

Sequence.txt
SEQUENCE LISTING

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<110>  Tocagen Inc.
      Jolly, Douglas
      Ibanez, Carlos

<120>  PRODUCER CELLS FOR REPLICATION COMPETENT RETROVIRAL VECTORS

<130>  00014-008wo1

<140>  Not yet known
<141>  2010-06-17

<150>  US 61/218,063
<151>  2009-06-17

<160>  30

<170>  PatentIn version 3.5

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

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

<400>  1
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
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

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

48

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

<220>
 <223> Synthetic Construct

<400> 4

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

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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

<210> 5
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Human codon optimized cytosine deaminase

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

<400> 5	
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 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	

Sequence.txt																
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
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<220>
<223> Synthetic Construct

<400> 6

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
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> 7
<211> 756
<212> DNA
<213> Saccharomyces cerevisiae
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<220>
<221> CDS
<222> (1)..(756)

<400> 7

Sequence.txt

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	

<210> 8
 <211> 251
 <212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

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

Sequence.txt

<210> 9
 <211> 1443
 <212> DNA
 <213> homo sapiens

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

<400> 9
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 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

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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		
			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		Ser	Leu	Ala	Thr		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		
					470					475					480		
taa																	1443

<210> 10
<211> 480

Sequence.txt

<212> PRT
 <213> homo sapiens

<400> 10

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

Sequence.txt

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

<210> 11
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct CDopt-UPRT

<220>
<221> CDS

Sequence.txt

<222> (1)..(1227)

<400> 11

atg gtg acc ggc ggc atg gcc tcc aag tgg gat caa aag ggc atg gat Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp 1 5 10 15	48
atc gct tac gag gag gcc ctg ctg ggc tac aag gag ggc ggc gtg cct Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro 20 25 30	96
atc ggc ggc tgt ctg atc aac aac aag gac ggc agt gtg ctg ggc agg Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg 35 40 45	144
ggc cac aac atg agg ttc cag aag ggc tcc gcc acc ctg cac ggc gag Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu 50 55 60	192
atc tcc acc ctg gag aac tgt ggc agg ctg gag ggc aag gtg tac aag Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys 65 70 75 80	240
gac acc acc ctg tac acc acc ctg tcc cct tgt gac atg tgt acc ggc Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly 85 90 95	288
gct atc atc atg tac ggc atc cct agg tgt gtg atc ggc gag aac gtg Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val 100 105 110	336
aac ttc aag tcc aag ggc gag aag tac ctg caa acc agg ggc cac gag Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu 115 120 125	384
gtg gtg gtt gtt gac gat gag agg tgt aag aag ctg atg aag cag ttc Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe 130 135 140	432
atc gac gag agg cct cag gac tgg ttc gag gat atc ggc gag aac ccg Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu Asn Pro 145 150 155 160	480
tta ttc ttt ttg gct tct cca ttc ttg tac ctt aca tat ctt ata tat Leu Phe Phe Leu Ala Ser Pro Phe Leu Tyr Leu Thr Tyr Leu Ile Tyr 165 170 175	528
tat cca aac aaa ggc tct ttc gtt agc aaa cct aga aat ctg caa aaa Tyr Pro Asn Lys Gly Ser Phe Val Ser Lys Pro Arg Asn Leu Gln Lys 180 185 190	576
atg tct tcg gaa cca ttt aag aac gtc tac ttg cta cct caa aca aac Met Ser Ser Glu Pro Phe Lys Asn Val Tyr Leu Leu Pro Gln Thr Asn 195 200 205	624
caa ttg ctg ggt ttg tac acc atc atc aga aat aag aat aca act aga Gln Leu Leu Gly Leu Tyr Thr Ile Ile Arg Asn Lys Asn Thr Thr Arg 210 215 220	672
cct gat ttc att ttc tac tcc gat aga atc atc aga ttg ttg gtt gaa Pro Asp Phe Ile Phe Tyr Ser Asp Arg Ile Ile Arg Leu Leu Val Glu 225 230 235 240	720
gaa ggt ttg aac cat cta cct gtg caa aag caa att gtg gaa act gac Glu Gly Leu Asn His Leu Pro Val Gln Lys Gln Ile Val Glu Thr Asp 245 250 255	768
acc aac gaa aac ttc gaa ggt gtc tca ttc atg ggt aaa atc tgt ggt	816

