SEQUENCE LISTING

<110> Fred Hutchinson Cancer Research Center
University of Washington

<120> RECOMBINANT AD35 VECTORS AND RELATED GENE THERAPY IMPROVEMENTS

<130> F053-0107PCT/19-132-WO-PCT

<140> PCT/US 2020/040756
<141> 2020-07-02

<150> US 62/869,907
<151> 2019-07-02

<150> US 62/935,507
<151> 2019-11-14

<150> US 63/009,385
<151> 2020-04-13

<160> 325

<170> PatentIn version 3.5

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<223> 5 end vector sequence, Sleeping Beauty IR/DR sequence,
integration junction (chr15, 6805206)

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cacaccctag ctgacacaag aatttgaaat acatccacag gtacacctcc aattgactca 180

aatgatgtca attagtctat cataatcttc taaagccatg acatcatttt aactggaatt 240

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ttgtgtcatg cacaaagtag atgtcctaac tgacttgcca aaactattgt ttgttaacaa 420

gaaatttgtg gagtagttga aaaacgagtt ttaatgactc caacttaagt gtatgtaaac 480

ttccgacttc aactgtaaga atggcccatt catctatagt agcacacaat atttgcattt 540

gtgcgacagt ataagggaca attatgctat caggcatttt tccaaagtga gtaatcgaag 600

tttttatacc tttgtgtgcc atgtttgcta ccatggtggg ataatcttac acgcgttctc 660

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<211> 607
<212> DNA
<213> Artificial Sequence

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<223> 5 end vector sequence, Sleeping Beauty IR/DR sequence,
integration junction (chrX, 16897322)

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<222> (594)..(594)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (602)..(602)
<223> n is a, c, g, or t

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aaatgatgtc aattagtcta tcataatctt ctaaagccat gacatcattt taactggaat 180

tttccaagct gtttaaaggc acagtcaact tagtgtatgt aaacttctga cccactggaa 240

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cttgtgtcat gcaaagtaga tgtcctaact gacttgccaa aactattgtt tgttaacaag 360

aaatttgtgg agtagttgaa aaacgagttt taatgactcc aacttaagtg tatgtaaact 420

tccgacttca actgtacaag tagaccaaat atccatatac ataaaagaaa aaaatagaaa 480

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tngaaat 607

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acaagtgtga taaaatcttg gaacaacctc ccagaggtct 520

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tgcccactac catg 74

<210> 5
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Sleeping beauty IR/DR sequence, Integration junction (repeat region)

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tcgccatatt tcatg 75

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<212> DNA
<213> Artificial Sequence

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<223> indels from HDAd-CRISPR-transduced CD34+ cells

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cctt 64

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<212> DNA
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<223> indels from HDAd-CRISPR-transduced CD34+ cells

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<210> 8
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> indels from HDAd-CRISPR-transduced CD34+ cells

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<211> 52
<212> DNA
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<210> 10
<211> 53
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<400> 10
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<210> 11
<211> 54
<212> DNA
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<210> 12
<211> 54
<212> DNA
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<211> 58
<212> DNA
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<223> indels from HDAd-CRISPR-transduced CD34+ cells

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<210> 14
<211> 59
<212> DNA
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<223> indels from HDAd-CRISPR-transduced CD34+ cells

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<210> 15
<211> 63
<212> DNA
<213> Artificial Sequence

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ctt 63

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<211> 63
<212> DNA
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ctt 63

<210> 17
<211> 64
<212> DNA
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<223> indels from HDAd-CRISPR-transduced CD34+ cells

<400> 17
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atcc 64

<210> 18
<211> 64
<212> DNA
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catc 64

<210> 19
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<212> DNA
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ccttaggcct cctccttcct 80

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<212> DNA
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cctcctcctt cct 73

<210> 21
<211> 75
<212> DNA
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ggcctcctcc ttcct 75

<210> 22
<211> 75
<212> DNA
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ggcctcctcc ttcct 75

<210> 23
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<212> DNA
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ggcctcctcc ttcct 75

<210> 24
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> microRNA regulated gene expression forward primer

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aagtctcgct ctctgcccct cattcaaaag tctcgctctc tgcccctcac 110

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<212> DNA
<213> Artificial Sequence

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<223> microRNA regulated gene expression reverse primer

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gaggggcaga gagcgagact ttgtgatgag gggcagagag cgagactttc 110

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<211> 76
<212> DNA
<213> Mus musculus

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aggcctcctc cttcct 76

<210> 27
<211> 77
<212> DNA
<213> Mus musculus

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taggcctcct ccttcct 77

<210> 28
<211> 77
<212> DNA
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taggcctcct ccttcct 77

<210> 29
<211> 77
<212> DNA
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taggcctcct ccttcct 77

<210> 30
<211> 77
<212> DNA
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taggcctcct ccttcct 77

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<210> 32
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<210> 33
<211> 26
<212> DNA
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<210> 34
<211> 77
<212> DNA
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taggcctcct ccttcct 77

<210> 35
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<212> DNA
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taggcctcct ccttcct 77

<210> 36
<211> 77
<212> DNA
<213> Mus musculus

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taggcctcct ccttcct 77

<210> 37
<211> 78
<212> DNA
<213> Mus musculus

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<210> 38
<211> 78
<212> DNA
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<210> 39
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<212> DNA
<213> Mus musculus

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<210> 40
<211> 78
<212> DNA
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<210> 41
<211> 78
<212> DNA
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<212> DNA
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<210> 43
<211> 78
<212> DNA
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ttaggcctcc tccttcct 78

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<212> DNA
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<210> 46
<211> 78
<212> DNA
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<210> 47
<211> 79
<212> DNA
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<210> 48
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<223> BCL11A binding site at HBG promoter

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gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg 180

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cgtgggaaaa tgacgtttta tgggggtgga gttttttgc aagttgtcgc gggaaatgtt 180

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<223> CMV (Complementary)

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<210> 65
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> top strand of GATAA motif

<400> 65
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<210> 66
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> bottom strand of GATAA motif

<400> 66
agtgcaagct aacagttgct tttatcacag gctccaggaa gggtttg 47

<210> 67
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> top strand of disrupted GATAA motif

<400> 67
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<210> 68
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> bottom strand of distrupted GATAA motif

<400> 68
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<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> HBG2 forward primer

<400> 69
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<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> HBB primer

<400> 70
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<210> 71
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> HDAd-BEHBG-106

<400> 71
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<210> 72
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> HBG2 reverse primer

<400> 72
cacttcattg tagttaccgt ggaaaga   27

<210> 73
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Sleeping Beauty transposase enzyme

<400> 73

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

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
            20   25   30

Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
        35   40   45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Tyr Leu
    50   55   60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65   70   75   80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
                85   90   95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100   105   110

Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115   120   125

```
Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
    130                 135                 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
    210                 215                 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
                245                 250                 255

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

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335
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Ala Thr Lys Tyr
            340

<210> 74
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Hyperactive Sleeping Beauty is SB100X

<400> 74

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

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
            20   25   30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
        35   40   45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Tyr Leu
    50   55   60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65   70   75   80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
                85   90   95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100   105   110

Lys Gly His Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115   120   125

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
    130   135   140

```
Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

Ile Asp Gly Ile Met Asp Ala Val Gln Tyr Val Asp Ile Leu Lys Gln
    210                 215                 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
                245                 250                 255

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

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Asn Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335
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Ala Thr Lys Tyr
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<210> 75
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> Flp (flippase)

<400> 75

Met Pro Gln Phe Gly Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
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Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
            20   25   30

Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
        35   40   45

Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
    50   55   60

Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
65   70   75   80

Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
                85   90   95

Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
            100   105   110

Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
        115   120   125

Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
    130   135   140

```
Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
145                 150                 155                 160

Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
                165                 170                 175

Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
            180                 185                 190

Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
        195                 200                 205

Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
    210                 215                 220

Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
225                 230                 235                 240

Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
                245                 250                 255

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

Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
        275                 280                 285

Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
    290                 295                 300

His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
305                 310                 315                 320

Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
                325                 330                 335

Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
            340                 345                 350
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```
His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
        355                 360                 365


Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
    370                 375                 380


Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
385                 390                 395                 400


Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
                405                 410                 415


Ser Tyr Ile Asn Arg Arg Ile
            420


<210>  76
<211>  34
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FRT recognition site

<400>  76
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<210>  77
<211>  374
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  variant of the Flp protein

<400>  77

Met Asn Glu Gln Ala Lys Gln Leu Val Ala Val Thr Arg Gln Pro Ala
1               5                   10                  15


Leu Asn Ala Gly Val Gly Leu Val Leu Ala Gln Leu Ala Glu Val Glu
            20                  25                  30
```

```
Ala Arg Gln Ile Pro Gly Ser Leu Ala Glu Ala Arg Ala His Cys Leu
        35                  40                  45

Ala Gln Gly Ala Pro Asp Ile Leu Leu Val Glu Val Glu Asn Pro Gln
    50                  55                  60

Thr Leu Ala Ala Asp Leu Ala Ala Leu Ala Glu Cys Cys Pro Pro Gln
65                  70                  75                  80

Met Arg Leu Val Leu Leu Gly Glu Arg Gly Asp Val Thr Leu Phe Arg
                85                  90                  95

Trp Leu Ile Ser Val Gly Val Asp Asp Tyr Tyr Pro Ala Pro Leu Asp
            100                 105                 110

Pro Asp Ala Leu Arg Thr Gly Leu Leu Arg Leu Leu Gly Val Pro Leu
        115                 120                 125

Val Thr Ser Leu Arg Lys Gly Arg Val Ile Cys Val Val Gly Ala Ala
    130                 135                 140

Gly Gly Val Gly Thr Ser Thr Val Ala Ala Asn Leu Ala Met Ala Leu
145                 150                 155                 160

Ala Asp Gln His His Arg Gln Val Ala Leu Leu Asp Leu Asn Leu His
                165                 170                 175

His Ser Arg His Pro Ile Leu Leu Gly Ser Asp Tyr Ala Pro Pro Gly
            180                 185                 190

Glu Gln Trp Trp Gln Ala Thr Asp Arg Leu Asp Gly Thr Leu Leu Ala
        195                 200                 205

His Thr Ala His Gln Leu Gly Pro Arg Leu Phe Leu Phe Tyr Asp Glu
    210                 215                 220
```

```
Gly Gln Glu Leu Val Leu Gly Ala Glu Gln Leu Val Ala Ala Val Asn
225                 230                 235                 240


Val Met Ala Glu His Tyr Ser Thr Leu Ile Ile Asp Val Pro Asp Leu
                245                 250                 255


Arg Thr His Gly Leu Arg Ala Leu Leu Gln Glu Ala Asp Val Val Leu
            260                 265                 270


Trp Leu His Asp Phe Ser Leu Gly Ala Leu Arg Leu Leu Gly Gln Cys
        275                 280                 285


Pro Gln Gly Gly Gln Ala Gln Arg Arg Leu Leu Val Gly Asn His Cys
    290                 295                 300


Arg Gly Lys Glu Gly Arg Val Pro Ala Gln Glu Leu Glu Arg Val Cys
305                 310                 315                 320


Gly Gln Pro His Ala Ala Val Leu Pro Tyr Asp His Gly Val Phe Val
                325                 330                 335


Arg Ala Glu Arg Ala Gly Gln Pro Leu Ile Gln Gln Lys Ser Lys Leu
            340                 345                 350


Ala Arg Ala Leu Thr Leu Leu Ala Gly Glu Leu Val Gly Ala Gln Val
        355                 360                 365


Thr Gly Arg Gly Arg Arg
    370
```

