

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

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att gcc tat gag gag gcg tta tta ggt tac aaa gag ggt ggt gtt cct Ile Ala Tyr Glu Glu Ala Leu Leu Gly Tyr Lys Glu Gly Gly Val Pro 20 25 30	96
att ggc gga tgt ctt atc aat aac aaa gac gga agt gtt ctc ggt cgt Ile Gly Gly Cys Leu Ile Asn Asn Lys Asp Gly Ser Val Leu Gly Arg 35 40 45	144
ggt cac aac atg aga ttt caa aag gga tcc gcc aca cta cat ggt gag Gly His Asn Met Arg Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu 50 55 60	192
atc tcc act ttg gaa aac tgt ggg aga tta gag ggc aaa gtg tac aaa Ile Ser Thr Leu Glu Asn Cys Gly Arg Leu Glu Gly Lys Val Tyr Lys 65 70 75 80	240
gat acc act ttg tat acg acg ctg tct cca tgc gac atg tgt aca ggt Asp Thr Thr Leu Tyr Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly 85 90 95	288
gcc atc atc atg tat ggt att cca cgc tgt gtc atc ggt gag aac gtt Ala Ile Ile Met Tyr Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val 100 105 110	336
aat ttc aaa agt aag ggc gag aaa tat tta caa act aga ggt cac gag Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu 115 120 125	384
gtt gtt gtt gtt gac gat gag agg tgt aaa aag tta atg aaa caa ttt Val Val Val Val Asp Asp Glu Arg Cys Lys Lys Leu Met Lys Gln Phe 130 135 140	432
atc gat gaa aga cct cag gat tgg ttt gaa gat att ggt gag tag Ile Asp Glu Arg Pro Gln Asp Trp Phe Glu Asp Ile Gly Glu 145 150 155	477

<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	

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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	

<210> 6
 <211> 158
 <212> PRT
 <213> Artificial Sequence

<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

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

<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
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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

Sequence.txt

<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)

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 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

Sequence.txt

Leu 225	Ser	Phe	Gly	Ala	Arg 230	Ala	Glu	Leu	Pro	Arg 235	Ile	His	Pro	Val	Ala 240	
tct Ser	aaa Lys	ctt Leu	ctt Leu	cgt Arg 245	ctt Leu	atg Met	caa Gln	aaa Lys	aaa Lys 250	gaa Glu	act Thr	aat Asn	ctt Leu	tgt Cys 255	ctt Leu	768
tct Ser	gct Ala	gat Asp	gtt Val 260	tct Ser	ctt Leu	gct Ala	cgt Arg	gaa Glu 265	ctt Leu	ctt Leu	caa Gln	ctt Leu	gct Ala 270	gat Asp	gct Ala	816
ctt Leu	ggt Gly	cct Pro 275	tct Ser	att Ile	tgt Cys	atg Met	ctt Leu 280	aaa Lys	act Thr	cat His	gtt Val	gat Asp 285	att Ile	ctt Leu	aat Asn	864
gat Asp	ttt Phe 290	act Thr	ctt Leu	gat Asp	gtt Val	atg Met 295	aaa Lys	gaa Glu	ctt Leu	att Ile	act Thr 300	ctt Leu	gct Ala	aaa Lys	tgt Cys	912
cat His 305	gaa Glu	ttt Phe	ctt Leu	att Ile	ttt Phe 310	gaa Glu	gat Asp	cgt Arg	aaa Lys	ttt Phe 315	gct Ala	gat Asp	att Ile	ggt Gly	aat Asn 320	960
act Thr	gtt Val	aaa Lys	aaa Lys	caa Gln 325	tat Tyr	gaa Glu	ggt Gly	ggt Gly	att Ile 330	ttt Phe	aaa Lys	att Ile	gct Ala	tct Ser 335	tgg Trp	1008
gct Ala	gat Asp	ctt Leu	gtt Val 340	aat Asn	gct Ala	cat His	gtt Val	gtt Val 345	cct Pro	ggt Gly	tct Ser	ggt Gly	gtt Val 350	gtt Val	aaa Lys	1056
ggt Gly	ctt Leu	caa Gln 355	gaa Glu	gtt Val	ggt Gly	ctt Leu	cct Pro 360	ctt Leu	cat His	cgt Arg	ggt Gly	tgt Cys 365	ctt Leu	ctt Leu	att Ile	1104
gct Ala	gaa Glu 370	atg Met	tct Ser	tct Ser	act Thr	ggt Gly 375	tct Ser	ctt Leu	gct Ala	act Thr	ggt Gly 380	gat Asp	tat Tyr	act Thr	cgt Arg	1152
gct Ala 385	gct Ala	gtt Val	cgt Arg	atg Met	gct Ala 390	gaa Glu	gaa Glu	cat His	tct Ser	gaa Glu 395	ttt Phe	gtt Val	gtt Val	ggt Gly	ttt Phe 400	1200
att Ile	tct Ser	ggt Gly	tct Ser	cgt Arg 405	gtt Val	tct Ser	atg Met	aaa Lys	cct Pro 410	gaa Glu	ttt Phe	ctt Leu	cat His	ctt Leu 415	act Thr	1248
cct Pro	ggt Gly	gtt Val	caa Gln 420	ctt Leu	gaa Glu	gct Ala	ggt Gly	ggt Gly 425	gat Asp	aat Asn	ctt Leu	ggt Gly	caa Gln 430	caa Gln	tat Tyr	1296
aat Asn	tct Ser	cct Pro 435	caa Gln	gaa Glu	gtt Val	att Ile	ggt Gly 440	aaa Lys	cgt Arg	ggt Gly	tct Ser	gat Asp 445	att Ile	att Ile	att Ile	1344
gtt Val	ggt Gly 450	cgt Arg	ggt Gly	att Ile	att Ile	tct Ser 455	gct Ala	gct Ala	gat Asp	cgt Arg	ctt Leu 460	gaa Glu	gct Ala	gct Ala	gaa Glu	1392
atg Met 465	tat Tyr	cgt Arg	aaa Lys	gct Ala	gct Ala 470	tgg Trp	gaa Glu	gct Ala	tat Tyr	ctt Leu 475	tct Ser	cgt Arg	ctt Leu	ggt Gly	gtt Val 480	1440
taa																1443