Sequence.txt

Thr	Asn	Glu	Asn	Phe	Glu	Gly	Val	Ser	Phe	Met	Gly	Lys	Ile	Cys	Gly		
			260					265					270				
ggt	tcc	att	gtc	aga	gct	ggg	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	ggg	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	ggg	ggg		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	ggg	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	ggg	gcc	ctc		1152
Lys	Tyr	His	Ala	Ala	Phe	Pro	Glu	Val	Arg	Ile	Val	Thr	Gly	Ala	Leu		
		370				375					380						
gac	aga	ggg	cta	gat	gaa	aac	aag	tat	cta	gtt	cca	ggg	ttg	ggg	gac		1200
Asp	Arg	Gly	Leu	Asp	Glu	Asn	Lys	Tyr	Leu	Val	Pro	Gly	Leu	Gly	Asp		
385					390					395					400		
ttt	ggg	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

Met Val Thr Gly Gly Met Ala Ser Lys Trp Asp Gln Lys Gly Met Asp
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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

Sequence.txt

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

Sequence.txt

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	
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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	

Sequence.txt																
atc Ile 145	gac Asp	gag Glu	agg Arg	cct Pro	cag Gln 150	gac Asp	tgg Trp	ttc Phe	gag Glu 155	gat Asp	atc Ile	ggc Gly	gag Glu	tcc Ser	ggc Gly 160	480
ggc Gly	ggc Gly	gcc Ala	tcc Ser	ggc Gly 165	ggc Gly	ggc Gly	gcc Ala	tcc Ser	ggc Gly 170	ggc Gly	ggc Gly	gcc Ala	tcc Ser	ggc Gly 175	ggc Gly	528
ggc Gly	gcc Ala	aac Asn	ccg Pro 180	tta Leu	ttc Phe	ttt Phe	ttg Leu	gct Ala 185	tct Ser	cca Pro	ttc Phe	ttg Leu	tac Tyr 190	ctt Leu	aca Thr	576
tat Tyr	ctt Leu	ata Ile 195	tat Tyr	tat Tyr	cca Pro	aac Asn	aaa Lys 200	ggg Gly	tct Ser	ttc Phe	gtt Val	agc Ser 205	aaa Lys	cct Pro	aga Arg	624
aat Asn 210	ctg Leu	caa Gln	aaa Lys	atg Met	tct Ser 215	tcg Ser	gaa Glu	cca Pro	ttt Phe	aag Lys	aac Asn 220	gtc Val	tac Tyr	ttg Leu	cta Leu	672