<210> 78
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of the Flp protein

<400> 78

```
Met Ala Pro Lys Lys Lys Arg Lys Val Met Ser Gln Phe Asp Ile Leu
1               5                   10                  15

Cys Lys Thr Pro Pro Lys Val Leu Val Arg Gln Phe Val Glu Arg Phe
            20                  25                  30

Glu Arg Pro Ser Gly Glu Lys Ile Ala Ser Cys Ala Ala Glu Leu Thr
        35                  40                  45

Tyr Leu Cys Trp Met Ile Thr His Asn Gly Thr Ala Ile Lys Arg Ala
    50                  55                  60

Thr Phe Met Ser Tyr Asn Thr Ile Ile Ser Asn Ser Leu Ser Phe Asp
65                  70                  75                  80

Ile Val Asn Lys Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr
                85                  90                  95

Ile Leu Glu Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr
            100                 105                 110

Ile Ile Pro Tyr Asn Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile
        115                 120                 125

Val Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys
    130                 135                 140

Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu Gly
145                 150                 155                 160

Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe Glu Tyr
                165                 170                 175

Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe Leu Phe Leu
            180                 185                 190

Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile Lys Asn Val Asp
        195                 200                 205
```

```
Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr Leu Gly Val Ile Ile
    210                 215                 220

Gln Cys Leu Val Thr Glu Thr Lys Thr Ser Val Ser Arg His Ile Tyr
225                 230                 235                 240

Phe Phe Ser Ala Arg Gly Arg Ile Asp Pro Leu Val Tyr Leu Asp Glu
                245                 250                 255

Phe Leu Arg Asn Ser Glu Pro Val Leu Lys Arg Val Asn Arg Thr Gly
            260                 265                 270

Asn Ser Ser Ser Asn Lys Gln Glu Tyr Gln Leu Leu Lys Asp Asn Leu
        275                 280                 285

Val Arg Ser Tyr Asn Lys Ala Leu Lys Lys Asn Ala Pro Tyr Pro Ile
    290                 295                 300

Phe Ala Ile Lys Asn Gly Pro Lys Ser His Ile Gly Arg His Leu Met
305                 310                 315                 320

Thr Ser Phe Leu Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val
                325                 330                 335

Gly Asn Trp Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr
            340                 345                 350

Thr His Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser
        355                 360                 365

Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys
    370                 375                 380

Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu Lys
385                 390                 395                 400
```

Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly Ile Ile
405 410 415

Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn Arg Arg Ile
420 425 430

<210> 79
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Cre

<400> 79

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

```
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

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

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

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

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335
```

Arg Leu Leu Glu Asp Gly Asp
340

<210> 80
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> loxP site

<400> 80
ataacttcgt atagcataca ttatacgaag ttat 34

<210> 81
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (lox2272)

<400> 81
ataacttcgt ataaagtatc ctatacgaag ttat 34

<210> 82
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (lox511)

<400> 82
ataacttcgt ataatgtatg ctatacgaag ttat 34

<210> 83
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (lox66)

<400> 83
ataacttcgt atagcataca ttatacgaac ggta 34

<210> 84
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (lox71

<400> 84
taccgttcgt atagcataca ttatacgaag ttat 34

<210> 85
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (loxM2)

<400> 85
ataacttcgt ataagaaacc atatacgaag ttat 34

<210> 86
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> lox recognition site (lox5171)

<400> 86
ataacttcgt ataatgtgta ctatacgaag ttat 34

<210> 87
<211> 380
<212> PRT
<213> Vibrio plasmid p0908

<400> 87

Met Ile Glu Asn Gln Leu Ser Leu Leu Gly Asp Phe Ser Gly Val Arg
1 5 10 15

```
Pro Asp Asp Val Lys Thr Ala Ile Gln Ala Ala Gln Lys Lys Gly Ile
            20                  25                  30

Asn Val Ala Glu Asn Glu Gln Phe Lys Ala Ala Phe Glu His Leu Leu
        35                  40                  45

Asn Glu Phe Lys Lys Arg Glu Glu Arg Tyr Ser Pro Asn Thr Leu Arg
    50                  55                  60

Arg Leu Glu Ser Ala Trp Thr Cys Phe Val Asp Trp Cys Leu Ala Asn
65                  70                  75                  80

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

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

Trp Ala Ile Ser Arg Val His Arg Val Ala Gly Cys Pro Asp Pro Cys
        115                 120                 125

Leu Asp Ile Tyr Val Glu Asp Arg Leu Lys Ala Ile Ala Arg Lys Lys
    130                 135                 140

Val Arg Glu Gly Glu Ala Val Lys Gln Ala Ser Pro Phe Asn Glu Gln
145                 150                 155                 160

His Leu Leu Lys Leu Thr Ser Leu Trp Tyr Arg Ser Asp Lys Leu Leu
                165                 170                 175

Leu Arg Arg Asn Leu Ala Leu Leu Ala Val Ala Tyr Glu Ser Met Leu
            180                 185                 190

Arg Ala Ser Glu Leu Ala Asn Ile Arg Val Ser Asp Met Glu Leu Ala
        195                 200                 205

Gly Asp Gly Thr Ala Ile Leu Thr Ile Pro Ile Thr Lys Thr Asn His
```

```
    210                 215                 220

Ser Gly Glu Pro Asp Thr Cys Ile Leu Ser Gln Asp Val Val Ser Leu
225                 230                 235                 240

Leu Met Asp Tyr Thr Glu Ala Gly Lys Leu Asp Met Ser Ser Asp Gly
                245                 250                 255

Phe Leu Phe Val Gly Val Ser Lys His Asn Thr Cys Ile Lys Pro Lys
            260                 265                 270

Lys Asp Lys Gln Thr Gly Glu Val Leu His Lys Pro Ile Thr Thr Lys
        275                 280                 285

Thr Val Glu Gly Val Phe Tyr Ser Ala Trp Glu Thr Leu Asp Leu Gly
    290                 295                 300

Arg Gln Gly Val Lys Pro Phe Thr Ala His Ser Ala Arg Val Gly Ala
305                 310                 315                 320

Ala Gln Asp Leu Leu Lys Lys Gly Tyr Asn Thr Leu Gln Ile Gln Gln
                325                 330                 335

Ser Gly Arg Trp Ser Ser Gly Ala Met Val Ala Arg Tyr Gly Arg Ala
            340                 345                 350

Ile Leu Ala Arg Asp Gly Ala Met Ala His Ser Arg Val Lys Thr Arg
        355                 360                 365

Ser Ala Pro Met Gln Trp Gly Lys Asp Glu Lys Asp
    370                 375                 380
```

<210> 88
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> VloxP recognition site

<400> 88
tcaatttccg agaatgacag ttctcagaaa ttga 34

<210> 89
<211> 342
<212> PRT
<213> Enterobacteria phage D6

<400> 89

Met Ser Glu Leu Ile Ile Ser Gly Ser Ser Gly Gly Phe Leu Arg Asn
1 5 10 15

Ile Gly Lys Glu Tyr Gln Glu Ala Ala Glu Asn Phe Met Arg Phe Met
20 25 30

Asn Asp Gln Gly Ala Tyr Ala Pro Asn Thr Leu Arg Asp Leu Arg Leu
35 40 45

Val Phe His Ser Trp Ala Arg Trp Cys His Ala Arg Gln Leu Ala Trp
50 55 60

Phe Pro Ile Ser Pro Glu Met Ala Arg Glu Tyr Phe Leu Gln Leu His
65 70 75 80

Asp Ala Asp Leu Ala Ser Thr Thr Ile Asp Lys His Tyr Ala Met Leu
85 90 95

Asn Met Leu Leu Ser His Cys Gly Leu Pro Pro Leu Ser Asp Asp Lys
100 105 110

Ser Val Ser Leu Ala Met Arg Arg Ile Arg Arg Glu Ala Ala Thr Glu
115 120 125

Lys Gly Glu Arg Thr Gly Gln Ala Ile Pro Leu Arg Trp Asp Asp Leu
130 135 140

Lys Leu Leu Asp Val Leu Leu Ser Arg Ser Glu Arg Leu Val Asp Leu
145 150 155 160

```
Arg Asn Arg Ala Phe Leu Phe Val Ala Tyr Asn Thr Leu Met Arg Met
                165                 170                 175

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

Thr Val Thr Leu His Ile Ser His Thr Lys Thr Ile Thr Thr Ala Ala
        195                 200                 205

Gly Leu Asp Lys Val Leu Ser Arg Arg Thr Thr Ala Val Leu Asn Asp
    210                 215                 220

Trp Leu Asp Val Ser Gly Leu Arg Glu His Pro Asp Ala Val Leu Phe
225                 230                 235                 240

Pro Pro Ile His Arg Ser Asn Lys Ala Arg Ile Thr Thr Thr Pro Leu
                245                 250                 255

Thr Ala Pro Ala Met Glu Lys Ile Phe Ser Asp Ala Trp Val Leu Leu
            260                 265                 270

Asn Lys Arg Asp Ala Thr Pro Asn Lys Gly Arg Tyr Arg Thr Trp Thr
        275                 280                 285

Gly His Ser Ala Arg Val Gly Ala Ala Ile Asp Met Ala Glu Lys Gln
    290                 295                 300

Val Ser Met Val Glu Ile Met Gln Glu Gly Thr Trp Lys Lys Pro Glu
305                 310                 315                 320

Thr Leu Met Arg Tyr Leu Arg Arg Gly Gly Val Ser Val Gly Ala Asn
                325                 330                 335

Ser Arg Leu Met Asp Ser
            340
```

<210> 90
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> rox recognition site

<400> 90
taactttaaa taattggcat tatttaaagt ta 32

<210> 91
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL1

<400> 91

Thr Ala Ser Ser Ser Val Asn Tyr Ile His
1 5 10

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL2

<400> 92

Thr Ser Lys Val Ala Ser
1 5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL3

<400> 93

Gln Gln Trp Arg Ser Tyr Pro Leu Thr
1   5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH1

<400> 94

Asp Tyr Val Val His
1   5

<210> 95
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH2

<400> 95

Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 96
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH3

<400> 96

Asp Tyr Arg Tyr Glu Val Tyr Gly Met Asp Tyr
1   5   10

<210> 97
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL1

<400> 97

Arg Ala Ser Glu Val Asp Asn Tyr Gly Ile Ser Phe Met Asn
1 5 10

<210> 98
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL2

<400> 98

Ala Ala Ser Asn Gln Gly Ser
1 5

<210> 99
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRL3

<400> 99

Gln Gln Ser Lys Glu Val Pro Trp
1 5

<210> 100
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH1

<400> 100

Asp Tyr Asn Met His
1 5

<210> 101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH2

<400> 101

Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Ser

<210> 102
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific CDRH3

<400> 102

Gly Arg Pro Ala Met Asp Tyr
1 5

<210> 103
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33-specific variable light chain

