SEQUENCE LISTING

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<120> GENE THERAPY VECTORS AND CYTOSINE DEAMINASES

<130> 00014-007JP1

<140> Not yet assinged
<141> 2011-03-24

<150> US 61/100,666
<151> 2008-09-26

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<151> 2008-12-08

<150> US 61/186,823
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<160> 48

<170> PatentIn version 3.5

<210> 1
<211> 477
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(477)

<400> 1

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atg gtg aca ggg gga atg gca agc aag tgg gat cag aag ggt atg gac          48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                  10                  15

att gcc tat gag gag gcg gcc tta ggt tac aaa gag ggt ggt gtt cct          96
Ile Ala Tyr Glu Glu Ala Ala Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

att ggc gga tgt ctt atc aat aac aaa gac gga agt gtt ctc ggt cgt         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggt cac aac atg aga ttt caa aag gga tcc gcc aca cta cat ggt gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc act ttg gaa aac tgt ggg aga tta gag ggc aaa gtg tac aaa         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
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65 70 75 80

gat acc act ttg tat acg acg ctg tct cca tgc gac atg tgt aca ggt 288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
85 90 95

gcc atc atc atg tat ggt att cca cgc tgt gtt gtc ggt gag aac gtt 336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Val Gly Glu Asn Val
100 105 110

aat ttc aaa agt aag ggc gag aaa tat tta caa act aga ggt cac gag 384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
115 120 125

gtt gtt gtt gtt gac gat gag agg tgt aaa aag atc atg aaa caa ttt 432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Ile Met Lys Gln Phe
130 135 140

atc gat gaa aga cct cag gat tgg ttt gaa gat att ggt gag tag 477
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145 150 155

<210> 2
<211> 158
<212> PRT
<213> Saccharomyces cerevisiae

<400> 2

Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1 5 10 15

Ile Ala Tyr Glu Glu Ala Ala Leu Gly Tyr Lys Glu Gly Gly Val Pro
20 25 30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
35 40 45

Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
50 55 60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65 70 75 80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
85 90 95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Val Gly Glu Asn Val
100 105 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
115 120 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Ile Met Lys Gln Phe

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    130                 135                 140

Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145                 150                 155


<210>  3
<211>  477
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Engineered cytosine deaminase


<220>
<221>  CDS
<222>  (1)..(477)

<400>  3
atg gtg aca ggg gga atg gca agc aag tgg gat cag aag ggt atg gac          48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

att gcc tat gag gag gcg tta tta ggt tac aaa gag ggt ggt gtt cct          96
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

att ggc gga tgt ctt atc aat aac aaa gac gga agt gtt ctc ggt cgt         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggt cac aac atg aga ttt caa aag gga tcc gcc aca cta cat ggt gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc act ttg gaa aac tgt ggg aga tta gag ggc aaa gtg tac aaa         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

gat acc act ttg tat acg acg ctg tct cca tgc gac atg tgt aca ggt         288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

gcc atc atc atg tat ggt att cca cgc tgt gtc atc ggt gag aac gtt         336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

aat ttc aaa agt aag ggc gag aaa tat tta caa act aga ggt cac gag         384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

gtt gtt gtt gtt gac gat gag agg tgt aaa aag tta atg aaa caa ttt         432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

atc gat gaa aga cct cag gat tgg ttt gaa gat att ggt gag tag             477
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145                 150                 155


<210>  4
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<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

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1               5                  10                  15

Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145                 150                 155
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<210> 5
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Human codon optimized cytosine deaminase

<220>
<221> CDS
<222> (1)..(480)

<400> 5

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Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

atc gct tac gag gag gcc gca ctg ggc tac aag gag ggc ggc gtg cct          96
Ile Ala Tyr Glu Glu Ala Ala Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc         288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

gct atc atc atg tac ggc atc cct agg tgt gtg gtc ggc gag aac gtg         336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Val Gly Glu Asn Val
            100                 105                 110

aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag         384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

gtg gtg gtt gtt gac gat gag agg tgt aag aag atc atg aag cag ttc         432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Ile Met Lys Gln Phe
    130                 135                 140

atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag tga taa         480
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145                 150                 155
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<210> 6
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

Ile Ala Tyr Glu Glu Ala Ala Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45
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```
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Val Gly Glu Asn Val
            100                 105                 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Ile Met Lys Gln Phe
    130                 135                 140

Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu
145                 150                 155


<210>  7
<211>  756
<212>  DNA
<213>  Saccharomyces cerevisiae


<220>
<221>  CDS
<222>  (1)..(756)

<400>  7
atg aac ccg tta ttc ttt ttg gct tct cca ttc ttg tac ctt aca tat          48
Met Asn Pro Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr Tyr
1               5                   10                  15

ctt ata tat tat cca aac aaa ggg tct ttc gtt agc aaa cct aga aat          96
Leu Ile Tyr Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg Asn
            20                  25                  30

ctg caa aaa atg tct tcg gaa cca ttt aag aac gtc tac ttg cta cct         144
Leu Gln Lys Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu Pro
        35                  40                  45

caa aca aac caa ttg ctg ggt ttg tac acc atc atc aga aat aag aat         192
Gln Thr Asn Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys Asn
    50                  55                  60

aca act aga cct gat ttc att ttc tac tcc gat aga atc atc aga ttg         240
Thr Thr Arg Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg Leu
65                  70                  75                  80

ttg gtt gaa gaa ggt ttg aac cat cta cct gtg caa aag caa att gtg         288
Leu Val Glu Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile Val
                85                  90                  95
```

```
gaa act gac acc aac gaa aac ttc gaa ggt gtc tca ttc atg ggt aaa        336
Glu Thr Asp Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly Lys
            100                 105                 110

atc tgt ggt gtt tcc att gtc aga gct ggt gaa tcg atg gag caa gga        384
Ile Cys Gly Val Ser Ile Val Arg Ala Gly Glu Ser Met Glu Gln Gly
        115                 120                 125

tta aga gac tgt tgt agg tct gtg cgt atc ggt aaa att tta att caa        432
Leu Arg Asp Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile Gln
    130                 135                 140

agg gac gag gag act gct tta cca aag tta ttc tac gaa aaa tta cca        480
Arg Asp Glu Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu Pro
145                 150                 155                 160

gag gat ata tct gaa agg tat gtc ttc cta tta gac cca atg ctg gcc        528
Glu Asp Ile Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu Ala
                165                 170                 175

