SEQUENCE LISTING

<110> JUNO THERAPEUTICS, INC.
EDITAS MEDICINE, INC.
BURLEIGH, Stephen Michael
BORGES, Christopher
NYE, Christopher Heath
SATHER, Blythe D.
VONG, Queenie
WELSTEAD, G. Grant

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<309> 1994-11-07

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<212> PRT
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Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
        115                 120                 125
Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
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Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
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Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
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Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
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Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys
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<220>
<223> EGFRt

<400> 13

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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
```

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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
                325                 330                 335


<210> 14
<211> 137
<212> PRT
<213> Mus musculus

<220>
<223> Mouse TCR alpha constant

<400> 14
Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg
 1               5                  10                  15
Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile
            20                  25                  30
Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr
        35                  40                  45
Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala
    50                  55                  60
Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr
65                  70                  75                  80
Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr
                85                  90                  95
Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser
            100                 105                 110
Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
        115                 120                 125
Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135


<210> 15
<211> 137
<212> PRT
<213> Mus musculus

<220>
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<223> Mouse TCR alpha constant

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


<210> 16
<211> 173
<212> PRT
<213> Mus musculus

<220>
<223> Mouse TCR beta constant

<300>
<308> Uniprot P01852
<309> 1986-07-21

<400> 16
Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1               5                  10                  15
Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
            20                  25                  30
Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35                  40                  45
Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
    50                  55                  60
Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65                  70                  75                  80
Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
                85                  90                  95
His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
            100                 105                 110

```
Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
        115                 120                 125
Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
    130                 135                 140
Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
145                 150                 155                 160
Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
                165                 170
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<210> 17
<211> 172
<212> PRT
<213> Mus musculus

<220>
<223> Mouse TCR beta constant

<400> 17

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Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser
 1               5                  10                  15
Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
            20                  25                  30
Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
        35                  40                  45
Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu
    50                  55                  60
Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
65                  70                  75                  80
Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His
                85                  90                  95
Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val
            100                 105                 110
Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile
        115                 120                 125
Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr
    130                 135                 140
Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Gly
145                 150                 155                 160
Leu Val Leu Met Ala Met Val Lys Arg Lys Asn Ser
                165                 170
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<210> 18
<211> 181
<212> DNA
<213> Artificial Sequence

<220>
<223> MND promoter

<400> 18
gggtctctct ggttagacca gatctgagcc tgggagctct ctggctaact agggaaccca 60
ctgcttaagc ctcaataaag cttgccttga gtgcttcaag tagtgtgtgc ccgtctgttg 120
tgtgactctg gtaactagag atccctcaga ccctttttagt cagtgtggaa aatctctagc 180
a 181

<210> 19
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<223> Human TCR alpha constant

<300>
<308> Uniprot P01848
<309> 2018-07-18

<400> 19
Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 1               5                  10                  15
Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
            20                  25                  30
Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
        35                  40                  45
Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
    50                  55                  60
Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
65                  70                  75                  80
Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
                85                  90                  95
Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
            100                 105                 110
Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val
        115                 120                 125
Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 20
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<223> Human TCR beta constant 1

<300>
<308> Uniprot P01850

<309> 2018-07-18

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



<210> 21
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<223> Human TCR beta constant 2

<300>
<308> Uniprot A0A5B9
<309> 2018-07-18

<400> 21
Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser
 1               5                  10                  15
Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala
            20                  25                  30
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
        35                  40                  45
Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
    50                  55                  60

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

<210> 22
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> REPEAT
<222> (0)...(0)
<223> SGGGG is repeated 5 or 6 times

<400> 22
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Pro Gly Gly Gly Ser Gly Gly Gly Gly Pro
 1               5                  10
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<210> 23
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 23
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Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
 1               5                  10                  15
Ser
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<210> 24
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> human TCR alpha constant

<300>
<308> CAA26636.1
<309> 2016-07-25

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


<210> 25
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<223> human TCR beta constant