cct Pro 225	caa Gln	aca Thr	aac Asn	caa Gln	ttg Leu 230	ctg Leu	ggg Gly	ttg Leu	tac Tyr	acc Thr 235	atc Ile	atc Ile	aga Arg	aat Asn	aag Lys 240	720
aat Asn	aca Thr	act Thr	aga Arg	cct Pro 245	gat Asp	ttc Phe	att Ile	ttc Phe	tac Tyr 250	tcc Ser	gat Asp	aga Arg	atc Ile	atc Ile 255	aga Arg	768
ttg Leu	ttg Leu	gtt Val	gaa Glu 260	gaa Glu	ggg Gly	ttg Leu	aac Asn	cat His 265	cta Leu	cct Pro	gtg Val	caa Gln 270	aag Lys	caa Gln	att Ile	816
gtg Val	gaa Glu	act Thr 275	gac Asp	acc Thr	aac Asn	gaa Glu	aac Asn 280	ttc Phe	gaa Glu	ggg Gly	gtc Val	tca Ser 285	ttc Phe	atg Met	ggg Gly	864
aaa Lys 290	atc Ile	tgt Cys	ggg Gly	gtt Val	tcc Ser	att Ile 295	gtc Val	aga Arg	gct Ala	ggg Gly	gaa Glu 300	tcg Ser	atg Met	gag Glu	caa Gln	912
gga Gly 305	tta Leu	aga Arg	gac Asp	tgt Cys	tgt Cys 310	agg Arg	tct Ser	gtg Val	cgt Arg	atc Ile 315	ggg Gly	aaa Lys	att Ile	tta Leu	att Ile 320	960
caa Gln	agg Arg	gac Asp	gag Glu	gag Glu 325	act Thr	gct Ala	tta Leu	cca Pro	aag Lys 330	tta Leu	ttc Phe	tac Tyr	gaa Glu	aaa Lys 335	tta Leu	1008
cca Pro	gag Glu	gat Asp	ata Ile 340	tct Ser	gaa Glu	agg Arg	tat Tyr	gtc Val 345	ttc Phe	cta Leu	tta Leu	gac Asp	cca Pro 350	atg Met	ctg Leu	1056
gcc Ala	acc Thr	ggg Gly 355	ggg Gly	agt Ser	gct Ala	atc Ile	atg Met 360	gct Ala	aca Thr	gaa Glu	gtc Val	ttg Leu 365	att Ile	aag Lys	aga Arg	1104
ggg Gly	gtt Val 370	aag Lys	cca Pro	gag Glu	aga Arg	att Ile 375	tac Tyr	ttc Phe	tta Leu	aac Asn	cta Leu 380	atc Ile	tgt Cys	agt Ser	aag Lys	1152
gaa Glu 385	ggg Gly	att Ile	gaa Glu	aaa Lys	tac Tyr 390	cat His	gcc Ala	gcc Ala	ttc Phe	cca Pro 395	gag Glu	gtc Val	aga Arg	att Ile	gtt Val 400	1200
act Thr	ggg Gly	gcc Ala	ctc Leu	gac Asp 405	aga Arg	ggg Gly	cta Leu	gat Asp	gaa Glu 410	aac Asn	aag Lys	tat Tyr	cta Leu	gtt Val 415	cca Pro	1248