acc ggt ggt agt gct atc atg gct aca gaa gtc ttg att aag aga ggt        576
Thr Gly Gly Ser Ala Ile Met Ala Thr Glu Val Leu Ile Lys Arg Gly
            180                 185                 190

gtt aag cca gag aga att tac ttc tta aac cta atc tgt agt aag gaa        624
Val Lys Pro Glu Arg Ile Tyr Phe Leu Asn Leu Ile Cys Ser Lys Glu
        195                 200                 205

ggg att gaa aaa tac cat gcc gcc ttc cca gag gtc aga att gtt act        672
Gly Ile Glu Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val Thr
    210                 215                 220

ggt gcc ctc gac aga ggt cta gat gaa aac aag tat cta gtt cca ggg        720
Gly Ala Leu Asp Arg Gly Leu Asp Glu Asn Lys Tyr Leu Val Pro Gly
225                 230                 235                 240

ttg ggt gac ttt ggt gac aga tac tac tgt gtt taa                       756
Leu Gly Asp Phe Gly Asp Arg Tyr Tyr Cys Val
                245                 250
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<210> 8
<211> 251
<212> PRT
<213> Saccharomyces cerevisiae

<400> 8

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Met Asn Pro Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr Tyr
1               5                   10                  15

Leu Ile Tyr Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg Asn
            20                  25                  30

Leu Gln Lys Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu Pro
        35                  40                  45

Gln Thr Asn Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys Asn
    50                  55                  60
```

```
Thr Thr Arg Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg Leu
65                  70                  75                  80

Leu Val Glu Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile Val
                85                  90                  95

Glu Thr Asp Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly Lys
            100                 105                 110

Ile Cys Gly Val Ser Ile Val Arg Ala Gly Glu Ser Met Glu Gln Gly
        115                 120                 125

Leu Arg Asp Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile Gln
    130                 135                 140

Arg Asp Glu Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu Pro
145                 150                 155                 160

Glu Asp Ile Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu Ala
                165                 170                 175

Thr Gly Gly Ser Ala Ile Met Ala Thr Glu Val Leu Ile Lys Arg Gly
            180                 185                 190

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

Gly Ile Glu Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val Thr
    210                 215                 220

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

Leu Gly Asp Phe Gly Asp Arg Tyr Tyr Cys Val
                245                 250
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<210> 9
<211> 1443
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(1443)

<400> 9

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atg gct gtt gct cgt gct gct ctt ggt cct ctt gtt act ggt ctt tat          48
Met Ala Val Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu Tyr
1               5                   10                  15
```

```
gat gtt caa gct ttt aaa ttt ggt gat ttt gtt ctt aaa tct ggt ctt          96
Asp Val Gln Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly Leu
            20                  25                  30

tct tct cct att tat att gat ctt cgt ggt att gtt tct cgt cct cgt         144
Ser Ser Pro Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro Arg
        35                  40                  45

ctt ctt tct caa gtt gct gat att ctt ttt caa act gct caa aat gct         192
Leu Leu Ser Gln Val Ala Asp Ile Leu Phe Gln Thr Ala Gln Asn Ala
    50                  55                  60

ggt att tct ttt gat act gtt tgt ggt gtt cct tat act gct ctt cct         240
Gly Ile Ser Phe Asp Thr Val Cys Gly Val Pro Tyr Thr Ala Leu Pro
65                  70                  75                  80

ctt gct act gtt att tgt tct act aat caa att cct atg ctt att cgt         288
Leu Ala Thr Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile Arg
                85                  90                  95

cgt aaa gaa act aaa gat tat ggt act aaa cgt ctt gtt gaa ggt act         336
Arg Lys Glu Thr Lys Asp Tyr Gly Thr Lys Arg Leu Val Glu Gly Thr
            100                 105                 110

att aat cct ggt gaa act tgt ctt att att gaa gat gtt gtt act tct         384
Ile Asn Pro Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr Ser
        115                 120                 125

ggt tct tct gtt ctt gaa act gtt gaa gtt ctt caa aaa gaa ggt ctt         432
Gly Ser Ser Val Leu Glu Thr Val Glu Val Leu Gln Lys Glu Gly Leu
    130                 135                 140

aaa gtt act gat gct att gtt ctt ctt gat cgt gaa caa ggt ggt aaa         480
Lys Val Thr Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly Lys
145                 150                 155                 160

gat aaa ctt caa gct cat ggt att cgt ctt cat tct gtt tgt act ctt         528
Asp Lys Leu Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr Leu
                165                 170                 175

tct aaa atg ctt gaa att ctt gaa caa caa aaa aaa gtt gat gct gaa         576
Ser Lys Met Leu Glu Ile Leu Glu Gln Gln Lys Lys Val Asp Ala Glu
            180                 185                 190

act gtt ggt cgt gtt aaa cgt ttt att caa gaa aat gtt ttt gtt gct         624
Thr Val Gly Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val Ala
        195                 200                 205

gct aat cat aat ggt tct cct ctt tct att aaa gaa gct cct aaa gaa         672
Ala Asn His Asn Gly Ser Pro Leu Ser Ile Lys Glu Ala Pro Lys Glu
    210                 215                 220

ctt tct ttt ggt gct cgt gct gaa ctt cct cgt att cat cct gtt gct         720
Leu Ser Phe Gly Ala Arg Ala Glu Leu Pro Arg Ile His Pro Val Ala
225                 230                 235                 240

tct aaa ctt ctt cgt ctt atg caa aaa aaa gaa act aat ctt tgt ctt         768
Ser Lys Leu Leu Arg Leu Met Gln Lys Lys Glu Thr Asn Leu Cys Leu
                245                 250                 255

tct gct gat gtt tct ctt gct cgt gaa ctt ctt caa ctt gct gat gct         816
Ser Ala Asp Val Ser Leu Ala Arg Glu Leu Leu Gln Leu Ala Asp Ala
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            260                 265                 270

ctt ggt cct tct att tgt atg ctt aaa act cat gtt gat att ctt aat        864
Leu Gly Pro Ser Ile Cys Met Leu Lys Thr His Val Asp Ile Leu Asn
        275                 280                 285

gat ttt act ctt gat gtt atg aaa gaa ctt att act ctt gct aaa tgt        912
Asp Phe Thr Leu Asp Val Met Lys Glu Leu Ile Thr Leu Ala Lys Cys
    290                 295                 300

cat gaa ttt ctt att ttt gaa gat cgt aaa ttt gct gat att ggt aat        960
His Glu Phe Leu Ile Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly Asn
305                 310                 315                 320