<300>
<308> A0A0G2JNG9

<400> 25
Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1               5                  10                  15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
            20                  25                  30

```
Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35                  40                  45
Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
    50                  55                  60
Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65                  70                  75                  80
Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
                85                  90                  95
Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
            100                 105                 110
Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
        115                 120                 125
Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
    130                 135                 140
Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145                 150                 155                 160
Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
                165                 170                 175
Ser Arg Gly
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<210> 26
<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA transcription sequence

<400> 26
agcgctctcg tacagagttg gcattataat acgactcact ataggggaga atcaaaatcg 60
gtgaatgttt tagagctaga aatagcaagt taaaataagg ctagtccgtt atcaacttga 120
aaaagtggca ccgagtcggt gctttttt 149

<210> 27
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA sequence

<400> 27
gagaaucaaa aucggugaau guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 28
<211> 20
<212> RNA

<213> Artificial Sequence

<220>
<223> TRAC-10 gRNA targeting domain

<400> 28
ucucucagcu gguacacggc 20

<210> 29
<211> 20
<212> RNA
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<220>
<223> TRAC-110 gRNA targeting domain

<400> 29
uggauuuaga gucucucagc 20

<210> 30
<211> 20
<212> RNA
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<220>
<223> TRAC-116 gRNA targeting domain

<400> 30
acacggcagg gucaggguuc 20

<210> 31
<211> 20
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<220>
<223> TRAC-16 gRNA targeting domain

<400> 31
gagaaucaaa aucggugaau 20

<210> 32
<211> 20
<212> RNA
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<220>
<223> TRAC-4 gRNA targeting domain

<400> 32

gcugguacac ggcaggguca 20

<210> 33
<211> 17
<212> RNA
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<220>
<223> TRAC-49 gRNA targeting domain

<400> 33
cucagcuggu acacggc 17

<210> 34
<211> 17
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<220>
<223> TRAC-2 gRNA targeting domain

<400> 34
ugguacacgg caggguc 17

<210> 35
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<220>
<223> TRAC-30 gRNA targeting domain

<400> 35
gcuagacaug aggucua 17

<210> 36
<211> 17
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<220>
<223> TRAC-43 gRNA targeting domain

<400> 36
gucagauuug uugcucc 17

<210> 37
<211> 17
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<220>
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<400> 37
ucagcuggua cacggca 17

<210> 38
<211> 17
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<220>
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<400> 38
gcagacagac uugucac 17

<210> 39
<211> 17
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<220>
<223> TRAC-25 gRNA targeting domain

<400> 39
gguacacggc aggguca 17

<210> 40
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<220>
<223> TRAC-128 gRNA targeting domain

<400> 40
cuucaagagc aacagugcug 20

<210> 41
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<220>
<223> TRAC-105 gRNA targeting domain

<400> 41
agagcaacag ugcuguggcc 20

<210> 42
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<220>
<223> TRAC-106 gRNA targeting domain

<400> 42
aaagucagau uuguugcucc 20

<210> 43
<211> 20
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<220>
<223> TRAC-123 gRNA targeting domain

<400> 43
acaaaacugu gcuagacaug 20

<210> 44
<211> 17
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<220>
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<400> 44
aaacugugcu agacaug 17

<210> 45
<211> 20
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<220>
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<400> 45
ugugcuagac augaggucua 20

<210> 46
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<212> RNA
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<220>
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<400> 46
ggcuggggaa gaaggugucu uc 22

<210> 47
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<220>
<223> TRAC-147 gRNA targeting domain

<400> 47
gcuggggaag aaggugucuu c 21

<210> 48
<211> 18
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<220>
<223> TRAC-234 gRNA targeting domain

<400> 48
ggggaagaag gugucuuc 18

<210> 49
<211> 22
<212> RNA
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<220>
<223> TRAC-167 gRNA targeting domain

<400> 49
guuuugucug ugauauacac au 22

<210> 50
<211> 24
<212> RNA
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<220>
<223> TRAC-177 gRNA targeting domain

<400> 50
ggcagacaga cuugucacug gauu 24

<210> 51
<211> 23
<212> RNA
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<220>
<223> TRAC-176 gRNA targeting domain

<400> 51
gcagacagac uugucacugg auu 23

<210> 52
<211> 20
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<220>
<223> TRAC-257 gRNA targeting domain

<400> 52
gacagacuug ucacuggauu 20

<210> 53
<211> 24
<212> RNA
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<220>
<223> TRAC-233 gRNA targeting domain

<400> 53
gugaauaggc agacagacuu guca 24

<210> 54
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<400> 54
gaauaggcag acagacuugu ca 22

<210> 55
<211> 22
<212> RNA
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<223> TRAC-163 gRNA targeting domain

<400> 55
gagucucuca gcugguacac gg 22

<210> 56
<211> 20
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<220>
<223> TRAC-241 gRNA targeting domain

<400> 56
gucucucagc ugguacacgg 20

<210> 57
<211> 22
<212> RNA
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<220>
<223> TRAC-179 gRNA targeting domain

<400> 57
gguacacggc agggucaggg uu 22

<210> 58
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC-178 gRNA targeting domain

<400> 58
guacacggca gggucagggu u 21

<210> 59
<211> 20
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<220>
<223> TRBC-40 gRNA targeting domain

<400> 59
cacccagauc gucagcgccg 20

<210> 60

<211> 20
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<220>
<223> TRBC-52 gRNA targeting domain

<400> 60
caaacacagc gaccucgggu 20

<210> 61
<211> 20
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<220>
<223> TRBC-25 gRNA targeting domain

<400> 61
ugacgagugg acccaggaua 20

<210> 62
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<220>
<223> TRBC-35 gRNA targeting domain

<400> 62
ggcucucgga gaaugacgag 20

<210> 63
<211> 20
<212> RNA
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<220>
<223> TRBC-50 gRNA targeting domain

<400> 63
ggccucggcg cugacgaucu 20

<210> 64
<211> 20
<212> RNA
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<220>
<223> TRBC-39 gRNA targeting domain

<400> 64
gaaaaacgug uucccacccg 20

<210> 65
<211> 20
<212> RNA
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<220>
<223> TRBC-49 gRNA targeting domain

<400> 65
augacgagug gacccaggau 20

<210> 66
<211> 20
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<220>
<223> TRBC-51 gRNA targeting domain

<400> 66
aguccaguuc uacgggcucu 20

<210> 67
<211> 20
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<220>
<223> TRBC-26 gRNA targeting domain

<400> 67
cgcugucaag uccaguucua 20

<210> 68
<211> 20
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<223> TRBC-47 gRNA targeting domain

<400> 68
aucgucagcg ccgaggccug 20

<210> 69
<211> 20

<212> RNA
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<220>
<223> TRBC-45 gRNA targeting domain

<400> 69
ucaaacacag cgaccucggg 20

<210> 70
<211> 20
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<220>
<223> TRBC-34 gRNA targeting domain

<400> 70
cguagaacug gacuugacag 20

<210> 71
<211> 20
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<220>
<223> TRBC-227 gRNA targeting domain

<400> 71
aggccucggc gcugacgauc 20

<210> 72
<211> 20
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<220>
<223> TRBC-41 gRNA targeting domain

<400> 72
ugacagcgga agugguugcg 20

<210> 73
<211> 20
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<220>
<223> TRBC-30 gRNA targeting domain

<400> 73
uugacagcgg aaguggguugc 20

<210> 74
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<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-206 gRNA targeting domain

<400> 74
ucuccgagag cccguagaac 20

<210> 75
<211> 20
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<220>
<223> TRBC-32 gRNA targeting domain

<400> 75
cgggugggaa cacguuuuuc 20

<210> 76
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-276 gRNA targeting domain

<400> 76
gacagguuug gcccuauccu 20

<210> 77
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-274 gRNA targeting domain

<400> 77
gaucgucagc gccgaggccu 20

<210> 78
<211> 20
<212> RNA

<213> Artificial Sequence

<220>
<223> TRBC-230 gRNA targeting domain

<400> 78
ggcucaaaca cagcgaccuc 20

<210> 79
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-235 gRNA targeting domain

<400> 79
ugagggucuc ggccaccuuc 20

<210> 80
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-38 gRNA targeting domain

<400> 80
aggcuucuac cccgaccacg 20

<210> 81
<211> 20
<212> RNA
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<220>
<223> TRBC-223 gRNA targeting domain

<400> 81
ccgaccacgu ggagcugagc 20

<210> 82
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<213> Artificial Sequence

<220>
<223> TRBC-221 gRNA targeting domain

<400> 82

ugacagguuu ggcccuaucc 20

<210> 83
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-48 gRNA targeting domain

<400> 83
cuugacagcg gaagugguug 20

<210> 84
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-216 gRNA targeting domain

<400> 84
agaucgucag cgccgaggcc 20

<210> 85
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-210 gRNA targeting domain

<400> 85
gcgcugacga ucugggugac 20

<210> 86
<211> 20
<212> RNA
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<220>
<223> TRBC-268 gRNA targeting domain

<400> 86
ugagggcggg cugcuccuug 20

<210> 87
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-193 gRNA targeting domain

<400> 87
guugcggggg uucugccaga 20

<210> 88
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-246 gRNA targeting domain

<400> 88
agcucagcuc cacguggucg 20

<210> 89
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-228 gRNA targeting domain

<400> 89
gcggcugcuc aggcaguauc 20

<210> 90
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-43 gRNA targeting domain

<400> 90
gcgggguuc ugccagaagg 20

<210> 91
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-272 gRNA targeting domain

<400> 91
uggcucaaac acagcgaccu 20

<210> 92
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-33 gRNA targeting domain

<400> 92
acuggacuug acagcggaag 20

<210> 93
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-44 gRNA targeting domain

<400> 93
gacagcggaa gugguugcgg 20

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

<220>
<223> TRBC-211 gRNA targeting domain

<400> 94
gcugucaagu ccaguucuac 20

<210> 95
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-253 gRNA targeting domain

<400> 95
guaucuggag ucauugaggg 20

<210> 96
<211> 17
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-18 gRNA targeting domain

<400> 96
cucggcgcug acgaucu 17

<210> 97
<211> 17
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-6 gRNA targeting domain

<400> 97
ccucggcgcu gacgauc 17

<210> 98
<211> 17
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-85 gRNA targeting domain

<400> 98
ccgagagccc guagaac 17

<210> 99
<211> 17
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-129 gRNA targeting domain

<400> 99
ccagaucguc agcgccg 17

<210> 100
<211> 17
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-93 gRNA targeting domain

<400> 100
gaaugacgag uggaccc 17

<210> 101
<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-415 gRNA targeting domain

<400> 101
gggugacagg uuuggcccua uc 22

<210> 102
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-414 gRNA targeting domain

<400> 102
ggugacaggu uuggcccuau c 21

<210> 103
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-310 gRNA targeting domain

<400> 103
gugacagguu uggcccuauc 20

<210> 104
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-308 gRNA targeting domain

<400> 104
gacagguuug gcccuauc 18

<210> 105
<211> 22
<212> RNA
<213> Artificial Sequence

<220>

<223> TRBC-401 gRNA targeting domain

<400> 105
gauacugccu gagcagccgc cu 22

<210> 106
<211> 24
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-468 gRNA targeting domain

<400> 106
gaccacgugg agcugagcug gugg 24

<210> 107
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-462 gRNA targeting domain

<400> 107
guggagcuga gcuggugg 18

<210> 108
<211> 24
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-424 gRNA targeting domain

<400> 108
gggcgggcug cuccuugagg ggcu 24

<210> 109
<211> 23
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-423 gRNA targeting domain

<400> 109
ggcgggcugc uccuugaggg gcu 23

<210> 110

<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-422 gRNA targeting domain

<400> 110
gcgggcugcu ccuugagggg cu 22

<210> 111
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-420 gRNA targeting domain

<400> 111
gggcugcucc uugaggggcu 20

<210> 112
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-419 gRNA targeting domain

<400> 112
ggcugcuccu ugaggggcu 19

<210> 113
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-418 gRNA targeting domain

<400> 113
gcugcuccuu gaggggcu 18

<210> 114
<211> 24
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-445 gRNA targeting domain

<400> 114
ggugaauggg aaggaggugc acag 24

<210> 115
<211> 23
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-444 gRNA targeting domain

<400> 115
gugaauggga aggaggugca cag 23

<210> 116
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC-442 gRNA targeting domain

<400> 116
gaaugggaag gaggugcaca g 21

<210> 117
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence

<400> 117
attcaccgat tttgattctc 20

<210> 118
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> TRBC target sequence

<400> 118
agatcgtcag cgccgaggcc 20

<210> 119
<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> HBB splice site acceptor

<400> 119
ctgacctctt ctcttcctcc cacag 25

<210> 120
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG splice site acceptor

<400> 120
tttctctcca cag 13

<210> 121
<211> 138
<212> PRT
<213> mus musculus

<220>
<223> Mouse TCR alpha constant

<300>
<308> Uniprot P01849
<309> 1986-07-21

<400> 121
Pro Tyr Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro
 1               5                  10                  15
Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln
            20                  25                  30
Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys
        35                  40                  45
Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile
    50                  55                  60
Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu
65                  70                  75                  80
Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu
                85                  90                  95
Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu
            100                 105                 110
Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn
        115                 120                 125
Leu Leu Met Thr Leu Arg Leu Trp Ser Ser

130 135

<210> 122
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified mouse TCR alpha constant

<400> 122
Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser
1 5 10 15
Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30
Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val
35 40 45
Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60
Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80
Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu
85 90 95
Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Leu Val
100 105 110
Ile Val Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125
Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 123
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified mouse TCR beta constant

<400> 123
Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
1 5 10 15
Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
20 25 30
Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys
50 55 60
Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala

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

<210> 124
<211> 611
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 5' homology arm

<400> 124
ctctatcaat gagagagcaa tctcctggta atgtgataga tttcccaact taatgccaac 60
ataccataaa cctcccattc tgctaatgcc cagcctaagt tggggagacc actccagatt 120
ccaagatgta cagtttgctt tgctgggcct ttttcccatg cctgccttta ctctgccaga 180
gttatattgc tggggttttg aagaagatcc tattaaataa aagaataagc agtattatta 240
agtagccctg catttcaggt ttccttgagt ggcaggccag gcctggccgt gaacgttcac 300
tgaaatcatg gcctcttggc caagattgat agcttgtgcc tgtccctgag tcccagtcca 360
tcacgagcag ctggtttcta agatgctatt tcccgtataa agcatgagac cgtgacttgc 420
cagccccaca gagccccgcc cttgtccatc actggcatct ggactccagc ctgggttggg 480
gcaaagaggg aaatgagatc atgtcctaac cctgatcctc ttgtcccaca gatatccaga 540
accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag tctgtctgcc 600
tattcaccga t 611

<210> 125
<211> 628
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 3' homology arm

<400> 125
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300

ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttgttc 360
tggcagtcca gagaatgaca cgggaaaaaa gcagatgaag agaaggtggc aggagagggc 420
acgtggccca gcctcagtct ctccaactga gttcctgcct gcctgccttt gctcagactg 480
tttgcccctt actgctcttc taggcctcat tctaagcccc ttctccaagt tgcctctcct 540
tatttctccc tgtctgccaa aaaatctttc ccagctcact aagtcagtct cacgcagtca 600
ctcattaacc caccaatcac tgattgtg 628

<210> 126
<211> 347
<212> DNA
<213> Artificial Sequence

<220>
<223> MND promoter

<400> 126
gaacagagaa acaggagaat atgggccaaa caggatatct gtggtaagca gttcctgccc 60
cggctcaggg ccaagaacag ttggaacagc agaatatggg ccaaacagga tatctgtggt 120
aagcagttcc tgccccggct cagggccaag aacagatggt ccccagatgc ggtcccgccc 180
tcagcagttt ctagagaacc atcagatgtt tccagggtgc cccaaggacc tgaaatgacc 240
ctgtgcctta tttgaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc 300
tccccgagct ctatataagc agagctcgtt tagtgaaccg tcagatc 347

<210> 127
<211> 544
<212> DNA
<213> Artificial Sequence

<220>
<223> Ef1alpha promoter with HTLV1 enhancer

<400> 127
ggatctgcga tcgctccggt gcccgtcagt gggcagagcg cacatcgccc acagtccccg 60
agaagttggg gggaggggtc ggcaattgaa ccggtgccta gagaaggtgg cgcggggtaa 120
actgggaaag tgatgtcgtg tactggctcc gccttttcc cgagggtggg ggagaaccgt 180
atataagtgc agtagtcgcc gtgaacgttc tttttcgcaa cgggtttgcc gccagaacac 240
agctgaagct tcgaggggct cgcatctctc cttcacgcgc ccgccgccct acctgaggcc 300
gccatccacg ccggttgagt cgcgttctgc cgcctcccgc ctgtggtgcc tcctgaactg 360
cgtccgccgt ctaggtaagt ttaaagctca ggtcgagacc gggcctttgt ccggcgctcc 420
cttggagcct acctagactc agccggctct ccacgctttg cctgaccctg cttgctcaac 480
tctacgtctt tgtttcgttt tctgttctgc gccgttacag atccaagctg tgaccggcgc 540
ctac 544

<210> 128
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> P2A nucleotide sequence

<400> 128
ggatctggag cgacgaattt tagtctactg aaacaagcgg gagacgtgga ggaaaaccct 60
ggacct 66

<210> 129
<211> 112
<212> PRT
<213> homo sapiens

<220>
<223> CD3 zeta

<400> 129
Arg Val Lys Phe Ser Arg Ser Ala Glu Pro 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> 130
<211> 112
<212> PRT
<213> homo sapiens

<220>
<223> CD3 zeta

<400> 130
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys 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

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                85                  90                  95
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            100                 105                 110


<210> 131
<211> 12
<212> PRT
<213> homo sapiens

<220>
<223> spacer (IgG4hinge)

<400> 131
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1               5                  10


<210> 132
<211> 36
<212> DNA
<213> homo sapiens

<220>
<223> spacer (IgG4hinge)

<400> 132
gaatctaagt acggaccgcc ctgccccct tgccct                          36

<210> 133
<211> 119
<212> PRT
<213> homo sapiens

<220>
<223> Hinge-CH3 spacer

<400> 133
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg
 1               5                  10                  15
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
            20                  25                  30
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
        35                  40                  45
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
    50                  55                  60
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
65                  70                  75                  80
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
                85                  90                  95
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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
100 105 110
Leu Ser Leu Ser Leu Gly Lys
115

<210> 134
<211> 229
<212> PRT
<213> homo sapiens

<220>
<223> Hinge-CH2-CH3 spacer

<400> 134
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45
Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110
Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125
Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190
Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220
Leu Ser Leu Gly Lys
225

<210> 135
<211> 282
<212> PRT

<213> homo sapiens

<220>
<223> IgD-hinge-Fc

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


<210> 136
<211> 27
<212> PRT
<213> homo sapiens

<220>

<223> CD28

<300>
<308> No. P10747
<309> 1989-07-01

<400> 136
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1               5                  10                  15
Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
            20                  25


<210> 137
<211> 66
<212> PRT
<213> homo sapiens

<220>
<223> CD28

<300>
<308> No. P10747
<309> 1989-07-01

<400> 137
Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
 1               5                  10                  15
Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
            20                  25                  30
Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
        35                  40                  45
Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
    50                  55                  60
Trp Val
65


<210> 138
<211> 41
<212> PRT
<213> homo sapiens

<220>
<223> CD28

<300>
<308> P10747
<309> 1989-07-01

<400> 138
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 1               5                  10                  15
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20                  25                  30
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        35                  40


<210> 139
<211> 41
<212> PRT
<213> homo sapiens

<220>
<223> CD28 (LL to GG)

<400> 139
Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
 1               5                  10                  15
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            20                  25                  30
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
        35                  40


<210> 140
<211> 42
<212> PRT
<213> homo sapiens

<220>
<223> 4-1BB

<300>
<308> Q07011.1
<309> 1995-02-01

<400> 140
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> 141
<211> 112
<212> PRT

<213> homo sapiens

<220>
<223> CD3 zeta

<400> 141
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> 142
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Partial recombinant TCRalpha constant region exon
      1 sequence

<400> 142
cagaacccag atcccgcggt atatcaactg cgcgactcaa aatcatccga taagagtgtc 60
tgtttgttta ctgacttcga cagtcaaact aatgtctctc agagcaaaga ttccgatgtc 120
tacatcactg acaagtgc                                              138

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV16 E7(11-19) peptide

<400> 143
Tyr Met Leu Asp Leu Gln Pro Glu Thr
 1               5


<210> 144

<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 144
nnnnnnnnnn nnnnnnnnnn guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugc 96

<210> 145
<211> 104
<212> RNA
<213> Artificial Sequence

<220>
<223> exemplary gRNA complementary domain

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 145
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcugaaa agcauagcaa guuaaaauaa 60
ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg gugc 104

<210> 146
<211> 106
<212> RNA
<213> Artificial Sequence

<220>

<223> TRAC gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 146
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuggaa acagcauagc aaguuaaaau 60
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 106

<210> 147
<211> 116
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 147
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuguuu uggaaacaaa acagcauagc 60
aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 116

<210> 148
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA

<220>
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<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 148
nnnnnnnnnn nnnnnnnnnn guauuagagc uagaaauagc aaguuaauau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugc 96

<210> 149
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA

<220>
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<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 149
nnnnnnnnnn nnnnnnnnnn guuuaagagc uagaaauagc aaguuuaaau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugc 96

<210> 150
<211> 116
<212> RNA
<213> Artificial Sequence

<220>
<223> TRAC gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 150
nnnnnnnnnn nnnnnnnnnn guauuagagc uaugcuguau uggaaacaau acagcauagc 60
aaguuaauau aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugc 116

<210> 151
<211> 47
<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 151
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcu 47

<210> 152
<211> 49
<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 152
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cgguggugc 49

<210> 153
<211> 51
<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 153
aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcggau c 51

<210> 154
<211> 31
<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 154
aaggcuaguc cguuaucaac uugaaaaagu g 31

<210> 155
<211> 18

<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 155
aaggcuaguc cguuauca 18

<210> 156
<211> 12
<212> RNA
<213> Artificial Sequence

<220>
<223> gRNA Proximal and tail domain

<400> 156
aaggcuaguc cg 12

<210> 157
<211> 102
<212> RNA
<213> Artificial Sequence

<220>
<223> Exemplary chimeric gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 157
nnnnnnnnnn nnnnnnnnnn guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60
cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uu 102

<210> 158
<211> 102
<212> RNA
<213> Artificial Sequence

<220>
<223> Exemplary chimeric gRNA

<220>
<221> modified_base
<222> (1)...(20)
<223> a, c, u, g, unknown or other

<220>
<221> misc_feature
<222> (1)...(20)
<223> n is a, c, g, or u

<400> 158
nnnnnnnnnn nnnnnnnnnn guuuuaguac ucuggaaaca gaaucuacua aaacaaggca 60
aaaugccgug uuuaucucgu caacuuguug gcgagauuuu uu 102

<210> 159
<211> 1344
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptococcus mutans Cas9

<400> 159
Lys Lys Pro Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val Gly
 1               5                  10                  15
Trp Ala Val Val Thr Asp Asp Tyr Lys Val Pro Ala Lys Lys Met Lys
            20                  25                  30
Val Leu Gly Asn Thr Asp Lys Ser His Ile Glu Lys Asn Leu Leu Gly
        35                  40                  45
Ala Leu Leu Phe Asp Ser Gly Asn Thr Ala Glu Asp Arg Arg Leu Lys
    50                  55                  60
Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Arg Asn Arg Ile Leu Tyr
65                  70                  75                  80
Leu Gln Glu Ile Phe Ser Glu Glu Met Gly Lys Val Asp Asp Ser Phe
                85                  90                  95
Phe His Arg Leu Glu Asp Ser Phe Leu Val Thr Glu Asp Lys Arg Gly
            100                 105                 110
Glu Arg His Pro Ile Phe Gly Asn Leu Glu Glu Glu Val Lys Tyr His
        115                 120                 125
Glu Asn Phe Pro Thr Ile Tyr His Leu Arg Gln Tyr Leu Ala Asp Asn
    130                 135                 140
Pro Glu Lys Val Asp Leu Arg Leu Val Tyr Leu Ala Leu Ala His Ile
145                 150                 155                 160
Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Lys Phe Asp Thr Arg
                165                 170                 175
Asn Asn Asp Val Gln Arg Leu Phe Gln Glu Phe Leu Ala Val Tyr Asp
            180                 185                 190
Asn Thr Phe Glu Asn Ser Ser Leu Gln Glu Gln Asn Val Gln Val Glu
        195                 200                 205
Glu Ile Leu Thr Asp Lys Ile Ser Lys Ser Ala Lys Lys Asp Arg Val

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    210                 215                 220
Leu Lys Leu Phe Pro Asn Glu Lys Ser Asn Gly Arg Phe Ala Glu Phe
225                 230                 235                 240
Leu Lys Leu Ile Val Gly Asn Gln Ala Asp Phe Lys Lys His Phe Glu
                245                 250                 255
Leu Glu Glu Lys Ala Pro Leu Gln Phe Ser Lys Asp Thr Tyr Glu Glu
            260                 265                 270
Glu Leu Glu Val Leu Leu Ala Gln Ile Gly Asp Asn Tyr Ala Glu Leu
        275                 280                 285
Phe Leu Ser Ala Lys Lys Leu Tyr Asp Ser Ile Leu Leu Ser Gly Ile
    290                 295                 300
Leu Thr Val Thr Asp Val Gly Thr Lys Ala Pro Leu Ser Ala Ser Met
305                 310                 315                 320
Ile Gln Arg Tyr Asn Glu His Gln Met Asp Leu Ala Gln Leu Lys Gln
                325                 330                 335
Phe Ile Arg Gln Lys Leu Ser Asp Lys Tyr Asn Glu Val Phe Ser Asp
            340                 345                 350
Val Ser Lys Asp Gly Tyr Ala Gly Tyr Ile Asp Gly Lys Thr Asn Gln
        355                 360                 365
Glu Ala Phe Tyr Lys Tyr Leu Lys Gly Leu Leu Asn Lys Ile Glu Gly
    370                 375                 380
Ser Gly Tyr Phe Leu Asp Lys Ile Glu Arg Glu Asp Phe Leu Arg Lys
385                 390                 395                 400
Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu Gln
                405                 410                 415
Glu Met Arg Ala Ile Ile Arg Arg Gln Ala Glu Phe Tyr Pro Phe Leu
            420                 425                 430
Ala Asp Asn Gln Asp Arg Ile Glu Lys Leu Leu Thr Phe Arg Ile Pro
        435                 440                 445
Tyr Tyr Val Gly Pro Leu Ala Arg Gly Lys Ser Asp Phe Ala Trp Leu
    450                 455                 460
Ser Arg Lys Ser Ala Asp Lys Ile Thr Pro Trp Asn Phe Asp Glu Ile
465                 470                 475                 480
Val Asp Lys Glu Ser Ser Ala Glu Ala Phe Ile Asn Arg Met Thr Asn
                485                 490                 495
Tyr Asp Leu Tyr Leu Pro Asn Gln Lys Val Leu Pro Lys His Ser Leu
            500                 505                 510
Leu Tyr Glu Lys Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys Tyr
        515                 520                 525
Lys Thr Glu Gln Gly Lys Thr Ala Phe Phe Asp Ala Asn Met Lys Gln
    530                 535                 540
Glu Ile Phe Asp Gly Val Phe Lys Val Tyr Arg Lys Val Thr Lys Asp
545                 550                 555                 560
Lys Leu Met Asp Phe Leu Glu Lys Glu Phe Asp Glu Phe Arg Ile Val
                565                 570                 575
