

tgtcaactct tgacagggct ctattttata ggcttcttct ctggaatctt cttcatcatc 360

ctcctgacaa tcgataggta cctggctgtc gtccatgctg tgtttgcttt aaaagccagg 420

acggtcacct ttggggtggt gacaagtgtg atcacttggg tggtggctgt gtttgcgtct 480

ctcccaggaa tcatctttac cagatctcaa aaagaaggtc ttcattacac ctgcagctct 540

cattttccat acagtcagta tcaattctgg aagaatttcc agacattaaa gatagtcatc 600

ttggggctgg tcctgccgct gcttgtcatg gtcatctgct actcgggaat cctaaaaact 660

ctgcttcggt gtcgaaatga gaagaagagg cacagggctg tgaggcttat cttcaccatc 720

atgattgttt attttctctt ctgggctccc tacaacattg tccttctcct gaacaccttc 780

caggaattct ttggcctgaa taattgcagt agctctaaca ggttggacca agctatgcag 840

gtgacagaga ctcttgggat gacgcactgc tgcatcaacc ccatcatcta tgcctttgtc 900

ggggagaagt tcagaaacta cctcttagtc ttcttccaaa agcacattgc caaacgcttc 960

tgcaaatgct gttctatttt ccagcaagag gctcccgagc gagcaagctc agtttacacc 1020

cgatccactg gggagcagga aatatctgtg ggcttgtga 1059

<210> 12
<211> 198
<212> PRT
<213> Planomicrobium okeanokoites

<220>
<223> FokI cleavage domain

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Lys Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala
20 25 30
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35 40 45
Phe Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg
50 55 60
Lys Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly
65 70 75 80
Val Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile
85 90 95
Gly Gln Ala Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg
100 105 110
Asn Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser
115 120 125
Val Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn
130 135 140
Tyr Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly
145 150 155 160
Ala Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys
165 170 175
Ala Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly
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<212> PRT
<213> Artificial Sequence

<220>
<223> CCR5-Mco-L

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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
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Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
35 40 45
Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
50 55 60
Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65 70 75 80
Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
85 90 95
Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
100 105 110
Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
115 120 125
Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
130 135 140
Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val
145 150 155 160
Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
165 170 175
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
180 185 190
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
195 200 205
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
210 215 220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225 230 235 240
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
245 250 255
Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
260 265 270
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
275 280 285
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
290 295 300
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
305 310 315 320
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
325 330 335
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
340 345 350
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
355 360 365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
370 375 380
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
385 390 395 400
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
405 410 415
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
420 425 430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
435 440 445
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
450 455 460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala

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465                 470                 475                 480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly
                485                 490                 495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
545                 550                 555                 560
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
            580                 585                 590
Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
                645                 650                 655
Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
    690                 695                 700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
705                 710                 715                 720
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
                725                 730                 735
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            740                 745                 750
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
        755                 760                 765
Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp
    770                 775                 780
Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys
785                 790                 795                 800
Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His
                805                 810                 815
Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr
            820                 825                 830
Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu Glu Glu
        835                 840                 845
Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His Glu Tyr
    850                 855                 860
Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg Ile Leu
865                 870                 875                 880
Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr Arg Gly
                885                 890                 895
Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr Thr Val
            900                 905                 910
Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala Tyr Ser
        915                 920                 925
Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln Arg Tyr
    930                 935                 940
Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn Glu Trp
945                 950                 955                 960
Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu Phe Val
                965                 970                 975
Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg Leu Asn
            980                 985                 990
His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu Leu Leu
        995                 1000                1005
Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu Glu Val
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1025 1030 1035

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<211> 1037
<212> PRT
<213> Artificial Sequence