Sequence.txt

1287

ggg ttg ggt gac ttt ggt gac aga tac tac tgt gtt taa
 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

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
 Page 17

Sequence.txt
220

210

215

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)

Sequence.txt

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<400> 15
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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 ggc 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

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Sequence.txt

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	
ggt 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

Sequence.txt

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

Sequence.txt

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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 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
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Sequence.txt

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Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	Gln	
			85					90					95			
agg	ctg	cgg	att	gtg	cga	ggc	acc	cag	ctc	ttt	gag	gac	aac	tat	gcc	513
Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	Ala	
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ctg	gcc	gtg	cta	gac	aat	gga	gac	ccg	ctg	aac	aat	acc	acc	cct	gtc	561
Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro	Val	
	115					120					125					
aca	ggg	gcc	tcc	cca	gga	ggc	ctg	cgg	gag	ctg	cag	ctt	cga	agc	ctc	609
Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	Leu	
130					135					140					145	
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Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	Leu	
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tgc	tac	cag	gac	acg	att	ttg	tgg	aag	gac	atc	ttc	cac	aag	aac	aac	705
Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	
			165					170					175			
cag	ctg	gct	ctc	aca	ctg	ata	gac	acc	aac	cgc	tct	cgg	gcc	tgc	cac	753
Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	
		180					185					190				
ccc	tgt	tct	ccg	atg	tgt	aag	ggc	tcc	cgc	tgc	tgg	gga	gag	agt	tct	801
Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	
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gag	gat	tgt	cag	agc	ctg	acg	cgc	act	gtc	tgt	gcc	ggt	ggc	tgt	gcc	849
Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	Ala	
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Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	Ala	
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gcc	ggc	tgc	acg	ggc	ccc	aag	cac	tct	gac	tgc	ctg	gcc	tgc	ctc	cac	945
Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	
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ttc	aac	cac	agt	ggc	atc	tgt	gag	ctg	cac	tgc	cca	gcc	ctg	gtc	acc	993
Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	
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Sequence.txt																
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Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	
	275					280				285						
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Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	Ser	
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acg	gac	gtg	gga	tcc	tgc	acc	ctc	gtc	tgc	ccc	ctg	cac	aac	caa	gag	1137
Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	Glu	
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Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	
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tgt	gcc	cga	gtg	tgc	tat	ggg	ctg	ggc	atg	gag	cac	ttg	cga	gag	gtg	1233
Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	
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Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	
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Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	
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Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	
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act	ctg	gaa	gag	atc	aca	ggg	tac	cta	tac	atc	tca	gca	tgg	ccg	gac	1425
Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	
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Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	
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Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	
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Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	Leu	
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gcc	ctc	atc	cac	cat	aac	acc	cac	ctc	tgc	ttc	gtg	cac	acg	gtg	ccc	1617
Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	Pro	
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tgg	gac	cag	ctc	ttt	cgg	aac	ccg	cac	caa	gct	ctg	ctc	cac	act	gcc	1665
Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	
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aac	cgg	cca	gag	gac	gag	tgt	gtg	ggc	gag	ggc	ctg	gcc	tgc	cac	cag	1713
Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	
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Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	
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aac	tgc	agc	cag	ttc	ctt	cgg	ggc	cag	gag	tgc	gtg	gag	gaa	tgc	cga	1809
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Sequence.txt																
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ccg	tgc	cac	cct	gag	tgt	cag	ccc	cag	aat	ggc	tca	gtg	acc	tgt	ttt	1905
Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	
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gga	ccg	gag	gct	gac	cag	tgt	gtg	gcc	tgt	gcc	cac	tat	aag	gac	cct	1953
Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	
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ccc	ttc	tgc	gtg	gcc	cgc	tgc	ccc	agc	ggc	gtg	aaa	cct	gac	ctc	tcc	2001
Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	
	595					600					605					
tac	atg	ccc	atc	tgg	aag	ttt	cca	gat	gag	gag	ggc	gca	tgc	cag	cct	2049
Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	Pro	
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tgc	ccc	atc	aac	tgc	acc	cac	tcc	tgt	gtg	gac	ctg	gat	gac	aag	ggc	2097
Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	Gly	
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tgc	ccc	gcc	gag	cag	aga	gcc	agc	cct	ctg	acg	tcc	atc	atc	tct	gcg	2145
Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser	Ala	
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gtg	gtt	ggc	att	ctg	ctg	gtc	gtg	gtc	ttg	ggg	gtg	gtc	ttt	ggg	atc	2193
Val	Val	Gly	Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	Ile	
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ctc	atc	aag	cga	cgg	cag	cag	aag	atc	cgg	aag	tac	acg	atg	cgg	aga	2241
Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	
	675					680					685					
ctg	ctg	cag	gaa	acg	gag	ctg	gtg	gag	ccg	ctg	aca	cct	agc	gga	gcg	2289
Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Ala	
					695				700					705		
atg	ccc	aac	cag	gcg	cag	atg	cgg	atc	ctg	aaa	gag	acg	gag	ctg	agg	2337
Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	Arg	
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aag	gtg	aag	gtg	ctt	gga	tct	ggc	gct	ttt	ggc	aca	gtc	tac	aag	ggc	2385
Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	
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Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	
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Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu	Asp	
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Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg	Leu	
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ctg	ggc	atc	tgc	ctg	aca	tcc	acg	gtg	cag	ctg	gtg	aca	cag	ctt	atg	2577
Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu	Met	
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ccc	tat	ggc	tgc	ctc	tta	gac	cat	gtc	cgg	gaa	aac	cgc	gga	cgc	ctg	2625
Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg	Leu	
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Sequence.txt