<400> 103

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

```
Glu Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Asn Tyr Ile
            20                  25                  30

His Trp Tyr Gln Gln Lys Ser Gly Asp Ser Pro Lys Arg Trp Ile Phe
        35                  40                  45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Arg Ser Tyr Pro Leu Thr
                85                  90                  95

Phe Gly Asp Gly Thr Arg Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro
            100                 105                 110

Thr Val Ser
        115


<210>  104
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD33-specific variable heavy chain

<400>  104

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

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

Val Val His Trp Leu Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Glu Val Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Tyr Arg Tyr Glu Val Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Ser Val Thr Val Ser Ser
        115   120

<210> 105
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> HBG1-seq primer

<400> 105
tttccttaga aaccactgct aactg   25

<210> 106
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> human CD33-specific variable heavy chain

<400> 106

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

Glu Lys Val Thr Met Thr Cys Ser Ala Asn Ser Ser Val Ser Tyr Ile
            20   25   30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Phe
        35   40   45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
65   70   75   80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser His Pro Leu Thr
                85   90   95

Phe Gly Thr Gly Thr Lys Leu Gln Leu Lys Arg Ala Asp Ala Ala Pro
            100   105   110

Thr Val Ser
        115

<210> 107
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRL1

<400> 107

Gly Tyr Ala Phe Ser Asn Tyr Trp Met Asn
1   5   10

<210> 108
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRL2

<400> 108

Gln Ile Tyr Pro Gly Asn Phe Asn Thr Asp Tyr Asn Gly Gln Phe Lys
1   5   10   15

Gly

<210> 109
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRL3

<400> 109

Phe Phe Asp Phe Gly Ala Tyr Phe Thr Leu Asp Tyr
1   5   10

<210> 110
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRH1

<400> 110

Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
1   5   10

<210> 111
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRH2

<400> 111

Tyr Ala Thr Thr Leu Ala Asp
1   5

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33FL-specific CDRH3

<400> 112

Leu His His Gly Glu Ser Pro Trp Thr
1   5

<210> 113
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> human CD33FL-specific variable light chain

<400> 113

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1   5   10   15

Gly Ser Thr Gly Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Ile Tyr
            20   25   30

Ala Ser Leu Gly Glu Arg Val Thr Ile Asn Cys Lys Ala Ser Gln Asp
        35   40   45

Ile Lys Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro
    50   55   60

Lys Thr Leu Ile Tyr Tyr Ala Thr Thr Leu Ala Asp Gly Val Pro Ser
65   70   75   80

Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser
                85   90   95

Ser Leu Glu Ser Asp Asp Thr Ala Thr Tyr Tyr Cys Leu His His Gly
            100   105   110

```
Glu Ser Pro Trp Thr Phe Gly Glu Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125


Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
    130                 135                 140


Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145                 150                 155                 160


Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
                165                 170                 175


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


Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
        195                 200                 205


His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
    210                 215                 220


Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230
```

<210> 114
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> human CD33FL-specific variable heavy chain

<400> 114

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Val
            20                  25                  30
```

```
Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Tyr Ala
        35                  40                  45

Phe Ser Asn Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Ile Gly Gln Ile Tyr Pro Gly Asn Phe Asn Thr Asp Tyr
65                  70                  75                  80

Asn Gly Gln Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
                85                  90                  95

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

Val Tyr Phe Cys Ala Arg Phe Phe Asp Phe Gly Ala Tyr Phe Thr Leu
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr
    130                 135                 140

Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr
145                 150                 155                 160

Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
        195                 200                 205

Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn
    210                 215                 220
```

```
Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro
225                 230                 235                 240

Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
                245                 250                 255

Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
            260                 265                 270

Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn
    290                 295                 300

Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
305                 310                 315                 320

Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
                325                 330                 335

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
            340                 345                 350

Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg
        355                 360                 365

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

Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
385                 390                 395                 400

Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
                405                 410                 415

Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
            420                 425                 430
```

Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
        435   440   445

Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
    450   455   460

Phe Ser Arg Thr Pro Gly Lys
465   470

<210> 115
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRL1

<400> 115

Gly Tyr Thr Phe Thr Thr Tyr Trp Met His
1   5   10

<210> 116
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRL2

<400> 116

Ala Ile Tyr Pro Gly Asn Ser Asp Thr Ser Tyr Asn Gln
1   5   10

<210> 117
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRL3

<400> 117

Tyr Asp Gly Tyr His Phe Ile
1 5

<210> 118
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRH1

<400> 118

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr
1 5 10 15

<210> 119
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRH2

<400> 119

Gln Met Ser Asn Leu Ala Ser
1 5

<210> 120
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD33 deltaE2-specific CDRH3

<400> 120

Ala Gln Asn Leu Glu Leu Pro Pro Thr
1 5

<210> 121
<211> 239

<212> PRT
<213> Artificial Sequence

<220>
<223> human CD33 deltaE2-specific variable light chain

<400> 121

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30

Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

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

Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro
130 135 140

Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe
145 150 155 160

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
165 170 175

```
Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp
            180                 185                 190


Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys
        195                 200                 205


Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys
    210                 215                 220


Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230                 235


<210>  122
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  human CD33 deltaE2-specific variable heavy chain

<400>  122

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala
            20                  25                  30


Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
        35                  40                  45


Phe Thr Thr Tyr Trp Met His Trp Ile Lys Gln Ser Pro Gly Gln Gly
    50                  55                  60


Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Thr Ser Tyr
65                  70                  75                  80


Asn Gln Lys Phe Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Ala
                85                  90                  95
```

```
Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Asn Glu Asp Ser Ala
            100                 105                 110

Val Tyr Tyr Cys Glu Ile Tyr Asp Gly Tyr His Phe Ile Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
    130                 135                 140

Val Tyr Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val
145                 150                 155                 160

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val
                165                 170                 175

Thr Trp Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala
            180                 185                 190

Leu Leu Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro
        195                 200                 205

Ser Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro
    210                 215                 220

Ala Ser Ser Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile
225                 230                 235                 240

Ser Thr Ile Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro
                245                 250                 255

Ala Pro Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn
            260                 265                 270

Ile Lys Asp Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val
        275                 280                 285
```

```
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
    290                 295                 300

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
305                 310                 315                 320

Asp Tyr Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Gln His
                325                 330                 335

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            340                 345                 350

Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu
        355                 360                 365

Val Arg Ala Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu
    370                 375                 380

Ser Arg Lys Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro
385                 390                 395                 400

Gly Asp Ile Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn
                405                 410                 415

Tyr Lys Asp Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile
            420                 425                 430

Tyr Ser Lys Leu Asn Met Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser
        435                 440                 445

Phe Ser Cys Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys
    450                 455                 460

Lys Thr Ile Ser Arg Ser Pro Gly Lys
465                 470
```

<210> 123
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRL1

<400> 123

Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala
1 5 10

<210> 124
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRL2

<400> 124

Ala Ser Tyr Arg Tyr Thr
1 5

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRL3

<400> 125

Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr
1 5

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRH1

<400> 126

Gly Phe Thr Phe Thr Asp Tyr Thr Met Asp
1 5 10

<210> 127
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRH2

<400> 127

Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe Lys
1 5 10 15

<210> 128
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2-specific CDRH3

<400> 128

Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
1 5

<210> 129
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRL1

<400> 129

Arg Ala Ser Lys Gly Val Ser Thr Ser Gly Tyr Ser Tyr Leu His
1 5 10 15

<210> 130
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRL2

<400> 130

Leu Ala Ser Tyr Leu Glu Ser
1   5

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRL3

<400> 131

Gln His Ser Arg Asp Leu Pro Leu Thr
1   5

<210> 132
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRH1

<400> 132

Asn Tyr Tyr Met Tyr
1   5

<210> 133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRH2

<400> 133

Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe Lys
1   5   10   15

Asn

<210> 134
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1-specific CDRH3

<400> 134

Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
1 5 10

<210> 135
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab variable heavy chain

<400> 135

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  136
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Avelumab variable light chain

<400>  136

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


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45


Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60


Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
                85                  90                  95


Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110
```

<210> 137
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRH1

<400> 137

Ser Gly Phe Thr Phe Ser Ser Tyr Ile Met Met
1 5 10

<210> 138
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRH2

<400> 138

Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val Lys
1 5 10 15

Gly

<210> 139
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRH3

<400> 139

Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
1 5 10

<210> 140
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRL1

<400> 140

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1   5   10

<210> 141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRL2

<400> 141

Asp Val Ser Asn Arg Pro Ser
1   5

<210> 142
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Avelumab-specific CDRL3

<400> 142

Ser Ser Tyr Thr Ser Ser Ser Thr Arg Val
1   5   10

<210> 143
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific variable heavy chain

<400> 143

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

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
            20                  25                  30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

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

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210>  144
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Atezolizumab-specific variable light chain

<400>  144

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 145
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRH1

<400> 145

Ser Gly Phe Thr Phe Ser Asp Ser Trp Ile His
1   5   10

<210> 146
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRH2

<400> 146

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

Gly

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRH3

<400> 147

Arg His Trp Pro Gly Gly Phe Asp Tyr
1 5

<210> 148
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRL1

<400> 148

Arg Ala Ser Gln Asp Val Ser Thr Ala Val Ala
1 5 10

<210> 149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRL2

<400> 149

Ser Ala Ser Phe Leu Tyr Ser
1 5

<210> 150
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Atezolizumab-specific CDRL3

<400> 150

Gln Gln Tyr Leu Tyr His Pro Ala Thr
1 5

<210> 151
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRL1

<400> 151

Lys Ala Ser Gln Asp Val Gly Thr Ala Val Asp
1 5 10

<210> 152
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRL2

<400> 152

Trp Ala Ser Thr Arg His Thr
1 5

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRL3

<400> 153

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 154
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRH1

<400> 154

Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His
1   5   10

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRH2

<400> 155

Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu
1   5   10   15

Asp

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PSMA-specific CDRH3

<400> 156

Gly Trp Asn Phe Asp Tyr
1   5

<210> 157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> MUC16-specific CDRL1

<400> 157

Ser Glu Asp Ile Tyr Ser Gly
1   5

<210> 158
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC16-specific CDRL3

<400> 158

Gly Tyr Ser Tyr Ser Ser Thr Leu
1   5

<210> 159
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC16-specific CDRH1

<400> 159

Thr Leu Gly Met Gly Val Gly
1   5

<210> 160
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC16-specific CDRH2

<400> 160

His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ala Leu Lys Ser
1   5   10   15

<210> 161
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> MUC16-specific CDRH3

<400> 161

Ile Gly Thr Ala Gln Ala Thr Asp Ala Leu Asp Tyr
1 5 10

<210> 162
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRL1

<400> 162

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

<210> 163
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRL2

<400> 163

Arg Ala Ser Asn Leu Glu Ala
1 5

<210> 164
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRL3

<400> 164

Gln Gln Ser Arg Glu Tyr Pro Tyr Thr
1 5

<210> 165
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRH1

<400> 165

Gly Tyr Phe Met Asn
1 5

<210> 166
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRH2

<400> 166

Arg Ile His Pro Tyr Asp Gly Asp Thr Phe Tyr Asn Gln Lys Phe Gln
1 5 10 15

Gly

<210> 167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FOLR-specific CDRH3

<400> 167

Tyr Asp Gly Ser Arg Ala Met Asp Tyr
1 5

<210> 168
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific variable heavy chain

<400> 168

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Ser Gly
100 105 110

Thr Pro Val Thr Val Ser Ser
115

<210> 169
<211> 106
<212> PRT
<213> Artificial Sequence

<220>

<223> Amatuximab-specific variable light chain

<400> 169

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu
65 70 75 80

Asp Asp Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Lys His Pro Leu Thr
85 90 95

Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105

<210> 170
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRH1

<400> 170

Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
1 5 10

<210> 171
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRH2

<400> 171

Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln
1   5   10

<210> 172
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRH3

<400> 172

Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr
1   5   10

<210> 173
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRL1

<400> 173

Ser Ala Ser Ser Ser Val Ser Tyr Met His
1   5   10

<210> 174
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRL2

<400> 174

Asp Thr Ser Lys Leu Ala Ser
1   5

<210> 175
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amatuximab-specific CDRL3

<400> 175

Gln Gln Trp Ser Lys His Pro Leu Thr
1   5

<210> 176
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Nef (66-97)

<400> 176

Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr
1   5   10   15

Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu
            20   25   30

<210> 177
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Nef (116-145)

<400> 177

His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
1   5   10   15

Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Leu Tyr Lys Leu
            20   25   30

<210> 178
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Gag p17 (17-35)

<400> 178

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
1   5   10   15

His Ile Val

<210> 179
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Gag p17-p24 (253-284)

<400> 179

Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu
1   5   10   15

Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp
            20   25   30

<210> 180
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Pol 325-355 (RT 158-188)

<400> 180

Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
1   5   10   15

Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr
            20   25   30

<210> 181
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 linker

<400> 181

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
1   5   10

<210> 182
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 linker

<400> 182

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
1   5   10

<210> 183
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> Residues (GGGGS) can be repeated n times, wherein n is an integer
       including, 1, 2, 3, 4, 5, 6, 7, 8, 9, or more

<400> 183

Gly Gly Gly Gly Ser
1   5

<210> 184
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> (EAAAK) can be repeated n times, wherein n is an integer
       including 1, 2, 3, 4, 5, 6, 7, 8, 9, or more

<400> 184

Glu Ala Ala Ala Lys
1   5

<210> 185
<211> 21531
<212> DNA
<213> Homo sapiens

<400> 185
gatctctatc ccctcctgtt ttctctacgt tatttatatg ggtatcatca ccatcctgga   60

caacatcagg acagatatcc ctcaccaagc caatgttcct ctctatgttg gctcaaatgt   120

ccttgaactt tcctttcacc acccctttcca cagtcaaaag gatattgtag tttaatgcct   180

cagagttcag cttttaagct tctgacaaat tattcttcct ctttaggttc tcctttatgg   240

aatcttctgt actgatggcc atgtccttta actactatgt agatatctgc tactacctgt   300

attatgcctc tacctttatt agcagagtta tctgtactgt tggcatgaca atcatttgtt   360

aatatgactt gcctttcctt tttctgctat tcttgatcaa atggctcctc tttcttgctc   420

ctctcatttc tcctgccttc acttggacgt gcttcacgta gtctgtgctt atgactggat   480

taaaaattga tatggactta tcctaatgtt gttcgtcata atatgggttt tatggtccat   540

tattatttcc tatgcattga tctggagaag gcttcaatcc ttttactctt tgtggaaaat 600

atctgtaaac cttctggttc actctgctat agcaatttca gtttaggcta gtaagcatga 660

ggatgcctcc ttctctgatt tttcccacag tctgttggtc acagaataac ctgagtgatt 720

actgatgaaa gagtgagaat gttattgata gtcacaatga caaaaaacaa acaactacag 780

tcaaaatgtt tctcttttta ttagtggatt atatttcctg acctatatct ggcaggactc 840

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<223> 32P-gamma-ATP labeled probes for miRNA 423-5p

<400> 235
aaagtctcgc tctctgcccc tca 23

<210> 236
<211> 37
<212> DNA
<213> Artificial Sequence

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<223> 32P-gamma-ATP labeled probes for U6 snRNA

<400> 236
gaatttgcgt gtcatccttg cgcaggggcc atgctaa 37

<210> 237
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<223> HBG2-seq primer

<400> 237
cttatttgga aaccaatgct tacta 25

<210> 238
<211> 22
<212> DNA
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<220>
<223> anti-mouse PDL1 forward primer

<400> 238
ggttcagcct ggtgggtctt tg 22

<210> 239
<211> 24
<212> DNA
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<220>
<223> anti-mouse PDL1 reverse primer

<400> 239
atctggaggt atgcggtgtt cttc 24

<210> 240
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<212> DNA
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<223> mouse PPIA forward primer

<400> 240
gcatacaggt cctggcatct 20

<210> 241
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<223> mouse PPIA reverse primer

<400> 241
atccagccat tcagtcttgg 20

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<223> forward primer for mouse beta-YAC (gamma-globin promoter)

<400> 242
aaacggtccc tggctaaact 20

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<223> reverse primer for mouse beta-YAC (gamma-globin promoter)

<400> 243
gctgaagggt gcttcctttt t 21

<210> 244
<211> 20
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<220>
<223> sgBCL

<400> 244
tttatcacag gctccaggaa 20

<210> 245
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<220>
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<400> 245
ttttatcaca ggctccagga 20

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<220>
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<220>
<223> forward BCL11A-seq primer

<400> 247
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<210> 248
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<220>

<223> sgBCL

<400> 248
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<210> 249
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<220>
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<400> 249
gataaaagca actgttagct 20

<210> 250
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<212> DNA
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<220>
<223> sgHBG

<400> 250
cttgaccaat agccttgaca 20

<210> 251
<211> 23
<212> DNA
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<220>
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<400> 251
aattctggct tatcggaggc aag 23

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<220>
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<400> 252
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<220>
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<400> 253
gtggggaagg ggcccccaag 20

<210> 254
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<220>
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<400> 254
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<220>
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<223> sgHBB_STOP

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cttgccccac agggcagtaa 20

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<211> 20
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<220>
<223> sgHBB_SKIP

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<210> 258
<211> 20
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<213> Artificial Sequence

<220>
<223> sgHBB_CRISPR

<400> 258
cttgtcaagg ctattggtca 20

<210> 259
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<220>
<223> sgNEG

<400> 259
ggtgtcgaaa tgagaagaag 20

<210> 260
<211> 594
<212> DNA
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<220>
<223> TadAN +32aa

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gcctgggacg aaagagaagt ccccgtcggc gccgtgctgg tgcacaacaa tcgcgtgatc 120

ggagaaggat ggaacaggcc aatcggacgc cacgacccta ccgcacacgc agagatcatg 180

gcactgaggc agggaggact ggtcatgcag aattatcgcc tgatcgatgc caccctgtat 240

gtgacactgg agccatgcgt gatgtgcgca ggagcaatga tccacagccg gatcggaaga 300

gtggtgttcg gagcacgaga cgccaagacc ggagcagcag gcagcctgat ggatgtgctg 360

caccacccag gcatgaacca ccgggtggag atcacagagg gcatcctggc agacgagtgc 420

gccgccctgc tgagcgattt ctttagaatg aggagacagg agatcaaggc ccagaagaag 480

gcacagagct ccaccgactc tggaggctct agcggaggat cctctggaag cgagacacca 540

ggcacatccg agtccgccac accagagtct tccggcggct cctccggagg atcc 594

<210> 261
<211> 594
<212> DNA
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<220>
<223> TadAN+ +32aa

<400> 261
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gcacgcgatg agagggaggt gcctgtggga gccgtgctgg tgctgaacaa tagagtgatc 120

ggcgagggct ggaacagagc catcggcctg cacgacccaa cagcccatgc cgaaattatg 180

gccctgagac agggcggcct ggtcatgcag aactacagac tgattgacgc caccctgtac 240

gtgacattcg agccttgcgt gatgtgcgcc ggcgccatga tccactctag gatcggccgc 300

gtggtgtttg gcgtgaggaa tgcaaaaact ggcgccgcag gctctctgat ggacgtgctg 360

cactaccccg gcatgaatca cagagtcgaa attaccgagg gaatcctggc agatgaatgt 420

gccgccctgc tgtgctattt ctttcggatg cctagacagg tgtttaatgc tcagaagaag 480

gcccagagct ccaccgatag tggcggatct agcgggggct cctctggctc tgagacccct 540

ggcacaagcg agagcgcaac acctgaaagc agcgggggca gcagcggggg gagc 594

<210> 262
<211> 600

<212> DNA
<213> Artificial Sequence

<220>
<223> vector

<400> 262
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gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg 180

gtgtgcgccg gtgtacagcc ctaggataac ttcgtatagc atacattata cgaagttata 240

ctagtacgcc cgggcgtatc gatacgatat cggtccggac aggaagtgac aattttcgcg 300

cggttttagg cggatgttgt agtaaatttg ggcgtaaccg agtaagattt ggccattttc 360

gcgggaaaac tgaataagag gaagtgaaat ctgaataatt ttgtgttact catagcgcgt 420

aatggatccg cgttaaccgg cggccgcatt ctagacggaa ttcataactt cgtatagcat 480

acattatacg aagttatgct agccgaagct tgagctcgtc gagggatctg ggcgtggtta 540

agggtgggaa agaatatata aggtgggggt cttatgtagt tttgtatctg ttttgcagca 600

<210> 263
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> BCL11A-seq reverse primer

<400> 263
ggcagctaga caggacttgg 20

<210> 264
<211> 370
<212> DNA
<213> Adenovirus serotype 35

<400> 264
catcatcaat aatatacctt atagatggaa tggtgccaat atgtaaatga ggtgatttta 60

aaaagtgtgg gccgtgtggt gattggctgt ggggttaacg gttaaaaggg gcggcgcggc 120

cgtgggaaaa tgacgttatt taaatataac ttcgtatagc atacattata cgaagttatg 180

aggtagtttt gttcaggggc aagtgaaaat tgacccatta cgcgcgaaaa ctgaatgagg 240

aagtgttttt ctgaataatg tggtatttat ggcagggtgg agtatttgac cggatccagg 300

tagactttgc tgattttcgt ggaggtttat aacttcgtat agcatacatt atacgaagtt 360

atatttaaat 370

<210> 265
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> TadA

<400> 265

Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu Thr
1 5 10 15

Leu Ala Lys Arg Ala Trp Asp Glu Arg Glu Val Pro Val Gly Ala Val
20 25 30

Leu Val His Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Pro Ile
35 40 45

Gly Arg His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg Gln
50 55 60

Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu Tyr
65 70 75 80

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

Arg Ile Gly Arg Val Val Phe Gly Ala Arg Asp Ala Lys Thr Gly Ala
100 105 110

Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His Arg

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        115                 120                 125

Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu Leu
    130                 135                 140

Ser Asp Phe Phe Arg Met Arg Arg Gln Glu Ile Lys Ala Gln Lys Lys
145                 150                 155                 160

Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly
                165                 170                 175

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly
            180                 185                 190

Gly Ser Ser Gly Gly Ser
        195


<210>  266
<211>  198
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  mutant TadA

<400>  266

Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu Thr
1               5                   10                  15

Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala Val
            20                  25                  30

Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala Ile
        35                  40                  45

Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg Gln
    50                  55                  60

Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu Tyr
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65 70 75 80

Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His Ser
85 90 95

Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly Ala
100 105 110

Ala Gly Ser Leu Met Asp Val Leu His Tyr Pro Gly Met Asn His Arg
115 120 125

Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu Leu
130 135 140

Cys Tyr Phe Phe Arg Met Pro Arg Gln Val Phe Asn Ala Gln Lys Lys
145 150 155 160

Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly
165 170 175

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly
180 185 190

Gly Ser Ser Gly Gly Ser
195

<210> 267
<211> 594
<212> DNA
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ggagagggat ggaacaggcc aatcggccgc cacgacccta ccgcacacgc agagatcatg 180

gcactgaggc agggaggcct ggtcatgcag aattaccgcc tgatcgatgc caccctgtat 240

gtgacactgg agccatgcgt gatgtgcgca ggagcaatga tccacagcag gatcggaaga 300

gtggtgttcg gagcacggga cgccaagacc ggcgcagcag gctccctgat ggatgtgctg 360

caccaccccg gcatgaacca ccgggtggag atcacagagg gaatcctggc agacgagtgc 420

gccgccctgc tgagcgattt ctttagaatg cggagacagg agatcaaggc ccagaagaag 480

gcacagagct ccaccgactc tggaggatct agcggaggat cctctggaag cgagacacca 540

ggcacaagcg agtccgccac accagagagc tccggcggct cctccggagg atcc 594

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<220>
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<400> 268
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gcacgcgatg agagggaggt gcctgtggga gccgtgctgg tgctgaacaa tagagtgatc 120

ggcgagggct ggaacagagc catcggcctg cacgacccaa cagcccatgc cgaaattatg 180

gccctgagga agggaggcct ggtcatgcag aactacagac tgattgacgc caccctgtac 240

gtgacattcg agccttgcgt gatgtgcgcc ggcgccatga tccactctag gatcggccgc 300

gtggtgtttg gcgtgaggaa cgcaaaaacc ggcgccgcag gctccctgat ggacgtgctg 360

cactaccccg gcatgaatca ccgcgtcgaa attaccgagg gaatcctggc agatgaatgt 420

gccgccctgc tgtgctattt ctttcggatg cctagacagg tgttcaatgc tcagaagaag 480

gcccagagct ccaccgactc cggaggatct agcggcggat cctctggctc tgagacacct 540

ggcacaagcg agagcgcaac acctgaaagc agcgggggca gcagcggggg gtca 594

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tttatcacag gctccaggaa ggg 23

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<212> DNA
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<400> 270
cagggtttct cctccagcat cttccacat 29

<210> 271
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<223> HBG1/2 reverse primer

<400> 271
agcagcagta tcctcttggg g 21

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<223> HBA primer

<400> 272
tcctgcaggg tgaggaagga agg 23

<210> 273
<211> 25
<212> DNA
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<220>
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<400> 273
tctatgcaca tcaattagca gaggc 25

<210> 274
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<212> DNA
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<220>
<223> HBA primer

<400> 274
ccccaaggca ctccagggac atag 24

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ttttatcaca ggctccagga agg 23

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gctattggtc aaggcaaggc tgg 23

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<400> 278
gtggggaagg ggcccccaag agg 23

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aggttctttg agtcctttgg ggatctgtcc actcctgatg ctgttatggg caaccctaag 180

gtgaaggctc atggcaagaa agtgctcggt gcctttagtg atggcctggc tcacctggac 240

aacctcaagg gcacctttgc cacactgagt gagctgcact gtgacaagct gcacgtggat 300

cctgagaact tcaggctcct gggcaacgtg ctggtctgtg tgctggccca tcactttggc 360

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gccctggccc acaagtatca ctaa 444

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ggagagggat ggaacaggcc aatcggccgc cacgacccta ccgcacacgc agagatcatg 180

gcactgaggc agggaggcct ggtcatgcag aattaccgcc tgatcgatgc caccctgtat 240

gtgacactgg agccatgcgt gatgtgcgca ggagcaatga tccacagcag gatcggaaga 300

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gccgccctgc tgagcgattt ctttagaatg cggagacagg agatcaaggc ccagaagaag 480

gcacagagct ccaccgactc tggaggatct agcggaggat cctctggaag cgagacacca 540

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ggcgagggct ggaacagagc catcggcctg cacgacccaa cagcccatgc cgcaattatg 180

gccctgagac agggcggcct ggtcatgcag aactacagac tgattgacgc caccctgtac 240

gtgacattcg agccttgcgt gatgtgcgcc ggcgccatga tccactctag gatcggccgc 300

gtggtgtttg gcgtgaggaa cgcaaaaacc ggcgccgcag gctccctgat ggacgtgctg 360

cactaccccg gcatgaatca ccgcgtcgaa attaccgagg gaatcctggc agatgaatgt 420

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<223> CMV (Complementary)

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<223> lambda-2

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<212> PRT
<213> Artificial Sequence

<220>

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<210> 291
<211> 594
<212> PRT
<213> Trichoplusia ni

<400> 291

Met Gly Ser Ser Leu Asp Asp Glu His Ile Leu Ser Ala Leu Leu Gln
1   5   10   15

Ser Asp Asp Glu Leu Val Gly Glu Asp Ser Asp Ser Glu Ile Ser Asp
            20   25   30

His Val Ser Glu Asp Asp Val Gln Ser Asp Thr Glu Glu Ala Phe Ile
        35   40   45

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

Asp Glu Gln Asn Val Ile Glu Gln Pro Gly Ser Ser Leu Ala Ser Asn
65   70   75   80

Arg Ile Leu Thr Leu Pro Gln Arg Thr Ile Arg Gly Lys Asn Lys His
                85   90   95

Cys Trp Ser Thr Ser Lys Ser Thr Arg Arg Ser Arg Val Ser Ala Leu
            100   105   110

Asn Ile Val Arg Ser Gln Arg Gly Pro Thr Arg Met Cys Arg Asn Ile
        115   120   125

Tyr Asp Pro Leu Leu Cys Phe Lys Leu Phe Phe Thr Asp Glu Ile Ile
    130   135   140