<210> 10
<211> 480

Sequence.txt

<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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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 85 Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly 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				
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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		
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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

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 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)

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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

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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	tcg Ser 215	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	ggc 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
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gtg Val	gaa Glu	act Thr 275	gac Asp	acc Thr	aac Asn	gaa Glu	aac Asn 280	ttc Phe	gaa Glu	ggc Gly	gtc Val	tca Ser 285	ttc Phe	atg Met	ggc Gly	864
aaa Lys	atc Ile 290	tgt Cys	ggc Gly	gtt Val	tcc Ser	att Ile 295	gtc Val	aga Arg	gct Ala	ggc 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	ggc 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	ggc Gly 355	ggc 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
ggc 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	ggc 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	ggc Gly	gcc Ala	ctc Leu	gac Asp 405	aga Arg	ggc 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
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 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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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 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

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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
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)

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1 5 10 15
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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 gcg gtc gct cgt gca gct ttg ggg cca ttg gtg acg ggt ctg 576
Gly Ala Ala Val Ala Arg Ala Ala Leu Gly Pro Leu Val Thr Gly Leu

Sequence.txt																
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Asn Phe Lys Ser Lys Gly Glu Lys Tyr Leu Gln Thr Arg Gly His Glu
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Sequence.txt

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Sequence.txt

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agc Ser 1100	ctc Leu	ccc Pro	aca Thr	cat His	gac Asp 1105	ccc Pro	agc Ser	cct Pro	cta Leu	cag Gln 1110	cgg Arg	tac Tyr	agt Ser	gag Glu	3516
gac Asp 1115	ccc Pro	aca Thr	gta Val	ccc Pro	ctg Leu 1120	ccc Pro	tct Ser	gag Glu	act Thr	gat Asp 1125	ggc Gly	tac Tyr	gtt Val	gcc Ala	3561
ccc Pro 1130	ctg Leu	acc Thr	tgc Cys	agc Ser	ccc Pro 1135	cag Gln	cct Pro	gaa Glu	tat Tyr	gtg Val 1140	aac Asn	cag Gln	cca Pro	gat Asp	3606
gtt Val 1145	cgg Arg	ccc Pro	cag Gln	ccc Pro	cct Pro 1150	tcg Ser	ccc Pro	cga Arg	gag Glu	ggc Gly 1155	cct Pro	ctg Leu	cct Pro	gct Ala	3651
gcc Ala 1160	cga Arg	cct Pro	gct Ala	ggt Gly	gcc Ala 1165	act Thr	ctg Leu	gaa Glu	agg Arg	ccc Pro 1170	aag Lys	act Thr	ctc Leu	tcc Ser	3696
cca Pro 1175	ggg Gly	aag Lys	aat Asn	ggg Gly	gtc Val 1180	gtc Val	aaa Lys	gac Asp	gtt Val	ttt Phe 1185	gcc Ala	ttt Phe	ggg Gly	ggt Gly	3741
gcc Ala 1190	gtg Val	gag Glu	aac Asn	ccc Pro	gag Glu 1195	tac Tyr	ttg Leu	aca Thr	ccc Pro	cag Gln 1200	gga Gly	gga Gly	gct Ala	gcc Ala	3786
cct Pro 1205	cag Gln	ccc Pro	cac His	cct Pro	cct Pro 1210	cct Pro	gcc Ala	ttc Phe	agc Ser	cca Pro 1215	gcc Ala	ttc Phe	gac Asp	aac Asn	3831