Asp Leu Thr Gly Leu Asp Lys Glu Asn Lys Val Phe Asn Ala Ser Tyr
            580                 585                 590
Gly Thr Tyr His Asp Leu Cys Lys Ile Leu Asp Lys Asp Phe Leu Asp
        595                 600                 605
Asn Ser Lys Asn Glu Lys Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
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    610                 615                 620
Leu Phe Glu Asp Arg Glu Met Ile Arg Lys Arg Leu Glu Asn Tyr Ser
625                 630                 635                 640
Asp Leu Leu Thr Lys Glu Gln Val Lys Lys Leu Glu Arg Arg His Tyr
                645                 650                 655
Thr Gly Trp Gly Arg Leu Ser Ala Glu Leu Ile His Gly Ile Arg Asn
            660                 665                 670
Lys Glu Ser Arg Lys Thr Ile Leu Asp Tyr Leu Ile Asp Asp Gly Asn
        675                 680                 685
Ser Asn Arg Asn Phe Met Gln Leu Ile Asn Asp Asp Ala Leu Ser Phe
    690                 695                 700
Lys Glu Glu Ile Ala Lys Ala Gln Val Ile Gly Glu Thr Asp Asn Leu
705                 710                 715                 720
Asn Gln Val Val Ser Asp Ile Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735
Ile Leu Gln Ser Leu Lys Ile Val Asp Glu Leu Val Lys Ile Met Gly
            740                 745                 750
His Gln Pro Glu Asn Ile Val Val Glu Met Ala Arg Glu Asn Gln Phe
        755                 760                 765
Thr Asn Gln Gly Arg Arg Asn Ser Gln Gln Arg Leu Lys Gly Leu Thr
    770                 775                 780
Asp Ser Ile Lys Glu Phe Gly Ser Gln Ile Leu Lys Glu His Pro Val
785                 790                 795                 800
Glu Asn Ser Gln Leu Gln Asn Asp Arg Leu Phe Leu Tyr Tyr Leu Gln
                805                 810                 815
Asn Gly Arg Asp Met Tyr Thr Gly Glu Glu Leu Asp Ile Asp Tyr Leu
            820                 825                 830
Ser Gln Tyr Asp Ile Asp His Ile Ile Pro Gln Ala Phe Ile Lys Asp
        835                 840                 845
Asn Ser Ile Asp Asn Arg Val Leu Thr Ser Ser Lys Glu Asn Arg Gly
    850                 855                 860
Lys Ser Asp Asp Val Pro Ser Lys Asp Val Val Arg Lys Met Lys Ser
865                 870                 875                 880
Tyr Trp Ser Lys Leu Leu Ser Ala Lys Leu Ile Thr Gln Arg Lys Phe
                885                 890                 895
Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Thr Asp Asp Asp Lys
            900                 905                 910
Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925
His Val Ala Arg Ile Leu Asp Glu Arg Phe Asn Thr Glu Thr Asp Glu
    930                 935                 940
Asn Asn Lys Lys Ile Arg Gln Val Lys Ile Val Thr Leu Lys Ser Asn
945                 950                 955                 960
Leu Val Ser Asn Phe Arg Lys Glu Phe Glu Leu Tyr Lys Val Arg Glu
                965                 970                 975
Ile Asn Asp Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val Ile
            980                 985                 990
Gly Lys Ala Leu Leu Gly Val Tyr Pro Gln Leu Glu Pro Glu Phe Val
        995                 1000                1005
Tyr Gly Asp Tyr Pro His Phe His Gly His Lys Glu Asn Lys Ala Thr
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    1010                1015                1020
Ala Lys Lys Phe Phe Tyr Ser Asn Ile Met Asn Phe Phe Lys Lys Asp
1025                1030                1035                1040
Asp Val Arg Thr Asp Lys Asn Gly Glu Ile Ile Trp Lys Lys Asp Glu
                1045                1050                1055
His Ile Ser Asn Ile Lys Lys Val Leu Ser Tyr Pro Gln Val Asn Ile
            1060                1065                1070
Val Lys Lys Val Glu Glu Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile
        1075                1080                1085
Leu Pro Lys Gly Asn Ser Asp Lys Leu Ile Pro Arg Lys Thr Lys Lys
    1090                1095                1100
Phe Tyr Trp Asp Thr Lys Lys Tyr Gly Gly Phe Asp Ser Pro Ile Val
1105                1110                1115                1120
Ala Tyr Ser Ile Leu Val Ile Ala Asp Ile Glu Lys Gly Lys Ser Lys
                1125                1130                1135
Lys Leu Lys Thr Val Lys Ala Leu Val Gly Val Thr Ile Met Glu Lys
            1140                1145                1150
Met Thr Phe Glu Arg Asp Pro Val Ala Phe Leu Glu Arg Lys Gly Tyr
        1155                1160                1165
Arg Asn Val Gln Glu Glu Asn Ile Ile Lys Leu Pro Lys Tyr Ser Leu
    1170                1175                1180
Phe Lys Leu Glu Asn Gly Arg Lys Arg Leu Leu Ala Ser Ala Arg Glu
1185                1190                1195                1200
Leu Gln Lys Gly Asn Glu Ile Val Leu Pro Asn His Leu Gly Thr Leu
                1205                1210                1215
Leu Tyr His Ala Lys Asn Ile His Lys Val Asp Glu Pro Lys His Leu
            1220                1225                1230
Asp Tyr Val Asp Lys His Lys Asp Glu Phe Lys Glu Leu Leu Asp Val
        1235                1240                1245
Val Ser Asn Phe Ser Lys Lys Tyr Thr Leu Ala Glu Gly Asn Leu Glu
    1250                1255                1260
Lys Ile Lys Glu Leu Tyr Ala Gln Asn Asn Gly Glu Asp Leu Lys Glu
1265                1270                1275                1280
Leu Ala Ser Ser Phe Ile Asn Leu Leu Thr Phe Thr Ala Ile Gly Ala
                1285                1290                1295
Pro Ala Thr Phe Lys Phe Phe Asp Lys Asn Ile Asp Arg Lys Arg Tyr
            1300                1305                1310
Thr Ser Thr Thr Glu Ile Leu Asn Ala Thr Leu Ile His Gln Ser Ile
        1315                1320                1325
Thr Gly Leu Tyr Glu Thr Arg Ile Asp Leu Asn Lys Leu Gly Gly Asp
    1330                1335                1340


<210> 160
<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptococcus pyogenes Cas9
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<400> 160
Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val Gly
 1               5                  10                  15
Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe Lys
            20                  25                  30
Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile Gly
        35                  40                  45
Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu Lys
    50                  55                  60
Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys Tyr
65                  70                  75                  80
Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser Phe
                85                  90                  95
Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys His
            100                 105                 110
Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr His
        115                 120                 125
Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp Ser
    130                 135                 140
Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His Met
145                 150                 155                 160
Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro Asp
                165                 170                 175
Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr Asn
            180                 185                 190
Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala Lys
        195                 200                 205
Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
    210                 215                 220
Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225                 230                 235                 240
Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe Asp
                245                 250                 255
Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp Asp
            260                 265                 270
Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp Leu
        275                 280                 285
Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp Ile
    290                 295                 300
Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser Met
305                 310                 315                 320
Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys Ala
                325                 330                 335
Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp
            340                 345                 350
Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser Gln
        355                 360                 365
Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp Gly
    370                 375                 380

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Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg Lys
385                 390                 395                 400
Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu Gly
                405                 410                 415
Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe Leu
            420                 425                 430
Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile Pro
        435                 440                 445
Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp Met
    450                 455                 460
Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu Val
465                 470                 475                 480
Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr Asn
                485                 490                 495
Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser Leu
            500                 505                 510
Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys Tyr
        515                 520                 525
Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln Lys
    530                 535                 540
Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr Val
545                 550                 555                 560
Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp Ser
                565                 570                 575
Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly Thr
            580                 585                 590
Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp Asn
        595                 600                 605
Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu
    610                 615                 620
Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala His
625                 630                 635                 640
Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr Thr
                645                 650                 655
Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp Lys
            660                 665                 670
Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
        675                 680                 685
Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
    690                 695                 700
Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu His
705                 710                 715                 720
Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly Ile
                725                 730                 735
Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly Arg
            740                 745                 750
His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln Thr
        755                 760                 765
Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile Glu
    770                 775                 780
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Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro Val
785                 790                 795                 800
Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu Gln
                805                 810                 815
Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg Leu
            820                 825                 830
Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys Asp
        835                 840                 845
Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg Gly
    850                 855                 860
Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys Asn
865                 870                 875                 880
Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys Phe
                885                 890                 895
Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp Lys
            900                 905                 910
Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925
His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940
Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser Lys
945                 950                 955                 960
Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg Glu
                965                 970                 975
Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val Val
            980                 985                 990
Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe Val
        995                 1000                1005
Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala Lys Ser
    1010                1015                1020
Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr Ser Asn
1025                1030                1035                1040
Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn Gly Glu Ile
                1045                1050                1055
Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu Thr Gly Glu Ile Val
            1060                1065                1070
Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val Leu Ser Met
        1075                1080                1085
Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly Phe
    1090                1095                1100
Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu Ile Ala
1105                1110                1115                1120
Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe Asp Ser Pro
                1125                1130                1135
Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val Glu Lys Gly Lys
            1140                1145                1150
Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met
        1155                1160                1165
Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys
    1170                1175                1180
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Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr
1185                1190                1195                1200
Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala
                1205                1210                1215
Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
            1220                1225                1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser Pro
        1235                1240                1245
Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys His Tyr
    1250                1255                1260
Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys Arg Val Ile
1265                1270                1275                1280
Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys His
                1285                1290                1295
Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile Ile His Leu Phe
            1300                1305                1310
Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr Phe Asp Thr
        1315                1320                1325
Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val Leu Asp Ala
    1330                1335                1340
Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr Arg Ile Asp
1345                1350                1355                1360
Leu Ser Gln Leu Gly Gly Asp
                1365
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<210> 161
<211> 1387
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptococcus thermophilus Cas9

<400> 161

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