```
Ser Glu Ile Val Lys Trp Thr Asn Ala Glu Ile Ser Leu Lys Arg Arg
145                 150                 155                 160

Glu Ser Met Thr Gly Ala Thr Phe Arg Asp Thr Asn Glu Asp Glu Ile
                165                 170                 175

Tyr Ala Phe Phe Gly Ile Leu Val Met Thr Ala Val Arg Lys Asp Asn
            180                 185                 190

His Met Ser Thr Asp Asp Leu Phe Asp Arg Ser Leu Ser Met Val Tyr
        195                 200                 205

Val Ser Val Met Ser Arg Asp Arg Phe Asp Phe Leu Ile Arg Cys Leu
    210                 215                 220

Arg Met Asp Asp Lys Ser Ile Arg Pro Thr Leu Arg Glu Asn Asp Val
225                 230                 235                 240

Phe Thr Pro Val Arg Lys Ile Trp Asp Leu Phe Ile His Gln Cys Ile
                245                 250                 255

Gln Asn Tyr Thr Pro Gly Ala His Leu Thr Ile Asp Glu Gln Leu Leu
            260                 265                 270

Gly Phe Arg Gly Arg Cys Pro Phe Arg Met Tyr Ile Pro Asn Lys Pro
        275                 280                 285

Ser Lys Tyr Gly Ile Lys Ile Leu Met Met Cys Asp Ser Gly Thr Lys
    290                 295                 300

Tyr Met Ile Asn Gly Met Pro Tyr Leu Gly Arg Gly Thr Gln Thr Asn
305                 310                 315                 320

Gly Val Pro Leu Gly Glu Tyr Tyr Val Lys Glu Leu Ser Lys Pro Val
                325                 330                 335

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

```
            340                 345                 350

Pro Leu Ala Lys Asn Leu Leu Gln Glu Pro Tyr Lys Leu Thr Ile Val
        355                 360                 365

Gly Thr Val Arg Ser Asn Lys Arg Glu Ile Pro Glu Val Leu Lys Asn
    370                 375                 380

Ser Arg Ser Arg Pro Val Gly Thr Ser Met Phe Cys Phe Asp Gly Pro
385                 390                 395                 400

Leu Thr Leu Val Ser Tyr Lys Pro Lys Pro Ala Lys Met Val Tyr Leu
                405                 410                 415

Leu Ser Ser Cys Asp Glu Asp Ala Ser Ile Asn Glu Ser Thr Gly Lys
            420                 425                 430

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

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

Trp Pro Met Ala Leu Leu Tyr Gly Met Ile Asn Ile Ala Cys Ile Asn
465                 470                 475                 480

Ser Phe Ile Ile Tyr Ser His Asn Val Ser Ser Lys Gly Glu Lys Val
                485                 490                 495

Gln Ser Arg Lys Lys Phe Met Arg Asn Leu Tyr Met Ser Leu Thr Ser
            500                 505                 510

Ser Phe Met Arg Lys Arg Leu Glu Ala Pro Thr Leu Lys Arg Tyr Leu
        515                 520                 525

Arg Asp Asn Ile Ser Asn Ile Leu Pro Asn Glu Val Pro Gly Thr Ser
    530                 535                 540
```

```
Asp Asp Ser Thr Glu Glu Pro Val Met Lys Lys Arg Thr Tyr Cys Thr
545                 550                 555                 560


Tyr Cys Pro Ser Lys Ile Arg Arg Lys Ala Asn Ala Ser Cys Lys Lys
                565                 570                 575


Cys Lys Lys Val Ile Cys Arg Glu His Asn Ile Asp Met Cys Gln Ser
            580                 585                 590


Cys Phe
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<210> 292
<211> 340
<212> PRT
<213> Rana pipiens

<400> 292

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Met Pro Arg Pro Lys Glu Ile Gln Glu Gln Leu Arg Lys Lys Val Ile
1               5                   10                  15


Glu Ile Tyr Gln Ser Gly Lys Gly Tyr Lys Ala Ile Ser Lys Ala Leu
            20                  25                  30


Gly Ile Gln Arg Thr Thr Val Arg Ala Ile Ile His Lys Trp Arg Arg
        35                  40                  45


His Gly Thr Val Val Asn Leu Pro Arg Ser Gly Arg Pro Pro Lys Ile
    50                  55                  60


Thr Pro Arg Ala Gln Arg Arg Leu Ile Gln Glu Val Thr Lys Asp Pro
65                  70                  75                  80


Thr Thr Thr Ser Lys Glu Leu Gln Ala Ser Leu Ala Ser Val Lys Val
                85                  90                  95


Ser Val His Ala Ser Thr Ile Arg Lys Arg Leu Gly Lys Asn Gly Leu
            100                 105                 110
```

```
His Gly Arg Val Pro Arg Arg Lys Pro Leu Leu Ser Lys Lys Asn Ile
        115                 120                 125

Lys Ala Arg Leu Asn Phe Ser Thr Thr His Leu Asp Asp Pro Gln Asp
    130                 135                 140

Phe Trp Asp Asn Ile Leu Trp Thr Asp Glu Thr Lys Val Glu Leu Phe
145                 150                 155                 160

Gly Arg Cys Val Ser Lys Tyr Ile Trp Arg Arg Arg Asn Thr Ala Phe
                165                 170                 175

His Lys Lys Asn Ile Ile Pro Thr Val Lys Tyr Gly Gly Gly Ser Val
            180                 185                 190

Met Val Trp Gly Cys Phe Ala Ala Ser Gly Pro Gly Arg Leu Ala Val
        195                 200                 205

Ile Lys Gly Thr Met Asn Ser Ala Val Tyr Gln Glu Ile Leu Lys Glu
    210                 215                 220

Asn Val Arg Pro Ser Val Arg Val Leu Lys Leu Lys Arg Thr Trp Val
225                 230                 235                 240

Leu Gln Gln Asp Asn Asp Pro Lys His Thr Ser Lys Ser Thr Thr Glu
                245                 250                 255

Trp Leu Lys Lys Asn Lys Met Lys Thr Leu Glu Trp Pro Ser Gln Ser
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Met Leu Trp Tyr Asp Leu Lys Lys Ala
        275                 280                 285

Val His Ala Arg Lys Pro Ser Asn Val Thr Glu Leu Gly Gln Phe Cys
    290                 295                 300
```

```
Lys Asp Glu Trp Ala Lys Ile Pro Pro Gly Arg Cys Lys Ser Leu Ile
305                 310                 315                 320


Ala Arg Tyr Arg Lys Arg Leu Val Ala Val Val Ala Ala Lys Gly Gly
                325                 330                 335


Pro Thr Ser Tyr
            340
```