act gtt aaa aaa caa tat gaa ggt ggt att ttt aaa att gct tct tgg       1008
Thr Val Lys Lys Gln Tyr Glu Gly Gly Ile Phe Lys Ile Ala Ser Trp
                325                 330                 335

gct gat ctt gtt aat gct cat gtt gtt cct ggt tct ggt gtt gtt aaa       1056
Ala Asp Leu Val Asn Ala His Val Val Pro Gly Ser Gly Val Val Lys
            340                 345                 350

ggt ctt caa gaa gtt ggt ctt cct ctt cat cgt ggt tgt ctt ctt att       1104
Gly Leu Gln Glu Val Gly Leu Pro Leu His Arg Gly Cys Leu Leu Ile
        355                 360                 365

gct gaa atg tct tct act ggt tct ctt gct act ggt gat tat act cgt       1152
Ala Glu Met Ser Ser Thr Gly Ser Leu Ala Thr Gly Asp Tyr Thr Arg
    370                 375                 380

gct gct gtt cgt atg gct gaa gaa cat tct gaa ttt gtt gtt ggt ttt       1200
Ala Ala Val Arg Met Ala Glu Glu His Ser Glu Phe Val Val Gly Phe
385                 390                 395                 400

att tct ggt tct cgt gtt tct atg aaa cct gaa ttt ctt cat ctt act       1248
Ile Ser Gly Ser Arg Val Ser Met Lys Pro Glu Phe Leu His Leu Thr
                405                 410                 415

cct ggt gtt caa ctt gaa gct ggt ggt gat aat ctt ggt caa caa tat       1296
Pro Gly Val Gln Leu Glu Ala Gly Gly Asp Asn Leu Gly Gln Gln Tyr
            420                 425                 430

aat tct cct caa gaa gtt att ggt aaa cgt ggt tct gat att att att       1344
Asn Ser Pro Gln Glu Val Ile Gly Lys Arg Gly Ser Asp Ile Ile Ile
        435                 440                 445

gtt ggt cgt ggt att att tct gct gct gat cgt ctt gaa gct gct gaa       1392
Val Gly Arg Gly Ile Ile Ser Ala Ala Asp Arg Leu Glu Ala Ala Glu
    450                 455                 460

atg tat cgt aaa gct gct tgg gaa gct tat ctt tct cgt ctt ggt gtt       1440
Met Tyr Arg Lys Ala Ala Trp Glu Ala Tyr Leu Ser Arg Leu Gly Val
465                 470                 475                 480

taa                                                                  1443
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<210> 10
<211> 480
<212> PRT
<213> homo sapiens

<400> 10

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

Asp Val Gln Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly Leu
            20                  25                  30

Ser Ser Pro Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro Arg
        35                  40                  45

Leu Leu Ser Gln Val Ala Asp Ile Leu Phe Gln Thr Ala Gln Asn Ala
    50                  55                  60

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

Leu Ala Thr Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile Arg
                85                  90                  95

Arg Lys Glu Thr Lys Asp Tyr Gly Thr Lys Arg Leu Val Glu Gly Thr
            100                 105                 110

Ile Asn Pro Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr Ser
        115                 120                 125

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

Lys Val Thr Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly Lys
145                 150                 155                 160

Asp Lys Leu Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr Leu
                165                 170                 175

Ser Lys Met Leu Glu Ile Leu Glu Gln Gln Lys Lys Val Asp Ala Glu
            180                 185                 190

Thr Val Gly Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val Ala
        195                 200                 205

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

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

Ser Lys Leu Leu Arg Leu Met Gln Lys Lys Glu Thr Asn Leu Cys Leu
                245                 250                 255
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Ser Ala Asp Val Ser Leu Ala Arg Glu Leu Leu Gln Leu Ala Asp Ala
            260                 265                 270

Leu Gly Pro Ser Ile Cys Met Leu Lys Thr His Val Asp Ile Leu Asn
        275                 280                 285

Asp Phe Thr Leu Asp Val Met Lys Glu Leu Ile Thr Leu Ala Lys Cys
    290                 295                 300

His Glu Phe Leu Ile Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly Asn
305                 310                 315                 320

Thr Val Lys Lys Gln Tyr Glu Gly Gly Ile Phe Lys Ile Ala Ser Trp
                325                 330                 335

Ala Asp Leu Val Asn Ala His Val Val Pro Gly Ser Gly Val Val Lys
            340                 345                 350

Gly Leu Gln Glu Val Gly Leu Pro Leu His Arg Gly Cys Leu Leu Ile
        355                 360                 365

Ala Glu Met Ser Ser Thr Gly Ser Leu Ala Thr Gly Asp Tyr Thr Arg
    370                 375                 380

Ala Ala Val Arg Met Ala Glu Glu His Ser Glu Phe Val Val Gly Phe
385                 390                 395                 400

Ile Ser Gly Ser Arg Val Ser Met Lys Pro Glu Phe Leu His Leu Thr
                405                 410                 415

Pro Gly Val Gln Leu Glu Ala Gly Gly Asp Asn Leu Gly Gln Gln Tyr
            420                 425                 430

Asn Ser Pro Gln Glu Val Ile Gly Lys Arg Gly Ser Asp Ile Ile Ile
        435                 440                 445

Val Gly Arg Gly Ile Ile Ser Ala Ala Asp Arg Leu Glu Ala Ala Glu
    450                 455                 460

Met Tyr Arg Lys Ala Ala Trp Glu Ala Tyr Leu Ser Arg Leu Gly Val
465                 470                 475                 480
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<210> 11
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct CDopt-UPRT

<220>
<221> CDS
<222> (1)..(1227)

<400> 11

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atg gtg acc ggc ggc atg gcc tcc aag tgg gat caa aag ggc atg gat          48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                  10                  15

atc gct tac gag gag gcc ctg ctg ggc tac aag gag ggc ggc gtg cct          96
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc         288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

gct atc atc atg tac ggc atc cct agg tgt gtg atc ggc gag aac gtg         336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag         384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

gtg gtg gtt gtt gac gat gag agg tgt aag aag ctg atg aag cag ttc         432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag aac ccg         480
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Asn Pro
145                 150                 155                 160

tta ttc ttt ttg gct tct cca ttc ttg tac ctt aca tat ctt ata tat         528
Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr Tyr Leu Ile Tyr
                165                 170                 175

tat cca aac aaa ggg tct ttc gtt agc aaa cct aga aat ctg caa aaa         576
Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg Asn Leu Gln Lys
            180                 185                 190

atg tct tcg gaa cca ttt aag aac gtc tac ttg cta cct caa aca aac         624
Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu Pro Gln Thr Asn
        195                 200                 205

caa ttg ctg ggt ttg tac acc atc atc aga aat aag aat aca act aga         672
Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys Asn Thr Thr Arg
```