```
        115                 120                 125
Asp Glu Phe Pro Thr Ile Tyr His Leu Arg Lys Tyr Leu Ala Asp Ser
    130                 135                 140
Thr Lys Lys Ala Asp Leu Arg Leu Val Tyr Leu Ala Leu Ala His Met
145                 150                 155                 160
Ile Lys Tyr Arg Gly His Phe Leu Ile Glu Gly Glu Phe Asn Ser Lys
                165                 170                 175
Asn Asn Asp Ile Gln Lys Asn Phe Gln Asp Phe Leu Asp Thr Tyr Asn
            180                 185                 190
Ala Ile Phe Glu Ser Asp Leu Ser Leu Glu Asn Ser Lys Gln Leu Glu
        195                 200                 205
Glu Ile Val Lys Asp Lys Ile Ser Lys Leu Glu Lys Lys Asp Arg Ile
    210                 215                 220
Leu Lys Leu Phe Pro Gly Glu Lys Asn Ser Gly Ile Phe Ser Glu Phe
225                 230                 235                 240
Leu Lys Leu Ile Val Gly Asn Gln Ala Asp Phe Arg Lys Cys Phe Asn
                245                 250                 255
Leu Asp Glu Lys Ala Ser Leu His Phe Ser Lys Glu Ser Tyr Asp Glu
            260                 265                 270
Asp Leu Glu Thr Leu Leu Gly Tyr Ile Gly Asp Asp Tyr Ser Asp Val
        275                 280                 285
Phe Leu Lys Ala Lys Lys Leu Tyr Asp Ala Ile Leu Leu Ser Gly Phe
    290                 295                 300
Leu Thr Val Thr Asp Asn Glu Thr Glu Ala Pro Leu Ser Ser Ala Met
305                 310                 315                 320
Ile Lys Arg Tyr Asn Glu His Lys Glu Asp Leu Ala Leu Leu Lys Glu
                325                 330                 335
Tyr Ile Arg Asn Ile Ser Leu Lys Thr Tyr Asn Glu Val Phe Lys Asp
            340                 345                 350
Asp Thr Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Lys Thr Asn Gln
        355                 360                 365
Glu Asp Phe Tyr Val Tyr Leu Lys Lys Leu Leu Ala Glu Phe Glu Gly
    370                 375                 380
Ala Asp Tyr Phe Leu Glu Lys Ile Asp Arg Glu Asp Phe Leu Arg Lys
385                 390                 395                 400
Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro Tyr Gln Ile His Leu Gln
                405                 410                 415
Glu Met Arg Ala Ile Leu Asp Lys Gln Ala Lys Phe Tyr Pro Phe Leu
            420                 425                 430
Ala Lys Asn Lys Glu Arg Ile Glu Lys Ile Leu Thr Phe Arg Ile Pro
        435                 440                 445
Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Asp Phe Ala Trp Ser
    450                 455                 460
Ile Arg Lys Arg Asn Glu Lys Ile Thr Pro Trp Asn Phe Glu Asp Val
465                 470                 475                 480
Ile Asp Lys Glu Ser Ser Ala Glu Ala Phe Ile Asn Arg Met Thr Ser
                485                 490                 495
Phe Asp Leu Tyr Leu Pro Glu Glu Lys Val Leu Pro Lys His Ser Leu
            500                 505                 510
Leu Tyr Glu Thr Phe Asn Val Tyr Asn Glu Leu Thr Lys Val Arg Phe
```

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        515                 520                 525
Ile Ala Glu Ser Met Arg Asp Tyr Gln Phe Leu Asp Ser Lys Gln Lys
    530                 535                 540
Lys Asp Ile Val Arg Leu Tyr Phe Lys Asp Lys Arg Lys Val Thr Asp
545                 550                 555                 560
Lys Asp Ile Ile Glu Tyr Leu His Ala Ile Tyr Gly Tyr Asp Gly Ile
                565                 570                 575
Glu Leu Lys Gly Ile Glu Lys Gln Phe Asn Ser Ser Leu Ser Thr Tyr
            580                 585                 590
His Asp Leu Leu Asn Ile Ile Asn Asp Lys Glu Phe Leu Asp Asp Ser
        595                 600                 605
Ser Asn Glu Ala Ile Ile Glu Glu Ile Ile His Thr Leu Thr Ile Phe
    610                 615                 620
Glu Asp Arg Glu Met Ile Lys Gln Arg Leu Ser Lys Phe Glu Asn Ile
625                 630                 635                 640
Phe Asp Lys Ser Val Leu Lys Lys Leu Ser Arg Arg His Tyr Thr Gly
                645                 650                 655
Trp Gly Lys Leu Ser Ala Lys Leu Ile Asn Gly Ile Arg Asp Glu Lys
            660                 665                 670
Ser Gly Asn Thr Ile Leu Asp Tyr Leu Ile Asp Asp Gly Ile Ser Asn
        675                 680                 685
Arg Asn Phe Met Gln Leu Ile His Asp Asp Ala Leu Ser Phe Lys Lys
    690                 695                 700
Lys Ile Gln Lys Ala Gln Ile Ile Gly Asp Glu Asp Lys Gly Asn Ile
705                 710                 715                 720
Lys Glu Val Val Lys Ser Leu Pro Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735
Ile Leu Gln Ser Ile Lys Ile Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750
Gly Arg Lys Pro Glu Ser Ile Val Val Glu Met Ala Arg Glu Asn Gln
        755                 760                 765
Tyr Thr Asn Gln Gly Lys Ser Asn Ser Gln Gln Arg Leu Lys Arg Leu
    770                 775                 780
Glu Lys Ser Leu Lys Glu Leu Gly Ser Lys Ile Leu Lys Glu Asn Ile
785                 790                 795                 800
Pro Ala Lys Leu Ser Lys Ile Asp Asn Asn Ala Leu Gln Asn Asp Arg
                805                 810                 815
Leu Tyr Leu Tyr Tyr Leu Gln Asn Gly Lys Asp Met Tyr Thr Gly Asp
            820                 825                 830
Asp Leu Asp Ile Asp Arg Leu Ser Asn Tyr Asp Ile Asp His Ile Ile
        835                 840                 845
Pro Gln Ala Phe Leu Lys Asp Asn Ser Ile Asp Asn Lys Val Leu Val
    850                 855                 860
Ser Ser Ala Ser Asn Arg Gly Lys Ser Asp Asp Val Pro Ser Leu Glu
865                 870                 875                 880
Val Val Lys Lys Arg Lys Thr Phe Trp Tyr Gln Leu Leu Lys Ser Lys
                885                 890                 895
Leu Ile Ser Gln Arg Lys Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly
            900                 905                 910
Gly Leu Ser Pro Glu Asp Lys Ala Gly Phe Ile Gln Arg Gln Leu Val
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        915                 920                 925
Glu Thr Arg Gln Ile Thr Lys His Val Ala Arg Leu Leu Asp Glu Lys
    930                 935                 940
Phe Asn Asn Lys Lys Asp Glu Asn Asn Arg Ala Val Arg Thr Val Lys
945                 950                 955                 960
Ile Ile Thr Leu Lys Ser Thr Leu Val Ser Gln Phe Arg Lys Asp Phe
                965                 970                 975
Glu Leu Tyr Lys Val Arg Glu Ile Asn Asp Phe His His Ala His Asp
            980                 985                 990
Ala Tyr Leu Asn Ala Val Val Ala Ser Ala Leu Leu Lys Lys Tyr Pro
        995                 1000                1005
Lys Leu Glu Pro Glu Phe Val Tyr Gly Asp Tyr Pro Lys Tyr Asn Ser
    1010                1015                1020
Phe Arg Glu Arg Lys Ser Ala Thr Glu Lys Val Tyr Phe Tyr Ser Asn
1025                1030                1035                1040
Ile Met Asn Ile Phe Lys Lys Ser Ile Ser Leu Ala Asp Gly Arg Val
                1045                1050                1055
Ile Glu Arg Pro Leu Ile Glu Val Asn Glu Glu Thr Gly Glu Ser Val
            1060                1065                1070
Trp Asn Lys Glu Ser Asp Leu Ala Thr Val Arg Arg Val Leu Ser Tyr
        1075                1080                1085
Pro Gln Val Asn Val Val Lys Lys Val Glu Glu Gln Asn His Gly Leu
    1090                1095                1100
Asp Arg Gly Lys Pro Lys Gly Leu Phe Asn Ala Asn Leu Ser Ser Lys
1105                1110                1115                1120
Pro Lys Pro Asn Ser Asn Glu Asn Leu Val Gly Ala Lys Glu Tyr Leu
                1125                1130                1135
Asp Pro Lys Lys Tyr Gly Gly Tyr Ala Gly Ile Ser Asn Ser Phe Thr
            1140                1145                1150
Val Leu Val Lys Gly Thr Ile Glu Lys Gly Ala Lys Lys Lys Ile Thr
        1155                1160                1165
Asn Val Leu Glu Phe Gln Gly Ile Ser Ile Leu Asp Arg Ile Asn Tyr
    1170                1175                1180
Arg Lys Asp Lys Leu Asn Phe Leu Leu Glu Lys Gly Tyr Lys Asp Ile
1185                1190                1195                1200
Glu Leu Ile Ile Glu Leu Pro Lys Tyr Ser Leu Phe Glu Leu Ser Asp
                1205                1210                1215
Gly Ser Arg Arg Met Leu Ala Ser Ile Leu Ser Thr Asn Asn Lys Arg
            1220                1225                1230
Gly Glu Ile His Lys Gly Asn Gln Ile Phe Leu Ser Gln Lys Phe Val
        1235                1240                1245
Lys Leu Leu Tyr His Ala Lys Arg Ile Ser Asn Thr Ile Asn Glu Asn
    1250                1255                1260
His Arg Lys Tyr Val Glu Asn His Lys Lys Glu Phe Glu Glu Leu Phe
1265                1270                1275                1280
Tyr Tyr Ile Leu Glu Phe Asn Glu Asn Tyr Val Gly Ala Lys Lys Asn
                1285                1290                1295
Gly Lys Leu Leu Asn Ser Ala Phe Gln Ser Trp Gln Asn His Ser Ile
            1300                1305                1310
Asp Glu Leu Cys Ser Ser Phe Ile Gly Pro Thr Gly Ser Glu Arg Lys
```