ggc tcc cag gac ctg ctg aac tgg tgt atg cag att gcc aag ggg atg Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly Met 820 825 830	2673
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aac gtg ctg gtc aag agt ccc aac cat gtc aaa att aca gac ttc ggg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly 850 855 860 865	2769
ctg gct cgg ctg ctg gac att gac gag aca gag tac cat gca gat ggg Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp Gly 870 875 880	2817
ggc aag gtg ccc atc aag tgg atg gcg ctg gag tcc att ctc cgc cgg Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg Arg 885 890 895	2865
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gag ctg atg act ttt ggg gcc aaa cct tac gat ggg atc cca gcc cgg Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala Arg 915 920 925	2961
gag atc cct gac ctg ctg gaa aag ggg gag cgg ctg ccc cag ccc ccc Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro 930 935 940 945	3009
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gac tct gaa tgt cgg cca aga ttc cgg gag ttg gtg tct gaa ttc tcc Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe Ser 965 970 975	3105
cgc atg gcc agg gac ccc cag cgc ttt gtg gtc atc cag aat gag gac Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu Asp 980 985 990	3153
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Sequence.txt

gta ttt gat ggt gac ctg gga atg ggg gca gcc aag ggg ctg caa Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln 1085 1090 1095	3471
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ccc ctg acc tgc agc ccc cag cct gaa tat gtg aac cag cca gat Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp 1130 1135 1140	3606
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gcc cga cct gct ggt gcc act ctg gaa agg ccc aag act ctc tcc Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu Ser 1160 1165 1170	3696
cca ggg aag aat ggg gtc gtc aaa gac gtt ttt gcc ttt ggg ggt Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly Gly 1175 1180 1185	3741
gcc gtg gag aac ccc gag tac ttg aca ccc cag gga gga gct gcc Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala Ala 1190 1195 1200	3786
cct cag ccc cac cct cct cct gcc ttc agc cca gcc ttc gac aac Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn 1205 1210 1215	3831
ctc tat tac tgg gac cag gac cca cca gag cgg ggg gct cca ccc Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro Pro 1220 1225 1230	3876
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Sequence.txt

<211> 1255
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<400> 24

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 20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 50 55 60

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

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
 85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
 100 105 110

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

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

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

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
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Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
 180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
 195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 245 250 255

Sequence.txt

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

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
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Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355 360 365

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

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
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Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
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Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Sequence.txt

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
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Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625 630 635 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
645 650 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
660 665 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
675 680 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
690 695 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785 790 795 800

Sequence.txt

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Sequence.txt

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1100 1105 1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1115 1120 1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1130 1135 1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1145 1150 1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu
1160 1165 1170

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
1235 1240 1245

Leu Gly Leu Asp Val Pro Val
1250 1255

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<212> DNA
<213> Homo sapiens

<220>
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Met Thr Ala Ile Ile Lys Glu Ile Val Ser Arg Asn Lys Arg Arg Tyr
1 5 10 15