<220>
<223> CCR5-Mco-R

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

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        435                 440                 445
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
    450                 455                 460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
465                 470                 475                 480
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
                485                 490                 495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
            500                 505                 510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
        515                 520                 525
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
    530                 535                 540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala
545                 550                 555                 560
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
                565                 570                 575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
            580                 585                 590
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
        595                 600                 605
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
    610                 615                 620
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val
625                 630                 635                 640
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
                645                 650                 655
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
            660                 665                 670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
        675                 680                 685
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
    690                 695                 700
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
705                 710                 715                 720
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
                725                 730                 735
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
            740                 745                 750
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
        755                 760                 765
Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp
    770                 775                 780
Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys
785                 790                 795                 800
Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His
                805                 810                 815
Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr
            820                 825                 830
Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu Glu Glu
        835                 840                 845
Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His Glu Tyr
    850                 855                 860
Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg Ile Leu
865                 870                 875                 880
Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr Arg Gly
                885                 890                 895
Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr Thr Val
            900                 905                 910
Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala Tyr Ser
        915                 920                 925
Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln Arg Tyr
    930                 935                 940
Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn Glu Trp
945                 950                 955                 960
Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu Phe Val
                965                 970                 975
Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg Leu Asn
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980 985 990
His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu Leu Leu
995 1000 1005
Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu Glu Val
1010 1015 1020
Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser
1025 1030 1035

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<212> DNA
<213> Homo sapiens

<400> 15
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<210> 16
<211> 18
<212> PRT
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Thr Thr

<210> 17
<211> 3788
<212> RNA
<213> Artificial Sequence

<220>
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ccagcagccg uagauuugag aacuuuggga uauucacagc agcagcagga aaagaucaag 180

cccaaaguga ggucgacagu cgcgcagcau cacgaagcgc ugguggguca uggguuuaca 240

caugcccaca ucguagccuu gucgcagcac ccugcagccc uuggcacggu cgccgucaag 300

uaccaggaca ugauugcggc guugccggaa gccacacaug aggcgaucgu cgguguggggg 360

aaacagugga gcggagcccg agcgcuugag gcccuguuga cggucgcggg agagcugaga 420

gggccucccc uucagcugga cacgggccag uugcugaaga ucgcgaagcg gggaggaguc 480

acggcggucg aggcggugca cgcguggcgc aaugcgcuca cgggagcacc ccucaaccug 540

accccagagc aggucguggc aauugcgagc aaccacgggg gaaagcaggc acucgaaacc 600

guccagaggu ugcugccugu gcugugccaa gcgcacggac uuacgccaga gcaggucgug 660

gcaauugcga gccaugacgg gggaaagcag gcacucgaaa ccguccagag guugcugccu 720

gugcugugcc aagcgcacgg acuaacccca gagcaggucg uggcaauugc gagcaacgga 780

gggggaaagc aggcacucga aaccguccag agguugcugc cugugcugug ccaagcgcac 840

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gaaaccgucc agagguugcu gccugugcug ugccaagcgc acggccugac cccagagcag 960

gucguggcaa uugcgagcaa ccacggggga aagcaggcac ucgaaaccgu ccagagguug 1020

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gugagcaacg gagggggaaa gcaggcacuc gaaaccgucc agagguugcu gccugugcug 1440

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gugcugugcc aagcgcacgg ccucacccca gagcaggucg uggcaauugc gagccaugac 1800

gggggaaagc aggcacucga aaccguccag agguugcugc cugugcugug ccaagcgcac 1860

ggacuuacgc cagagcaggu cguggcaauu gcgagcaaca ucgggggaaa gcaggcacuc 1920

gaaaccgucc agagguugcu gccugugcug ugccaagcgc acggacuaac cccagagcag 1980

gucguggcaa uugcgagcaa cggaggggga aagcaggcac ucgaaaccgu ccagagguug 2040

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caugacgggg gaaagcaggc acucgaaacc guccagaggu ugcugccugu gcugugccaa 2160

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gcauccaaca acgggggcag acccgcacug gagucaaucg uggcccagcu uucgaggccg 2460

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acgaaagccu acagcggugg guacaaucuu cccaucgggc aggcagauga gaugcaacgu 2940

uaugucgaag aaaaucagac caggaacaaa cacaucaauc caaaugagug guggaaagug 3000

uauccuucau cagugaccga guuuaaguuu uuguuugucu cugggcauuu caaaggcaac 3060

uauaaggccc agcucacacg guugaaucac auuacgaacu gcaauggugc gguuuugucc 3120

guagaggaac ugcucauugg uggagaaaug aucaaagcgg gaacucugac acuggaagaa 3180

gucagacgca aguuuaacaa uggcgagauc aauuuccgcu cauaaaaaau cagccucgac 3240

ugugccuucu aguugccagc caucuguugu uugccccucc cccgugccuu ccuugacccu 3300

ggaaggugcc acucccacug uccuuuccua auaaaaugag gaaauugcau cacaacacuc 3360

aacccuaucu cggucuauuc uuuugauuua uaagggauuu ugccgauuuc ggccuauugg 3420

uuaaaaaaug agcugauuua acaaaaauuu aacgcgaauu aauucugugg aauguguguc 3480

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ucaauuaguc agcaaccagg uguggaaagu ccccaggcuc cccagcaggc agaaguaugc 3600