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        1315                1320                1325
Gly Leu Phe Glu Leu Thr Ser Arg Gly Ser Ala Ala Asp Phe Glu Phe
    1330                1335                1340
Leu Gly Val Lys Ile Pro Arg Tyr Arg Asp Tyr Thr Pro Ser Ser Leu
1345                1350                1355                1360
Leu Lys Asp Ala Thr Leu Ile His Gln Ser Val Thr Gly Leu Tyr Glu
                1365                1370                1375
Thr Arg Ile Asp Leu Ala Lys Leu Gly Glu Gly
            1380                1385


<210> 162
<211> 1333
<212> PRT
<213> Artificial Sequence

<220>
<223> Listeria innocua Cas9

<400> 162
Lys Lys Pro Tyr Thr Ile Gly Leu Asp Ile Gly Thr Asn Ser Val Gly
 1               5                  10                  15
Trp Ala Val Leu Thr Asp Gln Tyr Asp Leu Val Lys Arg Lys Met Lys
            20                  25                  30
Ile Ala Gly Asp Ser Glu Lys Lys Gln Ile Lys Lys Asn Phe Trp Gly
        35                  40                  45
Val Arg Leu Phe Asp Glu Gly Gln Thr Ala Ala Asp Arg Arg Met Ala
    50                  55                  60
Arg Thr Ala Arg Arg Arg Ile Glu Arg Arg Arg Asn Arg Ile Ser Tyr
65                  70                  75                  80
Leu Gln Gly Ile Phe Ala Glu Glu Met Ser Lys Thr Asp Ala Asn Phe
                85                  90                  95
Phe Cys Arg Leu Ser Asp Ser Phe Tyr Val Asp Asn Glu Lys Arg Asn
            100                 105                 110
Ser Arg His Pro Phe Phe Ala Thr Ile Glu Glu Glu Val Glu Tyr His
        115                 120                 125
Lys Asn Tyr Pro Thr Ile Tyr His Leu Arg Glu Glu Leu Val Asn Ser
    130                 135                 140
Ser Glu Lys Ala Asp Leu Arg Leu Val Tyr Leu Ala Leu Ala His Ile
145                 150                 155                 160
Ile Lys Tyr Arg Gly Asn Phe Leu Ile Glu Gly Ala Leu Asp Thr Gln
                165                 170                 175
Asn Thr Ser Val Asp Gly Ile Tyr Lys Gln Phe Ile Gln Thr Tyr Asn
            180                 185                 190
Gln Val Phe Ala Ser Gly Ile Glu Asp Gly Ser Leu Lys Lys Leu Glu
        195                 200                 205
Asp Asn Lys Asp Val Ala Lys Ile Leu Val Glu Lys Val Thr Arg Lys
    210                 215                 220
Glu Lys Leu Glu Arg Ile Leu Lys Leu Tyr Pro Gly Glu Lys Ser Ala
225                 230                 235                 240
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Gly Met Phe Ala Gln Phe Ile Ser Leu Ile Val Gly Ser Lys Gly Asn
                245                 250                 255
Phe Gln Lys Pro Phe Asp Leu Ile Glu Lys Ser Asp Ile Glu Cys Ala
            260                 265                 270
Lys Asp Ser Tyr Glu Glu Asp Leu Glu Ser Leu Leu Ala Leu Ile Gly
        275                 280                 285
Asp Glu Tyr Ala Glu Leu Phe Val Ala Ala Lys Asn Ala Tyr Ser Ala
    290                 295                 300
Val Val Leu Ser Ser Ile Ile Thr Val Ala Glu Thr Glu Thr Asn Ala
305                 310                 315                 320
Lys Leu Ser Ala Ser Met Ile Glu Arg Phe Asp Thr His Glu Glu Asp
                325                 330                 335
Leu Gly Glu Leu Lys Ala Phe Ile Lys Leu His Leu Pro Lys His Tyr
            340                 345                 350
Glu Glu Ile Phe Ser Asn Thr Glu Lys His Gly Tyr Ala Gly Tyr Ile
        355                 360                 365
Asp Gly Lys Thr Lys Gln Ala Asp Phe Tyr Lys Tyr Met Lys Met Thr
    370                 375                 380
Leu Glu Asn Ile Glu Gly Ala Asp Tyr Phe Ile Ala Lys Ile Glu Lys
385                 390                 395                 400
Glu Asn Phe Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ala Ile Pro
                405                 410                 415
His Gln Leu His Leu Glu Glu Leu Glu Ala Ile Leu His Gln Gln Ala
            420                 425                 430
Lys Tyr Tyr Pro Phe Leu Lys Glu Asn Tyr Asp Lys Ile Lys Ser Leu
        435                 440                 445
Val Thr Phe Arg Ile Pro Tyr Phe Val Gly Pro Leu Ala Asn Gly Gln
    450                 455                 460
Ser Glu Phe Ala Trp Leu Thr Arg Lys Ala Asp Gly Glu Ile Arg Pro
465                 470                 475                 480
Trp Asn Ile Glu Glu Lys Val Asp Phe Gly Lys Ser Ala Val Asp Phe
                485                 490                 495
Ile Glu Lys Met Thr Asn Lys Asp Thr Tyr Leu Pro Lys Glu Asn Val
            500                 505                 510
Leu Pro Lys His Ser Leu Cys Tyr Gln Lys Tyr Leu Val Tyr Asn Glu
        515                 520                 525
Leu Thr Lys Val Arg Tyr Ile Asn Asp Gln Gly Lys Thr Ser Tyr Phe
    530                 535                 540
Ser Gly Gln Glu Lys Glu Gln Ile Phe Asn Asp Leu Phe Lys Gln Lys
545                 550                 555                 560
Arg Lys Val Lys Lys Lys Asp Leu Glu Leu Phe Leu Arg Asn Met Ser
                565                 570                 575
His Val Glu Ser Pro Thr Ile Glu Gly Leu Glu Asp Ser Phe Asn Ser
            580                 585                 590
Ser Tyr Ser Thr Tyr His Asp Leu Leu Lys Val Gly Ile Lys Gln Glu
        595                 600                 605
Ile Leu Asp Asn Pro Val Asn Thr Glu Met Leu Glu Asn Ile Val Lys
    610                 615                 620
Ile Leu Thr Val Phe Glu Asp Lys Arg Met Ile Lys Glu Gln Leu Gln
625                 630                 635                 640
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Gln Phe Ser Asp Val Leu Asp Gly Val Val Leu Lys Lys Leu Glu Arg
                645                 650                 655
Arg His Tyr Thr Gly Trp Gly Arg Leu Ser Ala Lys Leu Leu Met Gly
            660                 665                 670
Ile Arg Asp Lys Gln Ser His Leu Thr Ile Leu Asp Tyr Leu Met Asn
        675                 680                 685
Asp Asp Gly Leu Asn Arg Asn Leu Met Gln Leu Ile Asn Asp Ser Asn
    690                 695                 700
Leu Ser Phe Lys Ser Ile Ile Glu Lys Glu Gln Val Thr Thr Ala Asp
705                 710                 715                 720
Lys Asp Ile Gln Ser Ile Val Ala Asp Leu Ala Gly Ser Pro Ala Ile
                725                 730                 735
Lys Lys Gly Ile Leu Gln Ser Leu Lys Ile Val Asp Glu Leu Val Ser
            740                 745                 750
Val Met Gly Tyr Pro Pro Gln Thr Ile Val Val Glu Met Ala Arg Glu
        755                 760                 765
Asn Gln Thr Thr Gly Lys Gly Lys Asn Asn Ser Arg Pro Arg Tyr Lys
    770                 775                 780
Ser Leu Glu Lys Ala Ile Lys Glu Phe Gly Ser Gln Ile Leu Lys Glu
785                 790                 795                 800
His Pro Thr Asp Asn Gln Glu Leu Arg Asn Asn Arg Leu Tyr Leu Tyr
                805                 810                 815
Tyr Leu Gln Asn Gly Lys Asp Met Tyr Thr Gly Gln Asp Leu Asp Ile
            820                 825                 830
His Asn Leu Ser Asn Tyr Asp Ile Asp His Ile Val Pro Gln Ser Phe
        835                 840                 845
Ile Thr Asp Asn Ser Ile Asp Asn Leu Val Leu Thr Ser Ser Ala Gly
    850                 855                 860
Asn Arg Glu Lys Gly Asp Asp Val Pro Pro Leu Glu Ile Val Arg Lys
865                 870                 875                 880
Arg Lys Val Phe Trp Glu Lys Leu Tyr Gln Gly Asn Leu Met Ser Lys
                885                 890                 895
Arg Lys Phe Asp Tyr Leu Thr Lys Ala Glu Arg Gly Gly Leu Thr Glu
            900                 905                 910
Ala Asp Lys Ala Arg Phe Ile His Arg Gln Leu Val Glu Thr Arg Gln
        915                 920                 925
Ile Thr Lys Asn Val Ala Asn Ile Leu His Gln Arg Phe Asn Tyr Glu
    930                 935                 940
Lys Asp Asp His Gly Asn Thr Met Lys Gln Val Arg Ile Val Thr Leu
945                 950                 955                 960
Lys Ser Ala Leu Val Ser Gln Phe Arg Lys Gln Phe Gln Leu Tyr Lys
                965                 970                 975
Val Arg Asp Val Asn Asp Tyr His His Ala His Asp Ala Tyr Leu Asn
            980                 985                 990
Gly Val Val Ala Asn Thr Leu Leu Lys Val Tyr Pro Gln Leu Glu Pro
        995                 1000                1005
Glu Phe Val Tyr Gly Asp Tyr His Gln Phe Asp Trp Phe Lys Ala Asn
    1010                1015                1020
Lys Ala Thr Ala Lys Lys Gln Phe Tyr Thr Asn Ile Met Leu Phe Phe
1025                1030                1035                1040
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Ala Gln Lys Asp Arg Ile Ile Asp Glu Asn Gly Glu Ile Leu Trp Asp
                1045                1050                1055
Lys Lys Tyr Leu Asp Thr Val Lys Lys Val Met Ser Tyr Arg Gln Met
            1060                1065                1070
Asn Ile Val Lys Lys Thr Glu Ile Gln Lys Gly Glu Phe Ser Lys Ala
        1075                1080                1085
Thr Ile Lys Pro Lys Gly Asn Ser Ser Lys Leu Ile Pro Arg Lys Thr
    1090                1095                1100
Asn Trp Asp Pro Met Lys Tyr Gly Gly Leu Asp Ser Pro Asn Met Ala
1105                1110                1115                1120
Tyr Ala Val Val Ile Glu Tyr Ala Lys Gly Lys Asn Lys Leu Val Phe
                1125                1130                1135
Glu Lys Lys Ile Ile Arg Val Thr Ile Met Glu Arg Lys Ala Phe Glu
            1140                1145                1150
Lys Asp Glu Lys Ala Phe Leu Glu Glu Gln Gly Tyr Arg Gln Pro Lys
        1155                1160                1165
Val Leu Ala Lys Leu Pro Lys Tyr Thr Leu Tyr Glu Cys Glu Glu Gly
    1170                1175                1180
Arg Arg Arg Met Leu Ala Ser Ala Asn Glu Ala Gln Lys Gly Asn Gln
1185                1190                1195                1200
Gln Val Leu Pro Asn His Leu Val Thr Leu Leu His His Ala Ala Asn
                1205                1210                1215
Cys Glu Val Ser Asp Gly Lys Ser Leu Asp Tyr Ile Glu Ser Asn Arg
            1220                1225                1230
Glu Met Phe Ala Glu Leu Leu Ala His Val Ser Glu Phe Ala Lys Arg
        1235                1240                1245
Tyr Thr Leu Ala Glu Ala Asn Leu Asn Lys Ile Asn Gln Leu Phe Glu
    1250                1255                1260
Gln Asn Lys Glu Gly Asp Ile Lys Ala Ile Ala Gln Ser Phe Val Asp
1265                1270                1275                1280
Leu Met Ala Phe Asn Ala Met Gly Ala Pro Ala Ser Phe Lys Phe Phe
                1285                1290                1295
Glu Thr Thr Ile Glu Arg Lys Arg Tyr Asn Asn Leu Lys Glu Leu Leu
            1300                1305                1310
Asn Ser Thr Ile Ile Tyr Gln Ser Ile Thr Gly Leu Tyr Glu Ser Arg
        1315                1320                1325
Lys Arg Leu Asp Asp
    1330
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<210> 163
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence 2

<400> 163
gagaatcaaa atcggtgaat 20

<210> 164
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBC target sequence 2

<400> 164
ggcctcggcg ctgacgatct 20

<210> 165
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 3

<400> 165
gagaatcaaa atcggtgaat agg 23

<210> 166
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 4

<400> 166
ttcaaaacct gtcagtgatt ggg 23

<210> 167
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 5

<400> 167
tgtgctagac atgaggtcta tgg 23

<210> 168
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 6

<400> 168
cgtcatgagc agattaaacc cgg 23

<210> 169
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 7

<400> 169
tcagggttct ggatatctgt ggg 23

<210> 170
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 8

<400> 170
gtcagggttc tggatatctg tgg 23

<210> 171
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 9

<400> 171
ttcggaaccc aatcactgac agg 23

<210> 172
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 10

<400> 172
taaacccggc cactttcagg agg 23

<210> 173
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 11

<400> 173
aaagtcagat ttgttgctcc agg 23

<210> 174
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 12

<400> 174
aacaaatgtg tcacaaagta agg 23

<210> 175
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 13

<400> 175
tggatttaga gtctctcagc tgg 23

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

<220>
<223> TRAC target sequence with PAM 14

<400> 176
taggcagaca gacttgtcac tgg 23

<210> 177
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> TRAC target sequence with PAM 15

<400> 177
agctggtaca cggcagggtc agg 23

<210> 178
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 16

<400> 178
gctggtacac ggcagggtca ggg 23

<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 17

<400> 179
tctctcagct ggtacacggc agg 23

<210> 180
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 18

<400> 180
tttcaaaacc tgtcagtgat tgg 23

<210> 181
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 19

<400> 181
gattaaaccc ggccactttc agg 23

<210> 182

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 20

<400> 182
ctcgaccagc ttgacatcac agg 23

<210> 183
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 21

<400> 183
agagtctctc agctggtaca cgg 23

<210> 184
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 22

<400> 184
ctctcagctg gtacacggca ggg 23

<210> 185
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 23

<400> 185
aagttcctgt gatgtcaagc tgg 23

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 24

<400> 186
atcctcctcc tgaaagtggc cgg 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 25