Sequence.txt

caa gag gat gga ttc gac tta gac ttg acc tat att tat cca aac att Gln Glu Asp Gly Phe Asp Leu Asp Leu Thr Tyr Ile Tyr Pro Asn Ile 20 25 30	96
att gct atg gga ttt cct gca gaa aga ctt gaa ggc gta tac agg aac Ile Ala Met Gly Phe Pro Ala Glu Arg Leu Glu Gly Val Tyr Arg Asn 35 40 45	144
aat att gat gat gta gta agg ttt ttg gat tca aag cat aaa aac cat Asn Ile Asp Asp Val Val Arg Phe Leu Asp Ser Lys His Lys Asn His 50 55 60	192
tac aag ata tac aat ctt tgt gct gaa aga cat tat gac acc gcc aaa Tyr Lys Ile Tyr Asn Leu Cys Ala Glu Arg His Tyr Asp Thr Ala Lys 65 70 75 80	240
ttt aat tgc aga gtt gca caa tat cct ttt gaa gac cat aac cca cca Phe Asn Cys Arg Val Ala Gln Tyr Pro Phe Glu Asp His Asn Pro Pro 85 90 95	288
cag cta gaa ctt atc aaa ccc ttt tgt gaa gat ctt gac caa tgg cta Gln Leu Glu Leu Ile Lys Pro Phe Cys Glu Asp Leu Asp Gln Trp Leu 100 105 110	336
agt gaa gat gac aat cat gtt gca gca att cac tgt aaa gct gga aag Ser Glu Asp Asp Asn His Val Ala Ala Ile His Cys Lys Ala Gly Lys 115 120 125	384
gga cga act ggt gta atg ata tgt gca tat tta tta cat cgg ggc aaa Gly Arg Thr Gly Val Met Ile Cys Ala Tyr Leu Leu His Arg Gly Lys 130 135 140	432
ttt tta aag gca caa gag gcc cta gat ttc tat ggg gaa gta agg acc Phe Leu Lys Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu Val Arg Thr 145 150 155 160	480
aga gac aaa aag gga gta act att ccc agt cag agg cgc tat gtg tat Arg Asp Lys Lys Gly Val Thr Ile Pro Ser Gln Arg Arg Tyr Val Tyr 165 170 175	528
tat tat agc tac ctg tta aag aat cat ctg gat tat aga cca gtg gca Tyr Tyr Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val Ala 180 185 190	576
ctg ttg ttt cac aag atg atg ttt gaa act att cca atg ttc agt ggc Leu Leu Phe His Lys Met Met Phe Glu Thr Ile Pro Met Phe Ser Gly 195 200 205	624
gga act tgc aat cct cag ttt gtg gtc tgc cag cta aag gtg aag ata Gly Thr Cys Asn Pro Gln Phe Val Val Cys Gln Leu Lys Val Lys Ile 210 215 220	672
tat tcc tcc aat tca gga ccc aca cga cgg gaa gac aag ttc atg tac Tyr Ser Ser Asn Ser Gly Pro Thr Arg Arg Glu Asp Lys Phe Met Tyr 225 230 235 240	720
ttt gag ttc cct cag ccg tta cct gtg tgt ggt gat atc aaa gta gag Phe Glu Phe Pro Gln Pro Leu Pro Val Cys Gly Asp Ile Lys Val Glu 245 250 255	768
ttc ttc cac aaa cag aac aag atg cta aaa aag gac aaa atg ttt cac Phe Phe His Lys Gln Asn Lys Met Leu Lys Lys Asp Lys Met Phe His 260 265 270	816
ttt tgg gta aat aca ttc ttc ata cca gga cca gag gaa acc tca gaa Phe Trp Val Asn Thr Phe Phe Ile Pro Gly Pro Glu Glu Thr Ser Glu 275 280 285	864

Sequence.txt

aaa gta gaa aat gga agt cta tgt gat caa gaa atc gat agc att tgc Lys Val Glu Asn Gly Ser Leu Cys Asp Gln Glu Ile Asp Ser Ile Cys 290 295 300	912
agt ata gag cgt gca gat aat gac aag gaa tat cta gta ctt act tta Ser Ile Glu Arg Ala Asp Asn Asp Lys Glu Tyr Leu Val Leu Thr Leu 305 310 315 320	960
aca aaa aat gat ctt gac aaa gca aat aaa gac aaa gcc aac cga tac Thr Lys Asn Asp Leu Asp Lys Ala Asn Lys Asp Lys Ala Asn Arg Tyr 325 330 335	1008
ttt tct cca aat ttt aag gtg aag ctg tac ttc aca aaa aca gta gag Phe Ser Pro Asn Phe Lys Val Lys Leu Tyr Phe Thr Lys Thr Val Glu 340 345 350	1056
gag ccg tca aat cca gag gct agc agt tca act tct gta aca cca gat Glu Pro Ser Asn Pro Glu Ala Ser Ser Ser Thr Ser Val Thr Pro Asp 355 360 365	1104
gtt agt gac aat gaa cct gat cat tat aga tat tct gac acc act gac Val Ser Asp Asn Glu Pro Asp His Tyr Arg Tyr Ser Asp Thr Thr Asp 370 375 380	1152
tct gat cca gag aat gaa cct ttt gat gaa gat cag cat aca caa att Ser Asp Pro Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile 385 390 395 400	1200
aca aaa gtc tga Thr Lys Val	1212