```
    210                 215                 220

cct gat ttc att ttc tac tcc gat aga atc atc aga ttg ttg gtt gaa        720
Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg Leu Leu Val Glu
225                 230                 235                 240

gaa ggt ttg aac cat cta cct gtg caa aag caa att gtg gaa act gac        768
Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile Val Glu Thr Asp
                245                 250                 255

acc aac gaa aac ttc gaa ggt gtc tca ttc atg ggt aaa atc tgt ggt        816
Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly Lys Ile Cys Gly
            260                 265                 270

gtt tcc att gtc aga gct ggt gaa tcg atg gag caa gga tta aga gac        864
Val Ser Ile Val Arg Ala Gly Glu Ser Met Glu Gln Gly Leu Arg Asp
        275                 280                 285

tgt tgt agg tct gtg cgt atc ggt aaa att tta att caa agg gac gag        912
Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile Gln Arg Asp Glu
    290                 295                 300

gag act gct tta cca aag tta ttc tac gaa aaa tta cca gag gat ata        960
Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu Pro Glu Asp Ile
305                 310                 315                 320

tct gaa agg tat gtc ttc cta tta gac cca atg ctg gcc acc ggt ggt       1008
Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu Ala Thr Gly Gly
                325                 330                 335

agt gct atc atg gct aca gaa gtc ttg att aag aga ggt gtt aag cca       1056
Ser Ala Ile Met Ala Thr Glu Val Leu Ile Lys Arg Gly Val Lys Pro
            340                 345                 350

gag aga att tac ttc tta aac cta atc tgt agt aag gaa ggg att gaa       1104
Glu Arg Ile Tyr Phe Leu Asn Leu Ile Cys Ser Lys Glu Gly Ile Glu
        355                 360                 365

aaa tac cat gcc gcc ttc cca gag gtc aga att gtt act ggt gcc ctc       1152
Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val Thr Gly Ala Leu
    370                 375                 380

gac aga ggt cta gat gaa aac aag tat cta gtt cca ggg ttg ggt gac       1200
Asp Arg Gly Leu Asp Glu Asn Lys Tyr Leu Val Pro Gly Leu Gly Asp
385                 390                 395                 400

ttt ggt gac aga tac tac tgt gtt taa                                  1227
Phe Gly Asp Arg Tyr Tyr Cys Val
                405
```

<210> 12
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

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Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15
```

```
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Asn Pro
145                 150                 155                 160

Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr Tyr Leu Ile Tyr
                165                 170                 175

Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg Asn Leu Gln Lys
            180                 185                 190

Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu Pro Gln Thr Asn
        195                 200                 205

Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys Asn Thr Thr Arg
    210                 215                 220

Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg Leu Leu Val Glu
225                 230                 235                 240

Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile Val Glu Thr Asp
                245                 250                 255

Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly Lys Ile Cys Gly
```

260 265 270

Val Ser Ile Val Arg Ala Gly Glu Ser Met Glu Gln Gly Leu Arg Asp
275 280 285

Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile Gln Arg Asp Glu
290 295 300

Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu Pro Glu Asp Ile
305 310 315 320

Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu Ala Thr Gly Gly
325 330 335

Ser Ala Ile Met Ala Thr Glu Val Leu Ile Lys Arg Gly Val Lys Pro
340 345 350

Glu Arg Ile Tyr Phe Leu Asn Leu Ile Cys Ser Lys Glu Gly Ile Glu
355 360 365

Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val Thr Gly Ala Leu
370 375 380

Asp Arg Gly Leu Asp Glu Asn Lys Tyr Leu Val Pro Gly Leu Gly Asp
385 390 395 400

Phe Gly Asp Arg Tyr Tyr Cys Val
405

<210> 13
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construction - CDopt - linker - UPRT

<220>
<221> CDS
<222> (1)..(1287)

<400> 13
atg gtg acc ggc ggc atg gcc tcc aag tgg gat caa aag ggc atg gat 48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1 5 10 15

atc gct tac gag gag gcc ctg ctg ggc tac aag gag ggc ggc gtg cct 96
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
20 25 30

atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg 144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg

35 40 45

ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag 192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
50 55 60

atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag 240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65 70 75 80

gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc 288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
85 90 95

gct atc atc atg tac ggc atc cct agg tgt gtg atc ggc gag aac gtg 336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
100 105 110

aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag 384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
115 120 125

gtg gtg gtt gtt gac gat gag agg tgt aag aag ctg atg aag cag ttc 432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
130 135 140

atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag tcc ggc 480
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Ser Gly
145 150 155 160

ggc ggc gcc tcc ggc ggc ggc gcc tcc ggc ggc ggc gcc tcc ggc ggc 528
Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly
165 170 175

ggc gcc aac ccg tta ttc ttt ttg gct tct cca ttc ttg tac ctt aca 576
Gly Ala Asn Pro Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr
180 185 190

tat ctt ata tat tat cca aac aaa ggg tct ttc gtt agc aaa cct aga 624
Tyr Leu Ile Tyr Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg
195 200 205

aat ctg caa aaa atg tct tcg gaa cca ttt aag aac gtc tac ttg cta 672
Asn Leu Gln Lys Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu
210 215 220

cct caa aca aac caa ttg ctg ggt ttg tac acc atc atc aga aat aag 720
Pro Gln Thr Asn Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys
225 230 235 240

aat aca act aga cct gat ttc att ttc tac tcc gat aga atc atc aga 768
Asn Thr Thr Arg Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg
245 250 255

ttg ttg gtt gaa gaa ggt ttg aac cat cta cct gtg caa aag caa att 816
Leu Leu Val Glu Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile
260 265 270

gtg gaa act gac acc aac gaa aac ttc gaa ggt gtc tca ttc atg ggt 864
Val Glu Thr Asp Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly
275 280 285