aaagcaugca ucucaauuag ucagcaacca uagucccgcc ccuaacuccg cccaucccgc 3660

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augcagaggc cgaggccgcc ucugccucug agcuauucca gaaguaguga ggaggcuuuu 3780

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<210> 18
<211> 3788
<212> RNA
<213> Artificial Sequence

<220>
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ccagcagccg uagauuugag aacuuuggga uauucacagc agcagcagga aaagaucaag 180

cccaaaguga ggucgacagu cgcgcagcau cacgaagcgc ugguggguca uggguuuaca 240

caugcccaca ucguagccuu gucgcagcac ccugcagccc uuggcacggu cgccgucaag 300

uaccaggaca ugauugcggc guugccggaa gccacacaug aggcgaucgu cgguguggggg 360

aaacagugga gcggagcccg agcgcuugag gcccuguuga cggucgcggg agagcugaga 420

gggccucccc uucagcugga cacgggccag uugcugaaga ucgcgaagcg gggaggaguc 480

acggcggucg aggcggugca cgcguggcgc aaugcgcuca cgggagcacc ccucaaccug 540

accccagagc aggucguggc aauugcgagc aacaucgggg gaaagcaggc acucgaaacc 600

guccagaggu ugcugccugu gcugugccaa gcgcacggac uuacgccaga gcaggucgug 660

gcaauugcga gcaacaacgg gggaaagcag gcacucgaaa ccguccagag guugcugccu 720

gugcugugcc aagcgcacgg acuaacccca gagcaggucg uggcaauugc gagcaacauc 780

gggggaaagc aggcacucga aaccguccag agguugcugc cugugcugug ccaagcgcac 840

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gaaaccgucc agagguugcu gccugugcug ugccaagcgc acggccugac cccagagcag 960

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cugccugugc ugugccaagc gcacggacug acaccagagc aggucguggc aauugcgagc 1080

aacggagggg gaaagcaggc acucgaaacc guccagaggu ugcugccugu gcugugccaa 1140

gcgcacggac uuacacccga acaagucgug gcaauugcga gccaugacgg gggaaagcag 1200

gcacucgaaa ccguccagag guugcugccu gugcugugcc aagcgcacgg acuuacgcca 1260

gagcaggucg uggcaauugc gagcaacauc gggggaaagc aggcacucga aaccguccag 1320

agguugcugc cugugcugug ccaagcgcac ggacuaaccc cagagcaggu cguggcaauu 1380

gcgagcaacc acgggggaaa gcaggcacuc gaaaccgucc agagguugcu gccugugcug 1440

ugccaagcgc acggguugac cccagagcag gucguggcaa uugcgagcaa cggaggggga 1500

aagcaggcac ucgaaaccgu ccagagguug cugccugugc ugugccaagc gcacggccug 1560

accccagagc aggucguggc aauugcgagc caugacgggg gaaagcaggc acucgaaacc 1620

guccagaggu ugcugccugu gcugugccaa gcgcacggac ugacaccaga gcaggucgug 1680

gcaauugcga gcaacaucgg gggaaagcag gcacucgaaa ccguccagag guugcugccu 1740

gugcugugcc aagcgcacgg ccucacccca gagcaggucg uggcaauugc gagcaacgga 1800

gggggaaagc aggcacucga aaccguccag agguugcugc cugugcugug ccaagcgcac 1860

ggacuuacgc cagagcaggu cguggcaauu gcgagcaacc acgggggaaa gcaggcacuc 1920

gaaaccgucc agagguugcu gccugugcug ugccaagcgc acggacuaac cccagagcag 1980

gucguggcaa uugcgagcca ugacggggga aagcaggcac ucgaaaccgu ccagagguug 2040

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