<210> 26
<211> 403
<212> PRT
<213> Homo sapiens

<400> 26

Met Thr Ala Ile Ile Lys Glu Ile Val Ser Arg Asn Lys Arg Arg Tyr
1 5 10 15

Gln Glu Asp Gly Phe Asp Leu Asp Leu Thr Tyr Ile Tyr Pro Asn Ile
20 25 30

Ile Ala Met Gly Phe Pro Ala Glu Arg Leu Glu Gly Val Tyr Arg Asn
35 40 45

Asn Ile Asp Asp Val Val Arg Phe Leu Asp Ser Lys His Lys Asn His
50 55 60

Tyr Lys Ile Tyr Asn Leu Cys Ala Glu Arg His Tyr Asp Thr Ala Lys
65 70 75 80

Phe Asn Cys Arg Val Ala Gln Tyr Pro Phe Glu Asp His Asn Pro Pro
85 90 95

Gln Leu Glu Leu Ile Lys Pro Phe Cys Glu Asp Leu Asp Gln Trp Leu
100 105 110

Sequence.txt

Ser Glu Asp Asp Asn His Val Ala Ala Ile His Cys Lys Ala Gly Lys
115 120 125

Gly Arg Thr Gly Val Met Ile Cys Ala Tyr Leu Leu His Arg Gly Lys
130 135 140

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

Arg Asp Lys Lys Gly Val Thr Ile Pro Ser Gln Arg Arg Tyr Val Tyr
165 170 175

Tyr Tyr Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val Ala
180 185 190

Leu Leu Phe His Lys Met Met Phe Glu Thr Ile Pro Met Phe Ser Gly
195 200 205

Gly Thr Cys Asn Pro Gln Phe Val Val Cys Gln Leu Lys Val Lys Ile
210 215 220

Tyr Ser Ser Asn Ser Gly Pro Thr Arg Arg Glu Asp Lys Phe Met Tyr
225 230 235 240

Phe Glu Phe Pro Gln Pro Leu Pro Val Cys Gly Asp Ile Lys Val Glu
245 250 255

Phe Phe His Lys Gln Asn Lys Met Leu Lys Lys Asp Lys Met Phe His
260 265 270

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

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

Ser Ile Glu Arg Ala Asp Asn Asp Lys Glu Tyr Leu Val Leu Thr Leu
305 310 315 320

Thr Lys Asn Asp Leu Asp Lys Ala Asn Lys Asp Lys Ala Asn Arg Tyr
325 330 335

Phe Ser Pro Asn Phe Lys Val Lys Leu Tyr Phe Thr Lys Thr Val Glu
340 345 350

Glu Pro Ser Asn Pro Glu Ala Ser Ser Ser Thr Ser Val Thr Pro Asp
355 360 365

Val Ser Asp Asn Glu Pro Asp His Tyr Arg Tyr Ser Asp Thr Thr Asp
370 375 380

Sequence.txt

Ser Asp Pro Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile
 385 390 395 400

Thr Lys Val

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 <211> 597
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(597)