<400> 187
tgctcatgac gctgcggctg tgg 23

<210> 188
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 26

<400> 188
acaaaactgt gctagacatg agg 23

<210> 189
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 27

<400> 189
atttgtttga gaatcaaaat cgg 23

<210> 190
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 28

<400> 190
catcacagga actttctaaa agg 23

<210> 191
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 29

<400> 191
gtcgagaaaa gctttgaaac agg 23

<210> 192
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 30

<400> 192
ccactttcag gaggaggatt cgg 23

<210> 193
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 31

<400> 193
ctgacaggtt ttgaaagttt agg 23

<210> 194
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 32

<400> 194
agctttgaaa caggtaagac agg 23

<210> 195
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 33

<400> 195
tggaataatg ctgttgttga agg 23

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 34

<400> 196
agagcaacag tgctgtggcc tgg 23

<210> 197
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 35

<400> 197
ctgtggtcca gctgaggtga ggg 23

<210> 198
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 36

<400> 198
ctgcggctgt ggtccagctg agg 23

<210> 199
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 37

<400> 199
tgtggtccag ctgaggtgag ggg 23

<210> 200
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 38

<400> 200
cttcttcccc agcccaggta agg 23

<210> 201
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 39

<400> 201
acacggcagg gtcagggttc tgg 23

<210> 202
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 40

<400> 202
cttcaagagc aacagtgctg tgg 23

<210> 203
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 41

<400> 203
ctggggaaga aggtgtcttc tgg 23

<210> 204
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 42

<400> 204

tcctcctcct gaaagtggcc ggg 23

<210> 205
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 43

<400> 205
ttaatctgct catgacgctg cgg 23

<210> 206
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 44

<400> 206
acccggccac tttcaggagg agg 23

<210> 207
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 45

<400> 207
ttcttcccca gcccaggtaa ggg 23

<210> 208
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 46

<400> 208
cttacctggg ctggggaaga agg 23

<210> 209
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 47

<400> 209
gacaccttct tccccagccc agg 23

<210> 210
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 48

<400> 210
gctgtggtcc agctgaggtg agg 23

<210> 211
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC target sequence with PAM 49

<400> 211
ccgaatcctc ctcctgaaag tgg 23

<210> 212
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBC target sequence with PAM 3

<400> 212
gctgtcaagt ccagttctac ggg 23

<210> 213
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 1

<400> 213
ctatggactt caagagcaac agtgctgt 28

<210> 214
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 2

<400> 214
ctcatgtcta gcacagtttt gtctgtga 28

<210> 215
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 3

<400> 215
gtgctgtggc ctggagcaac aaatctga 28

<210> 216
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 4

<400> 216
ttgctcttga agtccataga cctcatgt 28

<210> 217
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 5

<400> 217
ctgtggcctg gagcaacaaa tctgact 27

<210> 218
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 6

<400> 218
ctgttgctct tgaagtccat agacctca 28

<210> 219
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 7

<400> 219
ctgtggcctg gagcaacaaa tctgactt 28

<210> 220
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 8

<400> 220
ctgactttgc atgtgcaaac gccttcaa 28

<210> 221
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 9

<400> 221
ttgttgctcc aggccacagc actgttgc 28

<210> 222
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 10

<400> 222
tgaaagtggc cgggtttaat ctgctcat 28

<210> 223
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 11

<400> 223
aggaggattc ggaacccaat cactgaca 28

<210> 224
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC ZFN target sequence 12

<400> 224
gaggaggatt cggaacccaa tcactgac 28

<210> 225
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBC ZFN target sequence 1

<400> 225
ccgtagaact ggacttgaca gcggaagt 28

<210> 226
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBC ZFN target sequence 2

<400> 226
tctcggagaa tgacgagtgg acccagga 28

<210> 227
<211> 1082
<212> PRT
<213> Artificial Sequence

<220>

<223> Neisseria meningitidis Cas9

<400> 227
Met Ala Ala Phe Lys Pro Asn Ser Ile Asn Tyr Ile Leu Gly Leu Asp
 1               5                  10                  15
Ile Gly Ile Ala Ser Val Gly Trp Ala Met Val Glu Ile Asp Glu Glu
            20                  25                  30
Glu Asn Pro Ile Arg Leu Ile Asp Leu Gly Val Arg Val Phe Glu Arg
        35                  40                  45
Ala Glu Val Pro Lys Thr Gly Asp Ser Leu Ala Met Ala Arg Arg Leu
    50                  55                  60
Ala Arg Ser Val Arg Arg Leu Thr Arg Arg Arg Ala His Arg Leu Leu
65                  70                  75                  80
Arg Thr Arg Arg Leu Leu Lys Arg Glu Gly Val Leu Gln Ala Ala Asn
                85                  90                  95
Phe Asp Glu Asn Gly Leu Ile Lys Ser Leu Pro Asn Thr Pro Trp Gln
            100                 105                 110
Leu Arg Ala Ala Ala Leu Asp Arg Lys Leu Thr Pro Leu Glu Trp Ser
        115                 120                 125
Ala Val Leu Leu His Leu Ile Lys His Arg Gly Tyr Leu Ser Gln Arg
    130                 135                 140
Lys Asn Glu Gly Glu Thr Ala Asp Lys Glu Leu Gly Ala Leu Leu Lys
145                 150                 155                 160
Gly Val Ala Gly Asn Ala His Ala Leu Gln Thr Gly Asp Phe Arg Thr
                165                 170                 175
Pro Ala Glu Leu Ala Leu Asn Lys Phe Glu Lys Glu Ser Gly His Ile
            180                 185                 190
Arg Asn Gln Arg Ser Asp Tyr Ser His Thr Phe Ser Arg Lys Asp Leu
        195                 200                 205
Gln Ala Glu Leu Ile Leu Leu Phe Glu Lys Gln Lys Glu Phe Gly Asn
    210                 215                 220
Pro His Val Ser Gly Gly Leu Lys Glu Gly Ile Glu Thr Leu Leu Met
225                 230                 235                 240
Thr Gln Arg Pro Ala Leu Ser Gly Asp Ala Val Gln Lys Met Leu Gly
                245                 250                 255
His Cys Thr Phe Glu Pro Ala Glu Pro Lys Ala Ala Lys Asn Thr Tyr
            260                 265                 270
Thr Ala Glu Arg Phe Ile Trp Leu Thr Lys Leu Asn Asn Leu Arg Ile
        275                 280                 285
Leu Glu Gln Gly Ser Glu Arg Pro Leu Thr Asp Thr Glu Arg Ala Thr
    290                 295                 300
Leu Met Asp Glu Pro Tyr Arg Lys Ser Lys Leu Thr Tyr Ala Gln Ala
305                 310                 315                 320
Arg Lys Leu Leu Gly Leu Glu Asp Thr Ala Phe Phe Lys Gly Leu Arg
                325                 330                 335
Tyr Gly Lys Asp Asn Ala Glu Ala Ser Thr Leu Met Glu Met Lys Ala
            340                 345                 350
Tyr His Ala Ile Ser Arg Ala Leu Glu Lys Glu Gly Leu Lys Asp Lys
        355                 360                 365
Lys Ser Pro Leu Asn Leu Ser Pro Glu Leu Gln Asp Glu Ile Gly Thr

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    370                 375                 380
Ala Phe Ser Leu Phe Lys Thr Asp Glu Asp Ile Thr Gly Arg Leu Lys
385                 390                 395                 400
Asp Arg Ile Gln Pro Glu Ile Leu Glu Ala Leu Leu Lys His Ile Ser
                405                 410                 415
Phe Asp Lys Phe Val Gln Ile Ser Leu Lys Ala Leu Arg Arg Ile Val
            420                 425                 430
Pro Leu Met Glu Gln Gly Lys Arg Tyr Asp Glu Ala Cys Ala Glu Ile
        435                 440                 445
Tyr Gly Asp His Tyr Gly Lys Lys Asn Thr Glu Glu Lys Ile Tyr Leu
    450                 455                 460
Pro Pro Ile Pro Ala Asp Glu Ile Arg Asn Pro Val Val Leu Arg Ala
465                 470                 475                 480
Leu Ser Gln Ala Arg Lys Val Ile Asn Gly Val Val Arg Arg Tyr Gly
                485                 490                 495
Ser Pro Ala Arg Ile His Ile Glu Thr Ala Arg Glu Val Gly Lys Ser
            500                 505                 510
Phe Lys Asp Arg Lys Glu Ile Glu Lys Arg Gln Glu Glu Asn Arg Lys
        515                 520                 525
Asp Arg Glu Lys Ala Ala Ala Lys Phe Arg Glu Tyr Phe Pro Asn Phe
    530                 535                 540
Val Gly Glu Pro Lys Ser Lys Asp Ile Leu Lys Leu Arg Leu Tyr Glu
545                 550                 555                 560
Gln Gln His Gly Lys Cys Leu Tyr Ser Gly Lys Glu Ile Asn Leu Gly
                565                 570                 575
Arg Leu Asn Glu Lys Gly Tyr Val Glu Ile Asp His Ala Leu Pro Phe
            580                 585                 590
Ser Arg Thr Trp Asp Asp Ser Phe Asn Asn Lys Val Leu Val Leu Gly
        595                 600                 605
Ser Glu Asn Gln Asn Lys Gly Asn Gln Thr Pro Tyr Glu Tyr Phe Asn
    610                 615                 620
Gly Lys Asp Asn Ser Arg Glu Trp Gln Glu Phe Lys Ala Arg Val Glu
625                 630                 635                 640
Thr Ser Arg Phe Pro Arg Ser Lys Lys Gln Arg Ile Leu Leu Gln Lys
                645                 650                 655
Phe Asp Glu Asp Gly Phe Lys Glu Arg Asn Leu Asn Asp Thr Arg Tyr
            660                 665                 670
Val Asn Arg Phe Leu Cys Gln Phe Val Ala Asp Arg Met Arg Leu Thr
        675                 680                 685
Gly Lys Gly Lys Lys Arg Val Phe Ala Ser Asn Gly Gln Ile Thr Asn
    690                 695                 700
Leu Leu Arg Gly Phe Trp Gly Leu Arg Lys Val Arg Ala Glu Asn Asp
705                 710                 715                 720
Arg His His Ala Leu Asp Ala Val Val Val Ala Cys Ser Thr Val Ala
                725                 730                 735
Met Gln Gln Lys Ile Thr Arg Phe Val Arg Tyr Lys Glu Met Asn Ala
            740                 745                 750
Phe Asp Gly Lys Thr Ile Asp Lys Glu Thr Gly Glu Val Leu His Gln
        755                 760                 765
Lys Thr His Phe Pro Gln Pro Trp Glu Phe Phe Ala Gln Glu Val Met
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    770                 775                 780
Ile Arg Val Phe Gly Lys Pro Asp Gly Lys Pro Glu Phe Glu Glu Ala
785                 790                 795                 800
Asp Thr Leu Glu Lys Leu Arg Thr Leu Leu Ala Glu Lys Leu Ser Ser
                805                 810                 815
Arg Pro Glu Ala Val His Glu Tyr Val Thr Pro Leu Phe Val Ser Arg
            820                 825                 830
Ala Pro Asn Arg Lys Met Ser Gly Gln Gly His Met Glu Thr Val Lys
        835                 840                 845
Ser Ala Lys Arg Leu Asp Glu Gly Val Ser Val Leu Arg Val Pro Leu
    850                 855                 860
Thr Gln Leu Lys Leu Lys Asp Leu Glu Lys Met Val Asn Arg Glu Arg
865                 870                 875                 880
Glu Pro Lys Leu Tyr Glu Ala Leu Lys Ala Arg Leu Glu Ala His Lys
                885                 890                 895
Asp Asp Pro Ala Lys Ala Phe Ala Glu Pro Phe Tyr Lys Tyr Asp Lys
            900                 905                 910
Ala Gly Asn Arg Thr Gln Gln Val Lys Ala Val Arg Val Glu Gln Val
        915                 920                 925
Gln Lys Thr Gly Val Trp Val Arg Asn His Asn Gly Ile Ala Asp Asn
    930                 935                 940
Ala Thr Met Val Arg Val Asp Val Phe Glu Lys Gly Asp Lys Tyr Tyr
945                 950                 955                 960
Leu Val Pro Ile Tyr Ser Trp Gln Val Ala Lys Gly Ile Leu Pro Asp
                965                 970                 975
Arg Ala Val Val Gln Gly Lys Asp Glu Glu Asp Trp Gln Leu Ile Asp
            980                 985                 990
Asp Ser Phe Asn Phe Lys Phe Ser Leu His Pro Asn Asp Leu Val Glu
        995                 1000                1005
Val Ile Thr Lys Lys Ala Arg Met Phe Gly Tyr Phe Ala Ser Cys His
    1010                1015                1020
Arg Gly Thr Gly Asn Ile Asn Ile Arg Ile His Asp Leu Asp His Lys
1025                1030                1035                1040
Ile Gly Lys Asn Gly Ile Leu Glu Gly Ile Gly Val Lys Thr Ala Leu
                1045                1050                1055
Ser Phe Gln Lys Tyr Gln Ile Asp Glu Leu Gly Lys Glu Ile Arg Pro
            1060                1065                1070
Cys Arg Leu Lys Lys Arg Pro Pro Val Arg
        1075                1080