aaa atc tgt ggt gtt tcc att gtc aga gct ggt gaa tcg atg gag caa 912

```
Lys Ile Cys Gly Val Ser Ile Val Arg Ala Gly Glu Ser Met Glu Gln
    290                 295                 300

gga tta aga gac tgt tgt agg tct gtg cgt atc ggt aaa att tta att        960
Gly Leu Arg Asp Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile
305                 310                 315                 320

caa agg gac gag gag act gct tta cca aag tta ttc tac gaa aaa tta       1008
Gln Arg Asp Glu Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu
                325                 330                 335

cca gag gat ata tct gaa agg tat gtc ttc cta tta gac cca atg ctg       1056
Pro Glu Asp Ile Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu
            340                 345                 350

gcc acc ggt ggt agt gct atc atg gct aca gaa gtc ttg att aag aga       1104
Ala Thr Gly Gly Ser Ala Ile Met Ala Thr Glu Val Leu Ile Lys Arg
        355                 360                 365

ggt gtt aag cca gag aga att tac ttc tta aac cta atc tgt agt aag       1152
Gly Val Lys Pro Glu Arg Ile Tyr Phe Leu Asn Leu Ile Cys Ser Lys
    370                 375                 380

gaa ggg att gaa aaa tac cat gcc gcc ttc cca gag gtc aga att gtt       1200
Glu Gly Ile Glu Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val
385                 390                 395                 400

act ggt gcc ctc gac aga ggt cta gat gaa aac aag tat cta gtt cca       1248
Thr Gly Ala Leu Asp Arg Gly Leu Asp Glu Asn Lys Tyr Leu Val Pro
                405                 410                 415

ggg ttg ggt gac ttt ggt gac aga tac tac tgt gtt taa                   1287
Gly Leu Gly Asp Phe Gly Asp Arg Tyr Tyr Cys Val
            420                 425
```

<210> 14
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

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Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
```

65 70 75 80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
85 90 95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
100 105 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
115 120 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
130 135 140

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

Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly
165 170 175

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

Tyr Leu Ile Tyr Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg
195 200 205

Asn Leu Gln Lys Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu
210 215 220

Pro Gln Thr Asn Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys
225 230 235 240

Asn Thr Thr Arg Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg
245 250 255

Leu Leu Val Glu Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile
260 265 270

Val Glu Thr Asp Thr Asn Glu Asn Phe Glu Gly Val Ser Phe Met Gly
275 280 285

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

Gly Leu Arg Asp Cys Cys Arg Ser Val Arg Ile Gly Lys Ile Leu Ile
305 310 315 320

```
Gln Arg Asp Glu Glu Thr Ala Leu Pro Lys Leu Phe Tyr Glu Lys Leu
                325                 330                 335

Pro Glu Asp Ile Ser Glu Arg Tyr Val Phe Leu Leu Asp Pro Met Leu
            340                 345                 350

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

Gly Val Lys Pro Glu Arg Ile Tyr Phe Leu Asn Leu Ile Cys Ser Lys
    370                 375                 380

Glu Gly Ile Glu Lys Tyr His Ala Ala Phe Pro Glu Val Arg Ile Val
385                 390                 395                 400

Thr Gly Ala Leu Asp Arg Gly Leu Asp Glu Asn Lys Tyr Leu Val Pro
                405                 410                 415

Gly Leu Gly Asp Phe Gly Asp Arg Tyr Tyr Cys Val
            420                 425


<210>  15
<211>  1200
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fusion Construct - CDopt3 - OPRT


<220>
<221>  CDS
<222>  (1)..(1200)

<400>  15
atg gtg acc ggc ggc atg gcc tcc aag tgg gat caa aag ggc atg gat          48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

atc gct tac gag gag gcc ctg ctg ggc tac aag gag ggc ggc gtg cct          96
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc         288
```

```
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

gct atc atc atg tac ggc atc cct agg tgt gtg atc ggc gag aac gtg      336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag      384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

gtg gtg gtt gtt gac gat gag agg tgt aag aag ctg atg aag cag ttc      432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag gcg gtc      480
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Ala Val
145                 150                 155                 160

gct cgt gca gct ttg ggg cca ttg gtg acg ggt ctg tac gac gtg cag      528
Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu Tyr Asp Val Gln
                165                 170                 175

gct ttc aag ttt ggg gac ttc gtg ctg aag agc ggg ctt tcc tcc ccc      576
Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly Leu Ser Ser Pro
            180                 185                 190

atc tac atc gat ctg cgg ggc atc gtg tct cga ccg cgt ctt ctg agt      624
Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro Arg Leu Leu Ser
        195                 200                 205

cag gtt gca gat att tta ttc caa act gcc caa aat gca ggc atc agt      672
Gln Val Ala Asp Ile Leu Phe Gln Thr Ala Gln Asn Ala Gly Ile Ser
    210                 215                 220

ttt gac acc gtg tgt gga gtg cct tat aca gct ttg cca ttg gct aca      720
Phe Asp Thr Val Cys Gly Val Pro Tyr Thr Ala Leu Pro Leu Ala Thr
225                 230                 235                 240

gtt atc tgt tca acc aat caa att cca atg ctt att aga agg aaa gaa      768
Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile Arg Arg Lys Glu
                245                 250                 255

aca aag gat tat gga act aag cgt ctt gta gaa gga act att aat cca      816
Thr Lys Asp Tyr Gly Thr Lys Arg Leu Val Glu Gly Thr Ile Asn Pro
            260                 265                 270

gga gaa acc tgt tta atc att gaa gat gtt gtc acc agt gga tct agt      864
Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr Ser Gly Ser Ser
        275                 280                 285

gtt ttg gaa act gtt gag gtt ctt cag aag gag ggc ttg aag gtc act      912
Val Leu Glu Thr Val Glu Val Leu Gln Lys Glu Gly Leu Lys Val Thr
    290                 295                 300

gat gcc ata gtg ctg ttg gac aga gag cag gga ggc aag gac aag ttg      960
Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly Lys Asp Lys Leu
305                 310                 315                 320

cag gcg cac ggg atc cgc ctc cac tca gtg tgt aca ttg tcc aaa atg     1008
Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr Leu Ser Lys Met
                325                 330                 335
```

```
ctg gag att ctc gag cag cag aaa aaa gtt gat gct gag aca gtt ggg       1056
Leu Glu Ile Leu Glu Gln Gln Lys Lys Val Asp Ala Glu Thr Val Gly
            340                 345                 350

aga gtg aag agg ttt att cag gag aat gtc ttt gtg gca gcg aat cat       1104
Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val Ala Ala Asn His
        355                 360                 365

aat ggt tct ccc ctt tct ata aag gaa gca ccc aaa gaa ctc agc ttc       1152
Asn Gly Ser Pro Leu Ser Ile Lys Glu Ala Pro Lys Glu Leu Ser Phe
    370                 375                 380

ggt gca cgt gca gag ctg ccc agg atc cac cca gtt gca tcg aag taa       1200
Gly Ala Arg Ala Glu Leu Pro Arg Ile His Pro Val Ala Ser Lys
385                 390                 395
```

<210> 16
<211> 399
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