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 Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met
 1 5 10 15
 gac gcc agg cag gcg gag cac ccc aag ccc tcg gcc tgc agg aac ctc 96
 Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
 20 25 30
 ttc ggc ccg gtg gac cac gaa gag tta acc cgg gac ttg gag aag cac 144
 Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45
 tgc aga gac atg gaa gag gcg agc cag cgc aag tgg aat ttc gat ttt 192
 Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60
 cag aat cac aaa ccc cta gag ggc aag tac gag tgg caa gag gtg gag 240
 Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80
 aag ggc agc ttg ccc gag ttc tac tac aga ccc ccg cgg ccc ccc aaa 288
 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95
 ggt gcc tgc aag gtg ccg gcg cag gag agc cag gat gtc agc ggg agc 336
 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110
 cgc ccg gcg gcg cct tta att ggg gct ccg gct aac tct gag gac acg 384
 Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
 115 120 125
 cat ttg gtg gac cca aag act gat ccg tcg gac agc cag acg ggg tta 432
 His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
 130 135 140
 gcg gag caa tgc gca gga ata agg aag cga cct gca acc gac gat tct 480
 Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160
 tct act caa aac aaa aga gcc aac aga aca gaa gaa aat gtt tca gac 528
 Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175
 ggt tcc cca aat gcc ggt tct gtg gag cag acg ccc aag aag cct ggc 576
 Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
 180 185 190

ctc aga aga cgt caa acg taa
 Leu Arg Arg Arg Gln Thr
 195

<210> 28
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met
 1 5 10 15

Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
 20 25 30

Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45

Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110

Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
 115 120 125

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

Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
 180 185 190

Leu Arg Arg Arg Gln Thr
 195

<210> 29
 <211> 894
 <212> DNA
 <213> Homo sapiens

Sequence.txt

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<220>
<221> CDS
<222> (1)..(894)

<400> 29
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1          5          10          15

atg aaa ggc cct att gct atg caa tct ggt cca aaa cca ctc ttc agg      96
Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
          20          25          30

agg atg tct tca ctg gtg ggc ccc acg caa agc ttc ttc atg agg gaa      144
Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
          35          40          45

tct aag act ttg ggg gct gtc cag att atg aat ggg ctc ttc cac att      192
Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
          50          55          60

gcc ctg ggg ggt ctt ctg atg atc cca gca ggg atc tat gca ccc atc      240
Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65          70          75          80

tgt gtg act gtg tgg tac cct ctc tgg gga ggc att atg tat att att      288
Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
          85          90          95

tcc gga tca ctc ttg gca gca acg gag aaa aac tct agg aag tgt ttg      336
Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
          100          105          110

gtc aaa gga aaa atg ata atg aat tca ttg agc ctc ttt gct gcc att      384
Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
          115          120          125

tct gga atg att ctt tca atc atg gac ata ctt aat att aaa att tcc      432
Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
          130          135          140

cat ttt tta aaa atg gag agt ctg aat ttt att aga gct cac aca cca      480
His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145          150          155          160

tat att aac ata tac aac tgt gaa cca gct aat ccc tct gag aaa aac      528
Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
          165          170          175

tcc cca tct acc caa tac tgt tac agc ata caa tct ctg ttc ttg ggc      576
Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
          180          185          190

att ttg tca gtg atg ctg atc ttt gcc ttc ttc cag gaa ctt gta ata      624
Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
          195          200          205

gct ggc atc gtt gag aat gaa tgg aaa aga acg tgc tcc aga ccc aaa      672
Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
          210          215          220

tct aac ata gtt ctc ctg tca gca gaa gaa aaa aaa gaa cag act att      720
Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225          230          235          240

gaa ata aaa gaa gaa gtg gtt ggg cta act gaa aca tct tcc caa cca      768

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Sequence.txt

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255

aag aat gaa gaa gac att gaa att att cca atc caa gaa gag gaa gaa 816
 Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
 260 265 270

gaa gaa aca gag acg aac ttt cca gaa cct ccc caa gat cag gaa tcc 864
 Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285

tca cca ata gaa aat gac agc tct cct taa 894
 Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 30
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
 20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
 35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110

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

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 Page 66

Sequence.txt

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180                               185                               190
Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195                               200                               205
Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210                               215                               220
Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                               230                               235                               240
Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245                               250                               255
Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
260                               265                               270
Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275                               280                               285
Ser Pro Ile Glu Asn Asp Ser Ser Pro
290                               295

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