<210> 293
<211> 636
<212> PRT
<213> Tribolium castaneum

<400> 293

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Met Met Leu Asn Trp Leu Lys Ser Gly Lys Leu Glu Ser Gln Ser Gln
1               5                   10                  15


Glu Gln Ser Ser Cys Tyr Leu Glu Asn Ser Asn Cys Leu Pro Pro Thr
            20                  25                  30


Leu Asp Ser Thr Asp Ile Ile Gly Glu Glu Asn Lys Ala Gly Thr Thr
        35                  40                  45


Ser Arg Lys Lys Arg Lys Tyr Asp Glu Asp Tyr Leu Asn Phe Gly Phe
    50                  55                  60


Thr Trp Thr Gly Asp Lys Asp Glu Pro Asn Gly Leu Cys Val Ile Cys
65                  70                  75                  80


Glu Gln Val Val Asn Asn Ser Ser Leu Asn Pro Ala Lys Leu Lys Arg
                85                  90                  95


His Leu Asp Thr Lys His Pro Thr Leu Lys Gly Lys Ser Glu Tyr Phe
            100                 105                 110


Lys Arg Lys Cys Asn Glu Leu Asn Gln Lys Lys His Thr Phe Glu Arg
        115                 120                 125
```

```
Tyr Val Arg Asp Asp Asn Lys Asn Leu Leu Lys Ala Ser Tyr Leu Val
    130                 135                 140

Ser Leu Arg Ile Ala Lys Gln Gly Glu Ala Tyr Thr Ile Ala Glu Lys
145                 150                 155                 160

Leu Ile Lys Pro Cys Thr Lys Asp Leu Thr Thr Cys Val Phe Gly Glu
                165                 170                 175

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

Ser Arg Arg Ile Glu Asp Met Ser Tyr Phe Cys Glu Ala Val Leu Val
        195                 200                 205

Asn Arg Leu Lys Asn Ala Lys Cys Gly Phe Thr Leu Gln Met Asp Glu
    210                 215                 220

Ser Thr Asp Val Ala Gly Leu Ala Ile Leu Leu Val Phe Val Arg Tyr
225                 230                 235                 240

Ile His Glu Ser Ser Phe Glu Glu Asp Met Leu Phe Cys Lys Ala Leu
                245                 250                 255

Pro Thr Gln Thr Thr Gly Glu Glu Ile Phe Asn Leu Leu Asn Ala Tyr
            260                 265                 270

Phe Glu Lys His Ser Ile Pro Trp Asn Leu Cys Tyr His Ile Cys Thr
        275                 280                 285

Asp Gly Ala Lys Ala Met Val Gly Val Ile Lys Gly Val Ile Ala Arg
    290                 295                 300

Ile Lys Lys Leu Val Pro Asp Ile Lys Ala Ser His Cys Cys Leu His
305                 310                 315                 320

Arg His Ala Leu Ala Val Lys Arg Ile Pro Asn Ala Leu His Glu Val
```

```
                325                 330                 335

Leu Asn Asp Ala Val Lys Met Ile Asn Phe Ile Lys Ser Arg Pro Leu
            340                 345                 350

Asn Ala Arg Val Phe Ala Leu Leu Cys Asp Asp Leu Gly Ser Leu His
        355                 360                 365

Lys Asn Leu Leu Leu His Thr Glu Val Arg Trp Leu Ser Arg Gly Lys
    370                 375                 380

Val Leu Thr Arg Phe Trp Glu Leu Arg Asp Glu Ile Arg Ile Phe Phe
385                 390                 395                 400

Asn Glu Arg Glu Phe Ala Gly Lys Leu Asn Asp Thr Ser Trp Leu Gln
                405                 410                 415

Asn Leu Ala Tyr Ile Ala Asp Ile Phe Ser Tyr Leu Asn Glu Val Asn
            420                 425                 430

Leu Ser Leu Gln Gly Pro Asn Ser Thr Ile Phe Lys Val Asn Ser Arg
        435                 440                 445

Ile Asn Ser Ile Lys Ser Lys Leu Lys Leu Trp Glu Glu Cys Ile Thr
    450                 455                 460

Lys Asn Asn Thr Glu Cys Phe Ala Asn Leu Asn Asp Phe Leu Glu Thr
465                 470                 475                 480

Ser Asn Thr Ala Leu Asp Pro Asn Leu Lys Ser Asn Ile Leu Glu His
                485                 490                 495

Leu Asn Gly Leu Lys Asn Thr Phe Leu Glu Tyr Phe Pro Pro Thr Cys
            500                 505                 510

Asn Asn Ile Ser Trp Val Glu Asn Pro Phe Asn Glu Cys Gly Asn Val
        515                 520                 525
```

```
Asp Thr Leu Pro Ile Lys Glu Arg Glu Gln Leu Ile Asp Ile Arg Thr
    530                 535                 540

Asp Thr Thr Leu Lys Ser Ser Phe Val Pro Asp Gly Ile Gly Pro Phe
545                 550                 555                 560

Trp Ile Lys Leu Met Asp Glu Phe Pro Glu Ile Ser Lys Arg Ala Val
                565                 570                 575

Lys Glu Leu Met Pro Phe Val Thr Thr Tyr Leu Cys Glu Lys Ser Phe
            580                 585                 590

Ser Val Tyr Val Ala Thr Lys Thr Lys Tyr Arg Asn Arg Leu Asp Ala
        595                 600                 605

Glu Asp Asp Met Arg Leu Gln Leu Thr Thr Ile His Pro Asp Ile Asp
    610                 615                 620

Asn Leu Cys Asn Asn Lys Gln Ala Gln Lys Ser His
625                 630                 635
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<210> 294
<211> 649
<212> PRT
<213> Oryzias latipes

<400> 294

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Met Glu Glu Val Cys Asp Ser Ser Ala Ala Ala Ser Ser Thr Val Gln
1               5                   10                  15

Asn Gln Pro Gln Asp Gln Glu His Pro Trp Pro Tyr Leu Arg Glu Phe
            20                  25                  30

Phe Ser Leu Ser Gly Val Asn Lys Asp Ser Phe Lys Met Lys Cys Val
        35                  40                  45

Leu Cys Leu Pro Leu Asn Lys Glu Ile Ser Ala Phe Lys Ser Ser Pro
    50                  55                  60
```

```
Ser Asn Leu Arg Lys His Ile Glu Arg Met His Pro Asn Tyr Leu Lys
65                  70                  75                  80

Asn Tyr Ser Lys Leu Thr Ala Gln Lys Arg Lys Ile Gly Thr Ser Thr
                85                  90                  95

His Ala Ser Ser Ser Lys Gln Leu Lys Val Asp Ser Val Phe Pro Val
            100                 105                 110

Lys His Val Ser Pro Val Thr Val Asn Lys Ala Ile Leu Arg Tyr Ile
        115                 120                 125

Ile Gln Gly Leu His Pro Phe Ser Thr Val Asp Leu Pro Ser Phe Lys
    130                 135                 140

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

Thr Leu Arg Ser Lys Ile Ala Glu Ala Ala Leu Ile Met Lys Gln Lys
                165                 170                 175

Val Thr Ala Ala Met Ser Glu Val Glu Trp Ile Ala Thr Thr Thr Asp
            180                 185                 190

Cys Trp Thr Ala Arg Arg Lys Ser Phe Ile Gly Val Thr Ala His Trp
        195                 200                 205

Ile Asn Pro Gly Ser Leu Glu Arg His Ser Ala Ala Leu Ala Cys Lys
    210                 215                 220

Arg Leu Met Gly Ser His Thr Phe Glu Val Leu Ala Ser Ala Met Asn
225                 230                 235                 240

Asp Ile His Ser Glu Tyr Glu Ile Arg Asp Lys Val Val Cys Thr Thr
                245                 250                 255
```

```
Thr Asp Ser Gly Ser Asn Phe Met Lys Ala Phe Arg Val Phe Gly Val
            260                 265                 270

Glu Asn Asn Asp Ile Glu Thr Glu Ala Arg Arg Cys Glu Ser Asp Asp
        275                 280                 285

Thr Asp Ser Glu Gly Cys Gly Glu Gly Ser Asp Gly Val Glu Phe Gln
    290                 295                 300

Asp Ala Ser Arg Val Leu Asp Gln Asp Asp Gly Phe Glu Phe Gln Leu
305                 310                 315                 320

Pro Lys His Gln Lys Cys Ala Cys His Leu Leu Asn Leu Val Ser Ser
                325                 330                 335

Val Asp Ala Gln Lys Ala Leu Ser Asn Glu His Tyr Lys Lys Leu Tyr
            340                 345                 350

Arg Ser Val Phe Gly Lys Cys Gln Ala Leu Trp Asn Lys Ser Ser Arg
        355                 360                 365

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

Leu Arg Pro Asn Gln Thr Arg Trp Asn Ser Thr Phe Met Ala Val Asp
385                 390                 395                 400

Arg Ile Leu Gln Ile Cys Lys Glu Ala Gly Glu Gly Ala Leu Arg Asn
                405                 410                 415