```
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                   10                  15

Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140
```

```
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Ala Val
145                 150                 155                 160

Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu Tyr Asp Val Gln
                165                 170                 175

Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly Leu Ser Ser Pro
            180                 185                 190

Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro Arg Leu Leu Ser
        195                 200                 205

Gln Val Ala Asp Ile Leu Phe Gln Thr Ala Gln Asn Ala Gly Ile Ser
    210                 215                 220

Phe Asp Thr Val Cys Gly Val Pro Tyr Thr Ala Leu Pro Leu Ala Thr
225                 230                 235                 240

Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile Arg Arg Lys Glu
                245                 250                 255

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

Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr Ser Gly Ser Ser
        275                 280                 285

Val Leu Glu Thr Val Glu Val Leu Gln Lys Glu Gly Leu Lys Val Thr
    290                 295                 300

Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly Lys Asp Lys Leu
305                 310                 315                 320

Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr Leu Ser Lys Met
                325                 330                 335

Leu Glu Ile Leu Glu Gln Gln Lys Lys Val Asp Ala Glu Thr Val Gly
            340                 345                 350

Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val Ala Ala Asn His
        355                 360                 365

Asn Gly Ser Pro Leu Ser Ile Lys Glu Ala Pro Lys Glu Leu Ser Phe
    370                 375                 380