<210> 228
<211> 1368
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptococcus pyogenes Cas9

<400> 228
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Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
 1               5                  10                  15
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45
Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
            340                 345                 350
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
        355                 360                 365
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
    370                 375                 380
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385                 390                 395                 400
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Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
                405                 410                 415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
            420                 425                 430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
        435                 440                 445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
    450                 455                 460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
                485                 490                 495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
                565                 570                 575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
            580                 585                 590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
        595                 600                 605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
    610                 615                 620
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625                 630                 635                 640
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
                645                 650                 655
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
            660                 665                 670
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
        675                 680                 685
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
    690                 695                 700
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705                 710                 715                 720
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
        755                 760                 765
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
    770                 775                 780
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785                 790                 795                 800
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Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
                805                 810                 815
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
    850                 855                 860
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975
Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990
Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
        995                 1000                1005
Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala Lys
    1010                1015                1020
Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr Ser
1025                1030                1035                1040
Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn Gly Glu
                1045                1050                1055
Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu Thr Gly Glu Ile
            1060                1065                1070
Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val Leu Ser
        1075                1080                1085
Met Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly
    1090                1095                1100
Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu Ile
1105                1110                1115                1120
Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe Asp Ser
                1125                1130                1135
Pro Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val Glu Lys Gly
            1140                1145                1150
Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile Thr Ile
        1155                1160                1165
Met Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala
    1170                1175                1180
Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys
1185                1190                1195                1200
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Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser
                1205                1210                1215
Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr
            1220                1225                1230
Val Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
        1235                1240                1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys His
    1250                1255                1260
Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys Arg Val
1265                1270                1275                1280
Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys
                1285                1290                1295
His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile Ile His Leu
            1300                1305                1310
Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr Phe Asp
        1315                1320                1325
Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val Leu Asp
    1330                1335                1340
Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr Arg Ile
1345                1350                1355                1360
Asp Leu Ser Gln Leu Gly Gly Asp
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<210> 229
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 50 bp 5' Homology Arm

<400> 229
agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 50

<210> 230
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 100 bp 5' Homology Arm

<400> 230
ctgatcctct tgtcccacag atatccagaa ccctgaccct gccgtgtacc agctgagaga 60
ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 100

<210> 231
<211> 200
<212> DNA

<213> Artificial Sequence

<220>
<223> TRAC 200 bp 5' Homology Arm

<400> 231
gtgacttgcc agccccacag agccccgccc ttgtccatca ctggcatctg gactccagcc 60
tgggttgggg caaagaggga aatgagatca tgtcctaacc ctgatcctct tgtcccacag 120
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 180
ctgtctgcct attcaccgat 200

<210> 232
<211> 300
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 300 bp 5' Homology Arm

<400> 232
cctcttggcc aagattgata gcttgtgcct gtccctgagt cccagtccat cacgagcagc 60
tggtttctaa gatgctattt cccgtataaa gcatgagacc gtgacttgcc agccccacag 120
agccccgccc ttgtccatca ctggcatctg gactccagcc tgggttgggg caaagaggga 180
aatgagatca tgtcctaacc ctgatcctct tgtcccacag atatccagaa ccctgaccct 240
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 300


<210> 233
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 400 bp 5' Homology Arm

<400> 233
attaaataaa agaataagca gtattattaa gtagccctgc atttcaggtt tccttgagtg 60
gcaggccagg cctggccgtg aacgttcact gaaatcatgg cctcttggcc aagattgata 120
gcttgtgcct gtccctgagt cccagtccat cacgagcagc tggtttctaa gatgctattt 180
cccgtataaa gcatgagacc gtgacttgcc agccccacag agccccgccc ttgtccatca 240
ctggcatctg gactccagcc tgggttgggg caaagaggga aatgagatca tgtcctaacc 300
ctgatcctct tgtcccacag atatccagaa ccctgaccct gccgtgtacc agctgagaga 360
ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 400

<210> 234
<211> 500
<212> DNA
<213> Artificial Sequence

<220>

<223> TRAC 500 bp 5' Homology Arm

<400> 234
ctccagattc caagatgtac agtttgcttt gctgggcctt tttcccatgc ctgcctttac 60
tctgccagag ttatattgct ggggttttga agaagatcct attaaataaa agaataagca 120
gtattattaa gtagccctgc atttcaggtt tccttgagtg gcaggccagg cctggccgtg 180
aacgttcact gaaatcatgg cctcttggcc aagattgata gcttgtgcct gtccctgagt 240
cccagtccat cacgagcagc tggtttctaa gatgctattt cccgtataaa gcatgagacc 300
gtgacttgcc agccccacag agccccgccc ttgtccatca ctggcatctg gactccagcc 360
tgggttgggg caaagaggga aatgagatca tgtcctaacc ctgatcctct tgtcccacag 420
atatccagaa ccctgaccct gccgtgtacc agctgagaga ctctaaatcc agtgacaagt 480
ctgtctgcct attcaccgat                                           500

<210> 235
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 600 bp 5' Homology Arm

<400> 235
agagagcaat ctcctggtaa tgtgatagat ttcccaactt aatgccaaca taccataaac 60
ctcccattct gctaatgccc agcctaagtt ggggagacca ctccagattc caagatgtac 120
agtttgcttt gctgggcctt tttcccatgc ctgcctttac tctgccagag ttatattgct 180
ggggttttga agaagatcct attaaataaa agaataagca gtattattaa gtagccctgc 240
atttcaggtt tccttgagtg gcaggccagg cctggccgtg aacgttcact gaaatcatgg 300
cctcttggcc aagattgata gcttgtgcct gtccctgagt cccagtccat cacgagcagc 360
tggtttctaa gatgctattt cccgtataaa gcatgagacc gtgacttgcc agccccacag 420
agccccgccc ttgtccatca ctggcatctg gactccagcc tgggttgggg caaagaggga 480
aatgagatca tgtcctaacc ctgatcctct tgtcccacag atatccagaa ccctgaccct 540
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat 600


<210> 236
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 50 bp 3' Homology Arm

<400> 236
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat            50

<210> 237
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 100 bp 3' Homology Arm

<400> 237
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca 100

<210> 238
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 200 bp 3' Homology Arm

<400> 238
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg 200

<210> 239
<211> 300
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 300 bp 3' Homology Arm

<400> 239
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300


<210> 240
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 400 bp 3' Homology Arm

<400> 240
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240

atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttgttc 360
tggcagtcca gagaatgaca cgggaaaaaa gcagatgaag 400

<210> 241
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 500 bp 3' Homology Arm

<400> 241
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttgttc 360
tggcagtcca gagaatgaca cgggaaaaaa gcagatgaag agaaggtggc aggagagggc 420
acgtggccca gcctcagtct ctccaactga gttcctgcct gcctgccttt gctcagactg 480
tttgcccctt actgctcttc 500

<210> 242
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> TRAC 600 bp 3' Homology Arm

<400> 242
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa 60
actgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac 120
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc 180
ttccccagcc caggtaaggg cagctttggt gccttcgcag gctgtttcct tgcttcagga 240
atggccaggt tctgcccaga gctctggtca atgatgtcta aaactcctct gattggtggt 300
ctcggcctta tccattgcca ccaaaaccct ctttttacta agaaacagtg agccttgttc 360
tggcagtcca gagaatgaca cgggaaaaaa gcagatgaag agaaggtggc aggagagggc 420
acgtggccca gcctcagtct ctccaactga gttcctgcct gcctgccttt gctcagactg 480
tttgcccctt actgctcttc taggcctcat tctaagcccc ttctccaagt tgcctctcct 540
tatttctccc tgtctgccaa aaaatctttc ccagctcact aagtcagtct cacgcagtca 600


<210> 243
<211> 141
<212> PRT
<213> Artificial Sequence

<220>

<223> Human TCR alpha constant

<400> 243
Asn Ile Gln Lys Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Ala Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 244
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 244
His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140

<210> 245
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 245
Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 246
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 246
Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80

```
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140
```

<210> 247
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 247

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

<210> 248
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 248

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

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


<210> 249
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 249
His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 250
<211> 141
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 250
Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 251
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 251
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala

```
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 252
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR alpha constant

<400> 252
Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
 1               5                  10                  15
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
            20                  25                  30
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
    50                  55                  60
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65                  70                  75                  80
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
                85                  90                  95
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
            100                 105                 110
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
        115                 120                 125
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
    130                 135                 140


<210> 253
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 253
Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1               5                  10                  15
Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
            20                  25                  30
Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
        35                  40                  45
Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
```

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

<210> 254
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 254

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

```
Asp Ser Arg Gly
            180


<210> 255
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 255
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
 1               5                  10                  15
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
            20                  25                  30
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
        35                  40                  45
Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu
    50                  55                  60
Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg
65                  70                  75                  80
Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg
                85                  90                  95
Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
            100                 105                 110
Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
        115                 120                 125
Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu
    130                 135                 140
Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
145                 150                 155                 160
Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys
                165                 170                 175
Asp Ser Arg Gly
            180


<210> 256
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 256
Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
 1               5                  10                  15
```

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

<210> 257
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 257

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

```
    130                 135                 140
Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
145                 150                 155                 160
Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys
                165                 170                 175
Asp Ser Arg Gly
            180


<210> 258
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TCR beta constant

<400> 258
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
 1               5                  10                  15
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
            20                  25                  30
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
        35                  40                  45
Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu
    50                  55                  60
Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg
65                  70                  75                  80
Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg
                85                  90                  95
Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
            100                 105                 110
Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
        115                 120                 125
Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu
    130                 135                 140
Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
145                 150                 155                 160
Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys
                165                 170                 175
Asp Ser Arg Gly
            180


<210> 259
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
```

<223> Partial TCR alpha constant region

<400> 259
Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
 1               5                  10                  15
Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
            20                  25                  30
Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
        35                  40                  45

<210> 260
<211> 131
<212> DNA
<213> Artificial Sequence

<220>
<223> Partial endogenous TCR alpha constant region

<400> 260
gtgctagaca tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa 60
tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc 120
cccagcccag g                                                      131

<210> 261
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Partial TCR alpha constant region

<400> 261
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
 1               5                  10                  15
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
            20                  25                  30
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
        35                  40