Ile Cys Thr Ser Leu Glu Val Pro Met Phe Asn Pro Ala Glu Met Leu
            420                 425                 430

Phe Leu Thr Glu Trp Ala Asn Thr Met Arg Pro Val Ala Lys Val Leu
        435                 440                 445

Asp Ile Leu Gln Ala Glu Thr Asn Thr Gln Leu Gly Trp Leu Leu Pro
    450                 455                 460
```

```
Ser Val His Gln Leu Ser Leu Lys Leu Gln Arg Leu His His Ser Leu
465                 470                 475                 480

Arg Tyr Cys Asp Pro Leu Val Asp Ala Leu Gln Gln Gly Ile Gln Thr
                485                 490                 495

Arg Phe Lys His Met Phe Glu Asp Pro Glu Ile Ile Ala Ala Ala Ile
            500                 505                 510

Leu Leu Pro Lys Phe Arg Thr Ser Trp Thr Asn Asp Glu Thr Ile Ile
        515                 520                 525

Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
    530                 535                 540

Lys Lys Glu Leu Ala Asn Ser Ser Ser Asp Asp Glu Asp Phe Phe Ala
545                 550                 555                 560

Ser Leu Lys Pro Thr Thr His Glu Ala Ser Lys Glu Leu Asp Gly Tyr
                565                 570                 575

Leu Ala Cys Val Ser Asp Thr Arg Glu Ser Leu Leu Thr Phe Pro Ala
            580                 585                 590

Ile Cys Ser Leu Ser Ile Lys Thr Asn Thr Pro Leu Pro Ala Ser Ala
        595                 600                 605

Ala Cys Glu Arg Leu Phe Ser Thr Ala Gly Leu Leu Phe Ser Pro Lys
    610                 615                 620

Arg Ala Arg Leu Asp Thr Asn Asn Phe Glu Asn Gln Leu Leu Leu Lys
625                 630                 635                 640

Leu Asn Leu Arg Phe Tyr Asn Phe Glu
                645
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<210> 295
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR encoding sequence Sleeping Beauty

<400> 295
acttaagtgt atgtaaactt ccgacttcaa ctg 33

<210> 296
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR and chromosomal sequence Sleeping Beauty

<400> 296
cagtcaactt agtgtatgta aacttctgac ccactggaat tgtgatacag tgaattataa 60

gtgaaataat ctgtctgtaa acaattgttg gaaaaatgac ttgtgtcatg cacaaagtag 120

atgtcctaac tgacttgcca aaactattgt ttgttaacaa gaaatttgtg gagtagttga 180

aaaacgagtt ttaatgactc caacttaagt gtatgtaaac ttccgacttc aactgtaaga 240

atggcccatt catctatagt agcacacaat atttgcattt gtgcgacagt ataagggaca 300

attatgctat caggcatttt tccaaagtga gtaatcgaag tttttatacc tttgtgtgcc 360

atgtttgcta 370

<210> 297
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR and chromosomal sequence Sleeping Beauty

<400> 297
cagtcaactt agtgtatgta aacttctgac ccactggaat tgtgatacag tgaattataa 60

gtgaaataat ctgtctgtaa acaattgttg gaaaaatgac ttgtgtcatg cacaaagtag 120

atgtcctaac tgacttgcca aaactattgt ttgttaacaa gaaatttgtg gagtagttga 180

aaaacgagtt ttaatgactc caacttaagt gtatgtaaac ttccgacttc aactgtacaa 240

gtagaccaaa tatccatata cataaaagaa aaaaatagaa aaaatttcta gtgacagaaa 300

aatgacaaag aacatactgc tttattacta ctattaagat gtttgcttcc attacactca 360

tatgagtca 369

<210> 298
<211> 227
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR of Sleeping Beauty

<400> 298
ttagtgtatg taaacttctg acccactgga attgtgatac agtgaattat aagtgaaata 60

atctgtctgt aaacaattgt tggaaaaatg acttgtgtca tgcacaaagt agatgtccta 120

actgacttgc caaaactatt gtttgttaac aagaaatttg tggagtagtt gaaaaacgag 180

ttttaatgac tccaacttaa gtgtatgtaa acttccgact tcaactg 227

<210> 299
<211> 371
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR and chromosomal sequence Sleeping Beauty

<400> 299
caacttgagt gtatgttaac ttctgaccca ctgggaatgt gatgaaagaa ataaaagctg 60

aaatgaatca ttctctctac tattattctg atatttcaca ttcttaaaat aaagtggtga 120

tcctaactga ccttaagaca gggaatcttt actcggatta aatgtcagga attgtgaaaa 180

agtgagttta aatgtatttg gctaaggtgt atgtaaactt ccgacttcaa ctgtatatcc 240

tccccgttgc accctcttga tgatgctgag atgaacacag atgctcactc cttgagggct 300

ctaagcttat gctgacacag acacaggtgc tcacttctat gaatggccta agatttgagg 360

acatcatgag g 371

<210> 300
<211> 229
<212> DNA
<213> Artificial Sequence

<220>
<223> IR/DR of Sleeping Beauty

<400> 300
ttgagtgtat gttaacttct gacccactgg gaatgtgatg aaagaaataa aagctgaaat 60

gaatcattct ctctactatt attctgatat ttcacattct taaaataaag tggtgatcct 120

aactgacctt aagacaggga atctttactc ggattaaatg tcaggaattg tgaaaaagtg 180

agtttaaatg tatttggcta aggtgtatgt aaacttccga cttcaactg 229

<210> 301
<211> 1468
<212> PRT
<213> Artificial Sequence

<220>
<223> ET3

<400> 301

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

Gly Phe Ser Ala Ile Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
20 25 30

Trp Asp Tyr Arg Gln Ser Glu Leu Leu Arg Glu Leu His Val Asp Thr
35 40 45

Arg Phe Pro Ala Thr Ala Pro Gly Ala Leu Pro Leu Gly Pro Ser Val
50 55 60

Leu Tyr Lys Lys Thr Val Phe Val Glu Phe Thr Asp Gln Leu Phe Ser
65 70 75 80

```
Val Ala Arg Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
                85                  90                  95

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

Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Phe Trp Lys Ser
        115                 120                 125

Ser Glu Gly Ala Glu Tyr Glu Asp His Thr Ser Gln Arg Glu Lys Glu
    130                 135                 140

Asp Asp Lys Val Leu Pro Gly Lys Ser Gln Thr Tyr Val Trp Gln Val
145                 150                 155                 160

Leu Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr
                165                 170                 175

Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu
            180                 185                 190

Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Thr Arg Glu Arg
        195                 200                 205

Thr Gln Asn Leu His Glu Phe Val Leu Leu Phe Ala Val Phe Asp Glu
    210                 215                 220

Gly Lys Ser Trp His Ser Ala Arg Asn Asp Ser Trp Thr Arg Ala Met
225                 230                 235                 240

Asp Pro Ala Pro Ala Arg Ala Gln Pro Ala Met His Thr Val Asn Gly
                245                 250                 255

Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Lys Lys Ser
            260                 265                 270

Val Tyr Trp His Val Ile Gly Met Gly Thr Ser Pro Glu Val His Ser
        275                 280                 285
```

```
Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg His His Arg Gln Ala
    290                 295                 300

Ser Leu Glu Ile Ser Pro Leu Thr Phe Leu Thr Ala Gln Thr Phe Leu
305                 310                 315                 320

Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His His
                325                 330                 335

His Gly Gly Met Glu Ala His Val Arg Val Glu Ser Cys Ala Glu Glu
            340                 345                 350

Pro Gln Leu Arg Arg Lys Ala Asp Glu Glu Glu Asp Tyr Asp Asp Asn
        355                 360                 365

Leu Tyr Asp Ser Asp Met Asp Val Val Arg Leu Asp Gly Asp Asp Val
    370                 375                 380

Ser Pro Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
        435                 440                 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480
```

```
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
                485                 490                 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500                 505                 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
        515                 520                 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530                 535                 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595                 600                 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610                 615                 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625                 630                 635                 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
                645                 650                 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660                 665                 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685
```

```
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ala Gln Asn Ser Arg Pro Pro
        755                 760                 765

Ser Ala Ser Ala Pro Lys Pro Pro Val Leu Arg Arg His Gln Arg Asp
    770                 775                 780

Ile Ser Leu Pro Thr Phe Gln Pro Glu Glu Asp Lys Met Asp Tyr Asp
785                 790                 795                 800

Asp Ile Phe Ser Thr Glu Thr Lys Gly Glu Asp Phe Asp Ile Tyr Gly
                805                 810                 815

Glu Asp Glu Asn Gln Asp Pro Arg Ser Phe Gln Lys Arg Thr Arg His
            820                 825                 830

Tyr Phe Ile Ala Ala Val Glu Gln Leu Trp Asp Tyr Gly Met Ser Glu
        835                 840                 845

Ser Pro Arg Ala Leu Arg Asn Arg Ala Gln Asn Gly Glu Val Pro Arg
    850                 855                 860

Phe Lys Lys Val Val Phe Arg Glu Phe Ala Asp Gly Ser Phe Thr Gln
865                 870                 875                 880
```

```
Pro Ser Tyr Arg Gly Glu Leu Asn Lys His Leu Gly Leu Leu Gly Pro
                885                 890                 895

Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Lys Asn
            900                 905                 910

Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Pro
        915                 920                 925

Asp Asp Gln Glu Gln Gly Ala Glu Pro Arg His Asn Phe Val Gln Pro
    930                 935                 940

Asn Glu Thr Arg Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro
945                 950                 955                 960

Thr Glu Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val
                965                 970                 975

Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Ile
            980                 985                 990

Cys Arg Ala Asn Thr Leu Asn Ala  Ala His Gly Arg Gln  Val Thr Val
        995                 1000                1005

Gln Glu  Phe Ala Leu Phe Phe  Thr Ile Phe Asp Glu  Thr Lys Ser
    1010                1015                1020

Trp Tyr  Phe Thr Glu Asn Val  Glu Arg Asn Cys Arg  Ala Pro Cys
    1025                1030                1035

His Leu  Gln Met Glu Asp Pro  Thr Leu Lys Glu Asn  Tyr Arg Phe
    1040                1045                1050

His Ala  Ile Asn Gly Tyr Val  Met Asp Thr Leu Pro  Gly Leu Val
    1055                1060                1065

Met Ala  Gln Asn Gln Arg Ile  Arg Trp Tyr Leu Leu  Ser Met Gly
    1070                1075                1080
```

```
Ser Asn  Glu Asn Ile His Ser  Ile His Phe Ser Gly  His Val Phe
    1085                1090                1095

Ser Val  Arg Lys Lys Glu Glu  Tyr Lys Met Ala Val  Tyr Asn Leu
    1100                1105                1110

Tyr Pro  Gly Val Phe Glu Thr  Val Glu Met Leu Pro  Ser Lys Val
    1115                1120                1125

Gly Ile  Trp Arg Ile Glu Cys  Leu Ile Gly Glu His  Leu Gln Ala
    1130                1135                1140

Gly Met  Ser Thr Thr Phe Leu  Val Tyr Ser Lys Lys  Cys Gln Thr
    1145                1150                1155

Pro Leu  Gly Met Ala Ser Gly  His Ile Arg Asp Phe  Gln Ile Thr
    1160                1165                1170

Ala Ser  Gly Gln Tyr Gly Gln  Trp Ala Pro Lys Leu  Ala Arg Leu
    1175                1180                1185

His Tyr  Ser Gly Ser Ile Asn  Ala Trp Ser Thr Lys  Glu Pro Phe
    1190                1195                1200

Ser Trp  Ile Lys Val Asp Leu  Leu Ala Pro Met Ile  Ile His Gly
    1205                1210                1215

Ile Lys  Thr Gln Gly Ala Arg  Gln Lys Phe Ser Ser  Leu Tyr Ile
    1220                1225                1230

Ser Gln  Phe Ile Ile Met Tyr  Ser Leu Asp Gly Lys  Lys Trp Gln
    1235                1240                1245

Thr Tyr  Arg Gly Asn Ser Thr  Gly Thr Leu Met Val  Phe Phe Gly
    1250                1255                1260
```

```
Asn Val  Asp Ser Ser Gly Ile  Lys His Asn Ile Phe  Asn Pro Pro
    1265                1270                1275

Ile Ile  Ala Arg Tyr Ile Arg  Leu His Pro Thr His  Tyr Ser Ile
    1280                1285                1290

Arg Ser  Thr Leu Arg Met Glu  Leu Met Gly Cys Asp  Leu Asn Ser
    1295                1300                1305

Cys Ser  Met Pro Leu Gly Met  Glu Ser Lys Ala Ile  Ser Asp Ala
    1310                1315                1320

Gln Ile  Thr Ala Ser Ser Tyr  Phe Thr Asn Met Phe  Ala Thr Trp
    1325                1330                1335

Ser Pro  Ser Lys Ala Arg Leu  His Leu Gln Gly Arg  Ser Asn Ala
    1340                1345                1350

Trp Arg  Pro Gln Val Asn Asn  Pro Lys Glu Trp Leu  Gln Val Asp
    1355                1360                1365

Phe Gln  Lys Thr Met Lys Val  Thr Gly Val Thr Thr  Gln Gly Val
    1370                1375                1380

Lys Ser  Leu Leu Thr Ser Met  Tyr Val Lys Glu Phe  Leu Ile Ser
    1385                1390                1395

Ser Ser  Gln Asp Gly His Gln  Trp Thr Leu Phe Phe  Gln Asn Gly
    1400                1405                1410

Lys Val  Lys Val Phe Gln Gly  Asn Gln Asp Ser Phe  Thr Pro Val
    1415                1420                1425

Val Asn  Ser Leu Asp Pro Pro  Leu Leu Thr Arg Tyr  Leu Arg Ile
    1430                1435                1440

His Pro  Gln Ser Trp Val His  Gln Ile Ala Leu Arg  Met Glu Val
    1445                1450                1455
```