Gly Ala Arg Ala Glu Leu Pro Arg Ile His Pro Val Ala Ser Lys
385                 390                 395
```

<210> 17
<211> 1260
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion Construct - CDopt3 - linker - OPRT

<220>
<221> CDS
<222> (1)..(1260)

<400> 17

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atg gtg acc ggc ggc atg gcc tcc aag tgg gat caa aag ggc atg gat          48
Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
1               5                  10                  15

atc gct tac gag gag gcc ctg ctg ggc tac aag gag ggc ggc gtg cct          96
Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro
            20                  25                  30

atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg         144
Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg
        35                  40                  45

ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag         192
Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu
    50                  55                  60

atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag         240
Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
65                  70                  75                  80

gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc         288
Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
                85                  90                  95

gct atc atc atg tac ggc atc cct agg tgt gtg atc ggc gag aac gtg         336
Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
            100                 105                 110

aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag         384
Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
        115                 120                 125

gtg gtg gtt gtt gac gat gag agg tgt aag aag ctg atg aag cag ttc         432
Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
    130                 135                 140

atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag tcc ggc         480
Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Ser Gly
145                 150                 155                 160

ggc ggc gcc tcc ggc ggc ggc gcc tcc ggc ggc ggc gcc tcc ggc ggc         528
Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly
                165                 170                 175

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Gly Ala Ala Val Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu
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tac gac gtg cag gct ttc aag ttt ggg gac ttc gtg ctg aag agc ggg          624
Tyr Asp Val Gln Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly
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ctt tcc tcc ccc atc tac atc gat ctg cgg ggc atc gtg tct cga ccg          672
Leu Ser Ser Pro Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro
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cgt ctt ctg agt cag gtt gca gat att tta ttc caa act gcc caa aat          720
Arg Leu Leu Ser Gln Val Ala Asp Ile Leu Phe Gln Thr Ala Gln Asn
225                 230                 235                 240

gca ggc atc agt ttt gac acc gtg tgt gga gtg cct tat aca gct ttg          768
Ala Gly Ile Ser Phe Asp Thr Val Cys Gly Val Pro Tyr Thr Ala Leu
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cca ttg gct aca gtt atc tgt tca acc aat caa att cca atg ctt att          816
Pro Leu Ala Thr Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile
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aga agg aaa gaa aca aag gat tat gga act aag cgt ctt gta gaa gga          864
Arg Arg Lys Glu Thr Lys Asp Tyr Gly Thr Lys Arg Leu Val Glu Gly
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act att aat cca gga gaa acc tgt tta atc att gaa gat gtt gtc acc          912
Thr Ile Asn Pro Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr
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agt gga tct agt gtt ttg gaa act gtt gag gtt ctt cag aag gag ggc          960
Ser Gly Ser Ser Val Leu Glu Thr Val Glu Val Leu Gln Lys Glu Gly
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ttg aag gtc act gat gcc ata gtg ctg ttg gac aga gag cag gga ggc         1008
Leu Lys Val Thr Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly
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aag gac aag ttg cag gcg cac ggg atc cgc ctc cac tca gtg tgt aca         1056
Lys Asp Lys Leu Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr
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gag aca gtt ggg aga gtg aag agg ttt att cag gag aat gtc ttt gtg         1152
Glu Thr Val Gly Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val
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Ala Ala Asn His Asn Gly Ser Pro Leu Ser Ile Lys Glu Ala Pro Lys
385                 390                 395                 400

gaa ctc agc ttc ggt gca cgt gca gag ctg ccc agg atc cac cca gtt         1248
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Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys
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Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly
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Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val
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Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
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Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe
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Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Ser Gly
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Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly Gly Ala Ser Gly Gly
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Gly Ala Ala Val Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu
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Tyr Asp Val Gln Ala Phe Lys Phe Gly Asp Phe Val Leu Lys Ser Gly
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Leu Ser Ser Pro Ile Tyr Ile Asp Leu Arg Gly Ile Val Ser Arg Pro
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Pro Leu Ala Thr Val Ile Cys Ser Thr Asn Gln Ile Pro Met Leu Ile
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Arg Arg Lys Glu Thr Lys Asp Tyr Gly Thr Lys Arg Leu Val Glu Gly
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Thr Ile Asn Pro Gly Glu Thr Cys Leu Ile Ile Glu Asp Val Val Thr
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Ser Gly Ser Ser Val Leu Glu Thr Val Glu Val Leu Gln Lys Glu Gly
305                 310                 315                 320

Leu Lys Val Thr Asp Ala Ile Val Leu Leu Asp Arg Glu Gln Gly Gly
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Lys Asp Lys Leu Gln Ala His Gly Ile Arg Leu His Ser Val Cys Thr
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Leu Ser Lys Met Leu Glu Ile Leu Glu Gln Gln Lys Lys Val Asp Ala
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Glu Thr Val Gly Arg Val Lys Arg Phe Ile Gln Glu Asn Val Phe Val
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Ala Ala Asn His Asn Gly Ser Pro Leu Ser Ile Lys Glu Ala Pro Lys
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<210> 28

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<223> Cytosine deaminase coding sequence with cloning sites

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gggggg 546

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<212> DNA
<213> Artificial Sequence

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<223> Cytosine deaminase codon optimized with cloning site

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gccaccctgc acggcgagat ctccaccctg gagaactgtg gcaggctgga gggcaaggtg 240

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gagaagtacc tgcaaaccag gggccacgag gtggtggttg ttgacgatga gaggtgtaag 420

aagatcatga agcagttcat cgacgagagg cctcaggact ggttcgagga tatcggcgag 480

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<223> Oligonucleotide Primer

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<210> 33
<211> 40
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<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

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<210> 34
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<223> Oligonucleotide Primer

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gcggcggcgc caacccgtta tt 82

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<220>
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ccgccgccgg atcactcgcc ga 82

<210> 36
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<213> Artificial Sequence