ctc Leu 1220	tat Tyr	tac Tyr	tgg Trp	gac Asp	cag Gln 1225	gac Asp	cca Pro	cca Pro	gag Glu	cgg Arg 1230	ggg Gly	gct Ala	cca Pro	ccc Pro	3876
agc Ser 1235	acc Thr	ttc Phe	aaa Lys	ggg Gly	aca Thr 1240	cct Pro	acg Thr	gca Ala	gag Glu	aac Asn 1245	cca Pro	gag Glu	tac Tyr	ctg Leu	3921
ggt Gly 1250	ctg Leu	gac Asp	gtg Val	cca Pro	gtg Val 1255	tga	accagaaggc	caagtccgca	gaagccctga						3972
tggtgtcctca	gggagcaggg	aaggcctgac	ttctgtctggc	atcaagaggt	gggagggccc										4032
tccgaccact	tccaggggaa	cctgccatgc	caggaacctg	tcctaaggaa	ccttccttcc										4092
tgcttgagtt	cccagatggc	tggaaggggt	ccagcctcgt	tggaagagga	acagcactgg										4152
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tgagagggga	agcggcccta	agggagtgtc	taagaacaaa	agcgacccat	tcagagactg										4332
tccctgaaac	ctagtactgc	cccccatgag	gaaggaacag	caatgggtgtc	agtatccagg										4392
ctttgtacag	agtgtctttc	tgtttagttt	ttactttttt	tgttttgttt	ttttaaagat										4452
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Sequence.txt

<211> 1255
 <212> PRT
 <213> Homo sapiens

<400> 24

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Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
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Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
      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
      165      170      175

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
275 280 285

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
450 455 460

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
485 490 495

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
530 535 540

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

<210> 25
<211> 1212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1212)

<400> 25
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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	912
Lys Val Glu Asn Gly Ser Leu Cys Asp Gln Glu Ile Asp Ser Ile Cys	
290 295 300	
agt ata gag cgt gca gat aat gac aag gaa tat cta gta ctt act tta	960
Ser Ile Glu Arg Ala Asp Asn Asp Lys Glu Tyr 315 Leu Val Leu Thr Leu	
305 310 315 320	
aca aaa aat gat ctt gac aaa gca aat aaa gac aaa gcc aac cga tac	1008
Thr Lys Asn Asp Leu Asp Lys Ala Asn Lys Asp Lys Ala Asn Arg Tyr	
325 330 335	
ttt tct cca aat ttt aag gtg aag ctg tac ttc aca aaa aca gta gag	1056
Phe Ser Pro Asn Phe Lys Val Lys Leu Tyr Phe Thr Lys Thr Val Glu	
340 345 350	
gag ccg tca aat cca gag gct agc agt tca act tct gta aca cca gat	1104
Glu Pro Ser Asn Pro Glu Ala Ser Ser Ser Thr Ser Val Thr Pro Asp	
355 360 365	
gtt agt gac aat gaa cct gat cat tat aga tat tct gac acc act gac	1152
Val Ser Asp Asn Glu Pro Asp His Tyr Arg Tyr Ser Asp Thr Thr Asp	
370 375 380	
tct gat cca gag aat gaa cct ttt gat gaa gat cag cat aca caa att	1200
Ser Asp Pro Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile	
385 390 395 400	
aca aaa gtc tga	1212
Thr Lys Val	

<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

<210> 27
 <211> 597
 <212> DNA
 <213> Homo sapiens

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

<400> 27
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 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

<220>

<221> CDS

<222> (1)..(894)

<400> 29

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Met	Thr	Thr	Pro	Arg	Asn	Ser	Val	Asn	Gly	Thr	Phe	Pro	Ala	Glu	Pro	
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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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										

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 <211> 297
 <212> PRT
 <213> Homo sapiens
 <400> 30

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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

Sequence.txt

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