Leu Gly Cys Glu Ala Gln Asp Leu Tyr Val
    1460   1465

<210> 302
<211> 147
<212> PRT
<213> Homo sapiens

<400> 302

Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp
1   5   10   15

Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
            20   25   30

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

Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His
    50   55   60

Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp
65   70   75   80

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

Leu His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn Val Leu Val
            100   105   110

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

Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His
    130   135   140

Lys Tyr His

145

<210> 303
<211> 147
<212> PRT
<213> Homo sapiens

<400> 303

Met Gly His Phe Thr Glu Glu Asp Lys Ala Thr Ile Thr Ser Leu Trp
1 5 10 15

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

Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Asp Ser Phe Gly Asn
35 40 45

Leu Ser Ser Ala Ser Ala Ile Met Gly Asn Pro Lys Val Lys Ala His
50 55 60

Gly Lys Lys Val Leu Thr Ser Leu Gly Asp Ala Thr Lys His Leu Asp
65 70 75 80

Asp Leu Lys Gly Thr Phe Ala Gln Leu Ser Glu Leu His Cys Asp Lys
85 90 95

Leu His Val Asp Pro Glu Asn Phe Lys Leu Leu Gly Asn Val Leu Val
100 105 110

Thr Val Leu Ala Ile His Phe Gly Lys Glu Phe Thr Pro Glu Val Gln
115 120 125

Ala Ser Trp Gln Lys Met Val Thr Ala Val Ala Ser Ala Leu Ser Ser
130 135 140

Arg Tyr His
145

<210> 304
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<212> DNA
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<223> HDAd35-T4-Ef1a-mgmt

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<222> (1)..(481)
<223> Ad35 5'end

<220>
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<222> (14126)..(14159)
<223> FRT (Complementary)

<220>
<221> misc_feature
<222> (14220)..(14463)
<223> pT4 LIR

<220>
<221> misc_feature
<222> (14491)..(15825)
<223> EF1a

<220>
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<222> (15843)..(16466)
<223> mgmt

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<221> misc_feature
<222> (16484)..(16705)
<223> pA

<220>
<221> misc_feature
<222> (16735)..(17000)
<223> pT4 RIR

<220>
<221> misc_feature
<222> (17107)..(17140)
<223> FRT (Complementary)

<220>

<221> misc_feature
<222> (28823)..(29230)
<223> Ad35 3'end

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aaaagtgtgg gccgtgtggt gattggctgt ggggttaacg gttaaaaggg gcggcgcggc 120

cgtgggaaaa tgacgtttta tgggggtgga gttttttttgc aagttgtcgc gggaaatgtt 180

acgcataaaa aggcttcttt tctcacggaa ctacttagtt ttcccacggt atttaacagg 240

aaatgaggta gttttgaccg gatgcaagtg aaaattgctg attttcgcgc gaaaactgaa 300

tgaggaagtg tttttctgaa taatgtggta tttatggcag ggtggagtat ttgttcaggg 360

ccaggtagac tttgacccat tacgtggagg tttcgattac cgtgtttttt acctgaattt 420

ccgcgtaccg tgtcaaagtc ttctgttttt acgtaggtgt cagctgatcg ctagggtatt 480

taccggtatt caaggattac atgagcttag aaatgtaatt agcatagtgt gtggcatagt 540

gtagatacca aataaatatg atctctcctt ctactcttga aaatgcaaac acattcttgg 600

tggtcctaaa atagcctgta acatggttta ctcagcagca tttgctattc aaggcagatc 660

tgcctttagt cattggctgc gctcctgaac agctgtgtga aaggctaact tttgtaaacc 720

aaatcaaaat aaaatgcagc aaaaatttgt cactgaaagg aaatcctcag tatatccttt 780

tatgaaatga aagatccctc atccaaactt aacttttta aaagtgcgca tttggagata 840

tagccctttc ttatgaatcc taattcaatt ttggccataa acacacgttg atgttcccca 900

ccccaaagca catagcaaca agagtaggtt ctatattgaa aataatgaca atttaaaaac 960

atgtacttat ttcactgtat gtggacagtg tctatgattg catcatgaag tgtcatataa 1020

ccatgtacgt gtacatgaga gagagataga gagagaagtg gtagggtggt ggtggtagag 1080

gggatggcga tagtaatcat ggtaatggta gaggtgatgg aggtggtaat gacggaggta 1140

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tagtgaaggt gagggtagtg gtggtggagg tggtggtgct ggtagcaata gtgatggtgg 1320

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ttgtaccact ctgtcaacag caccactgac tgggacagag gaagaaggca cactctgaat 1440

gtgttattaa cagaaacctc aaaacagtct gtctccttgt agtcattcaa aattatcttt 1500

ttcttacctg gaaaactgaa actgaattac cgggaaaaac acaggagatt tttgtttgtt 1560

aatatgctgc caataaagta attttatgtc aaatttaact acaggaaagg gcaaggcatt 1620

ttctaagttc cttagatgtc atgtggctaa aaaaaacaaa aggatggaca gcagttagat 1680

actgtacact tagctgtttg aagccatata ttcagaaagc agatgttggg agttggtgtt 1740

tgaggactga tttcctggag gtattttata taggccaagt tcattgttct aaactctaag 1800

ggcttgactt gagggaggaa aagaggcaag aacatgttta gttttgctga cagcatcaca 1860

tgggcagccc taaggctaga caactttagg gcctgaagct tattctagga aagaagcacc 1920

tacagagtgg cactgggctc ccctccacta tagagatgaa gtcatatgac agtaaagggc 1980

aggcagggct gcctaggggg cccagaactg acacttccat tagaatgagc acaggccagg 2040

gagagaagtg gggaaccaga gagaaggagc tggaattcta gtaggacaaa cggtaagtga 2100

acaacaagaa caagttaaga gtgtgtgcag tattctttca aagactgaaa aaatagtgat 2160

gtgatagaat ggcaggtggc tctgagcagg ccaggagaag gactgggggc agagcatccc 2220

aggcaggagg gcagcaagtg ggaaggccct ggggtggggc ttttggactg ttccagtgac 2280

gggcaggcag ccagtgtgcc tgtcacacaa tgcaccaggg aagtagtcgt gaatttgcag 2340

agggtcttgc aggctatggg aaagggattg gattgtattt tgtttgtagg gaagccatcg 2400

ggggacttaa gcagaggaag gattggcttc atctctttga aaaagttctc tctggatgct 2460

gatgggagga gaaatggaag gaaaagaaac acttttaggg gcaagaactt ttgagaaggg 2520

tggaattggg agtgtggagt tggggccagc tttggcacag gaggggaagc taaacacgtg 2580

gccgcatgag ggcctgtaat tctacctgaa atgggtacca tttgttaggg taaacaaatg 2640

aaccaaatgc ccagtgatac agaccaagtg ttggcaaact tcttctgtga tggcccaggt 2700

agtaaatgtc tcaggcttcg caggccatgt ggtctctgtt gaagctctgt gtagtagaca 2760

atatgttaat gactgggcgt gactgtgtgc taataaaagt ttatttacaa aaacagcccg 2820

tgggctggat ttagctcaca ggctgtagtt tgccaacctc tgacctagag catgaactga 2880

gcatcttctt ggagggaaat aagttctttc caagttgccc tcctcacatt gcaggggcc 2940

atgtaggccc attattcaca gaagagtggg tgggcaacct ttctggagca gaaaaacgta 3000

aagatttctt ccgtagtgca agtaaggtga ccatttctaa accgtgcaag tgatccagca 3060

gtcccaaaag ttgtttcact tctcattgtg cgcccgttct caggtgctcc gaagcttcca 3120

gtcctttgta gggacatgga tgaaattgga aatcatcatt ctcagtaaac tatcgcaaga 3180

acaaaaaacc aaacaccgca tattctcact cataggtggg aattgaacaa tgagatcaca 3240

tggacacggg aaggggaaca tcacattctg gggactgttg tggggtgggg ggaggggga 3300

gggatagcat tgggagatat acctaatgct agatgacaag ttagtgggtg cagcgcacca 3360

gtgtggcaca tgtatacata tgtaactaac ctgcacaatg tgcacatgta ccctaaaact 3420

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