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<223> Cytosine deaminase heat stabilized

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gccgcgccat agataaaata aaagatttta tttagtctcc agaaaaaggg ggg 533

<210> 37
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atgaagcagt tcatcgacga gaggcctcag gactggttcg aggatatcgg cgagtgataa 480

<210> 38
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> CD human codon optimized heat stabilitized cloning sites

<400> 38
aacacgatta taaatggtga ccggcggcat ggcctccaag tgggatcaaa agggcatgga 60

tatcgcttac gaggaggccc tgctgggcta caaggagggc ggcgtgccta tcggcggctg 120

tctgatcaac aacaaggacg gcagtgtgct gggcaggggc cacaacatga ggttccagaa 180

gggctccgcc accctgcacg gcgagatctc caccctggag aactgtggca ggctggaggg 240

caaggtgtac aaggacacca ccctgtacac caccctgtcc ccttgtgaca tgtgtaccgg 300

cgctatcatc atgtacggca tccctaggtg tgtgatcggc gagaacgtga acttcaagtc 360

caagggcgag aagtacctgc aaaccagggg ccacgaggtg gtggttgttg acgatgagag 420

gtgtaagaag ctgatgaagc agttcatcga cgagaggcct caggactggt tcgaggatat 480

cggcgagtaa gcggccgcgc catagataaa ataaaagatt ttatttagtc tccagaaaaa 540

gggggg 546

<210> 39
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 39
tcgaggatat cggcgagtga aacccgttat tctttttggc 40

<210> 40
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 40
gccaaaaaga ataacgggtt tcactcgccg atatcctcga 40

<210> 41
<211> 52
<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 41
ccaagctcct atagccgctc actatctact tgggcaataa gaaaaaccga ag 52

<210> 42
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer

<400> 42
ggttcgagga tatcggcgag tgatagatga acccgttatt ctttttggct tc 52

<210> 43
<211> 1296
<212> DNA
<213> Artificial Sequence

<220>
<223> CD codon optimized-UPRT

<400> 43
aacacgatta taaatggtga ccggcggcat ggcctccaag tgggatcaaa agggcatgga 60

tatcgcttac gaggaggccc tgctgggcta caaggagggc ggcgtgccta tcggcggctg 120

tctgatcaac aacaaggacg gcagtgtgct gggcaggggc cacaacatga ggttccagaa 180

gggctccgcc accctgcacg gcgagatctc caccctggag aactgtggca ggctggaggg 240

caaggtgtac aaggacacca ccctgtacac caccctgtcc ccttgtgaca tgtgtaccgg 300

cgctatcatc atgtacggca tccctaggtg tgtgatcggc gagaacgtga acttcaagtc 360

caagggcgag aagtacctgc aaaccagggg ccacgaggtg gtggttgttg acgatgagag 420

gtgtaagaag ctgatgaagc agttcatcga cgagaggcct caggactggt tcgaggatat 480

cggcgagaac ccgttattct ttttggcttc tccattcttg taccttacat atcttatata 540

ttatccaaac aaagggtctt tcgttagcaa acctagaaat ctgcaaaaaa tgtcttcgga 600

accatttaag aacgtctact tgctacctca aacaaaccaa ttgctgggtt tgtacaccat 660

catcagaaat aagaatacaa ctagacctga tttcattttc tactccgata gaatcatcag 720

attgttggtt gaagaaggtt tgaaccatct acctgtgcaa aagcaaattg tggaaactga 780

caccaacgaa aacttcgaag gtgtctcatt catgggtaaa atctgtggtg tttccattgt 840

cagagctggt gaatcgatgg agcaaggatt aagagactgt tgtaggtctg tgcgtatcgg 900

taaaatttta attcaaaggg acgaggagac tgctttacca aagttattct acgaaaaatt 960

accagaggat atatctgaaa ggtatgtctt cctattagac ccaatgctgg ccaccggtgg 1020

tagtgctatc atggctacag aagtcttgat taagagaggt gttaagccag agagaattta 1080

cttcttaaac ctaatctgta gtaaggaagg gattgaaaaa taccatgccg ccttcccaga 1140

ggtcagaatt gttactggtg ccctcgacag aggtctagat gaaaacaagt atctagttcc 1200

agggttgggt gactttggtg acagatacta ctgtgtttaa gcggccgcgc catagataaa 1260

ataaaagatt ttatttagtc tccagaaaaa gggggg 1296

<210> 44
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 44
tcggcgagtg atccggcggc ggcgcctccg gcggcggcgc ctccggcggc ggcgcctccg 60

gcggcggcgc caacccgtta tt 82

<210> 45
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 45
aataacgggt tggcgccgcc gccggaggcg ccgccgccgg aggcgccgcc gccggaggcg 60

ccgccgccgg atcactcgcc ga 82

<210> 46
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> CD human codon optimized-linker-UPRT

<400> 46
aacacgatta taaatggtga ccggcggcat ggcctccaag tgggatcaaa agggcatgga 60

tatcgcttac gaggaggccc tgctgggcta caaggagggc ggcgtgccta tcggcggctg 120

tctgatcaac aacaaggacg gcagtgtgct gggcaggggc cacaacatga ggttccagaa 180

gggctccgcc accctgcacg gcgagatctc caccctggag aactgtggca ggctggaggg 240

caaggtgtac aaggacacca ccctgtacac caccctgtcc ccttgtgaca tgtgtaccgg 300

cgctatcatc atgtacggca tccctaggtg tgtgatcggc gagaacgtga acttcaagtc 360

caagggcgag aagtacctgc aaaccagggg ccacgaggtg gtggttgttg acgatgagag 420

gtgtaagaag ctgatgaagc agttcatcga cgagaggcct caggactggt tcgaggatat 480

cggcgagtcc ggcggcggcg cctccggcgg cggcgcctcc ggcggcggcg cctccggcgg 540

cggcgccaac ccgttattct ttttggcttc tccattcttg taccttacat atcttatata 600

ttatccaaac aaagggtctt tcgttagcaa acctagaaat ctgcaaaaaa tgtcttcgga 660

accatttaag aacgtctact tgctacctca aacaaaccaa ttgctgggtt tgtacaccat 720

catcagaaat aagaatacaa ctagacctga tttcattttc tactccgata gaatcatcag 780

attgttggtt gaagaaggtt tgaaccatct acctgtgcaa aagcaaattg tggaaactga 840

caccaacgaa aacttcgaag gtgtctcatt catgggtaaa atctgtggtg tttccattgt 900

cagagctggt gaatcgatgg agcaaggatt aagagactgt tgtaggtctg tgcgtatcgg 960

taaaatttta attcaaaggg acgaggagac tgctttacca aagttattct acgaaaaatt 1020

accagaggat atatctgaaa ggtatgtctt cctattagac ccaatgctgg ccaccggtgg 1080

tagtgctatc atggctacag aagtcttgat taagagaggt gttaagccag agagaattta 1140

cttcttaaac ctaatctgta gtaaggaagg gattgaaaaa taccatgccg ccttcccaga 1200

ggtcagaatt gttactggtg ccctcgacag aggtctagat gaaaacaagt atctagttcc 1260

agggttgggt gactttggtg acagatacta ctgtgtttaa gcggccgcgc catagataaa 1320

ataaaagatt ttatttagtc tccagaaaaa gggggg 1356

<210> 47
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> CD human codon optimized-OPRT

<400> 47
aacacgatta taaatggtga ccggcggcat ggcctccaag tgggatcaaa agggcatgga 60

tatcgcttac gaggaggccc tgctgggcta caaggagggc ggcgtgccta tcggcggctg 120

tctgatcaac aacaaggacg gcagtgtgct gggcaggggc cacaacatga ggttccagaa 180

gggctccgcc accctgcacg gcgagatctc caccctggag aactgtggca ggctggaggg 240

caaggtgtac aaggacacca ccctgtacac caccctgtcc ccttgtgaca tgtgtaccgg 300

cgctatcatc atgtacggca tccctaggtg tgtgatcggc gagaacgtga acttcaagtc 360

caagggcgag aagtacctgc aaaccagggg ccacgaggtg gtggttgttg acgatgagag 420

gtgtaagaag ctgatgaagc agttcatcga cgagaggcct caggactggt tcgaggatat 480

cggcgaggcg gtcgctcgtg cagctttggg gccattggtg acgggtctgt acgacgtgca 540

ggctttcaag tttggggact tcgtgctgaa gagcgggctt tcctcccccа tctacatcga 600

tctgcggggc atcgtgtctc gaccgcgtct tctgagtcag gttgcagata ttttattcca 660

aactgcccaa aatgcaggca tcagttttga caccgtgtgt ggagtgcctt atacagcttt 720

gccattggct acagttatct gttcaaccaa tcaaattcca atgcttatta gaaggaaaga 780

aacaaaggat tatggaacta agcgtcttgt agaaggaact attaatccag gagaaacctg 840

tttaatcatt gaagatgttg tcaccagtgg atctagtgtt ttggaaactg ttgaggttct 900

tcagaaggag ggcttgaagg tcactgatgc catagtgctg ttggacagag agcagggagg 960

caaggacaag ttgcaggcgc acgggatccg cctccactca gtgtgtacat tgtccaaaat 1020

gctggagatt ctcgagcagc agaaaaaagt tgatgctgag acagttggga gagtgaagag 1080

gtttattcag gagaatgtct ttgtggcagc gaatcataat ggttctcccc tttctataaa 1140

ggaagcaccc aaagaactca gcttcggtgc acgtgcagag ctgcccagga tccacccagt 1200

tgcatcgaag taagcggccg cgccatagat aaaataaaag attttattta gtctccagaa 1260

aaaggggggg 1269

<210> 48
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> CD codon optimized-linker-OPRT

<400> 48
aacacgatta taaatggtga ccggcggcat ggcctccaag tgggatcaaa agggcatgga 60

tatcgcttac gaggaggccc tgctgggcta caaggagggc ggcgtgccta tcggcggctg 120

tctgatcaac aacaaggacg gcagtgtgct gggcaggggc cacaacatga ggttccagaa 180

gggctccgcc accctgcacg gcgagatctc caccctggag aactgtggca ggctggaggg 240

caaggtgtac aaggacacca ccctgtacac caccctgtcc ccttgtgaca tgtgtaccgg 300

cgctatcatc atgtacggca tccctaggtg tgtgatcggc gagaacgtga acttcaagtc 360

caagggcgag aagtacctgc aaaccagggg ccacgaggtg gtggttgttg acgatgagag 420

gtgtaagaag ctgatgaagc agttcatcga cgagaggcct caggactggt tcgaggatat 480

cggcgagtcc ggcggcggcg cctccggcgg cggcgcctcc ggcggcggcg cctccggcgg 540

cggcgccgcg gtcgctcgtg cagctttggg gccattggtg acgggtctgt acgacgtgca 600

ggctttcaag tttggggact tcgtgctgaa gagcgggctt tcctccccca tctacatcga 660

tctgcggggc atcgtgtctc gaccgcgtct tctgagtcag gttgcagata ttttattcca 720

aactgcccaa aatgcaggca tcagttttga caccgtgtgt ggagtgcctt atacagcttt 780

gccattggct acagttatct gttcaaccaa tcaaattcca atgcttatta gaaggaaaga 840

aacaaaggat tatggaacta agcgtcttgt agaaggaact attaatccag gagaaacctg 900

tttaatcatt gaagatgttg tcaccagtgg atctagtgtt ttggaaactg ttgaggttct 960

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caaggacaag ttgcaggcgc acgggatccg cctccactca gtgtgtacat tgtccaaaat 1080

gctggagatt ctcgagcagc agaaaaaagt tgatgctgag acagttggga gagtgaagag 1140

gtttattcag gagaatgtct ttgtggcagc gaatcataat ggttctcccc tttctataaa 1200

ggaagcaccc aaagaactca gcttcggtgc acgtgcagag ctgcccagga tccacccagt 1260

tgcatcgaag taagcggccg cgccatagat aaaataaaag attttattta gtctccagaa 1320

aaaggggggg 1329