

SEQUENCE LISTING

<110> EISAI R&D MANAGEMENT CO., LTD.

<120> A METHOD OF PRODUCING A TUMOUR CELL FROM A NORMAL HUMAN MAMMARY
GLAND EPITHELIAL CELL

<130> PCT11-0026

<150> JP 2010-154744

<151> 2010-07-07

<160> 10

<170> PatentIn version 3.4

<210> 1

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(312)

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Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro

20 25 30

ctg gat gga gaa tat ttc acc ctt cag atc cgt ggg cgt gag cgc ttc 144

Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe

35 40 45

gag atg ttc cga gag ctg aat gag gcc ttg gaa ctc aag gat gcc cag	192
Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln	
50 55 60	

gct ggg aag gag cca ggg ggg agc agg gct cac tcc agc cac ctg aag	240
Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys	
65 70 75 80	

tcc aaa aag ggt cag tct acc tcc cgc cat aaa aaa ctc atg ttc aag	288
Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys	
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aca gaa ggg cct gac tca gac tga	312
Thr Glu Gly Pro Asp Ser Asp	
100	

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 <212> PRT
 <213> Homo sapiens

<400> 2

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Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro
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Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe
35 40 45

Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln

60

Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys
85 90 95

Thr Glu Gly Pro Asp Ser Asp
100

$\langle 210 \rangle$	3
$\langle 211 \rangle$	1581
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Rous sarcoma virus

$\langle 220 \rangle$	
$\langle 221 \rangle$	CDS
$\langle 222 \rangle$	(1)..(1581)

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agc ctg gag cca ccc gac agc acc cac cac ggg gga ttc cca gcc tcg 96
Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser
20 25 30

cag acc ccc aac aag aca gca gcc ccc gac acg cac cgc acc ccc agc 144
Gln Thr Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser
35 40 45

cgc tcc ttc ggg acc gtg gcc acc gag ccc aag ctc ttc ggg ggc ttc	192
Arg Ser Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe	
50 55 60	
aac act tct gac acc gtt acg tcg ccg cag cgt gcc ggg gca ctg gct	240
Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala	
65 70 75 80	
ggc ggc gtc acc act ttc gtg gct ctc tac gac tac gag tcc tgg att	288
Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Trp Ile	
85 90 95	
gaa acg gac ttg tcc ttc aag aaa gga gaa cgg ctg cag att gtc aac	336
Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn	
100 105 110	
aac acg gaa ggt aac tgg tgg ctg gct cat tcc ctc act aca gga cag	384
Asn Thr Glu Gly Asn Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln	
115 120 125	
acg ggc tac atc ccc agt aac tat gtc gcg ccc tca gac tcc atc cag	432
Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln	
130 135 140	
gct gaa gag tgg tac ttt ggg aag atc act cgt cgg gag tcc gag cgg	480
Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg	
145 150 155 160	
ctg ctg ctc aac ccc gaa aac ccc cgg gga acc ttc ttg gtc cgg gag	528
Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu	
165 170 175	
agc gag acg aca aaa ggt gcc tat tgc ctc tcc gtt tct gac ttt gac	576
Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp	
180 185 190	
aac gcc aag ggg ctc aat gtg aag cac tac aag atc cgc aag ctg gac	624
Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp	

195	200	205	
agc ggc ggc ttc tac atc acc tca cgc aca cag ttc agc agc ctg cag			672
Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln			
210	215	220	
cag ctg gtg gcc tac tac tcc aaa cat gct gat ggc ttg tgc cac cgc			720
Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg			
225	230	235	240
ctg acc aac gtc tgc ccc acg tcc aag ccc cag acc cag gga ctc gcc			768
Leu Thr Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala			
245	250	255	
aag gac gcg tgg gaa atc ccc cgg gag tcg ctg cgg ctg gag gtg aag			816
Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys			
260	265	270	
ctg ggg cag ggc tgc ttt gga gag gtc tgg atg ggg acc tgg aac ggc			864
Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly			
275	280	285	
acc acc aga gtg gcc ata aag act ctg aag ccc ggc acc atg tcc ccg			912
Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro			
290	295	300	
gag gcc ttc ctg cag gaa gcc caa gtg atg aag aag ctc cgg cat gag			960
Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu			
305	310	315	320
aag ctg gtt caa ctg tac gca gtg gtg tcg gaa gag ccc atc tac atc			1008
Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile			
325	330	335	
gtc att gag tac atg agc aag ggg agc ctc ctg gat ttc ctg aag gga			1056
Val Ile Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly			
340	345	350	

gag atg ggc aag tac ctg cgg ctg cca cag ctc gtt gat atg gct gct	1104
Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala	
355 360 365	
cag att gca tcc ggc atg gcc tat gtg gag agg atg aac tac gtg cac	1152
Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His	
370 375 380	
cga gac ctg cgg gcg gcc aac atc ctg gtg ggg gag aac ctg gtg tgc	1200
Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys	
385 390 395 400	
aag gtg gct gac ttt ggg ctg gca cgc ctc atc gag gac aac gag tac	1248
Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr	
405 410 415	
aca gca cgg caa ggt gcc aag ttc ccc atc aag tgg aca gcc ccc gag	1296
Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu	
420 425 430	
gca gcc ctc tat ggc cgg ttc acc atc aag tgc gat gtc tgg tcc ttc	1344
Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe	
435 440 445	
ggc atc ctg ctg act gag ctg acc acc aag ggc cgg gtg cca tac cca	1392
Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro	
450 455 460	
ggg atg ggc aac ggg gag gtg ctg gac cgg gtg gag agg ggc tac cgc	1440
Gly Met Gly Asn Gly Glu Val Leu Asp Arg Val Glu Arg Gly Tyr Arg	
465 470 475 480	
atg ccc tgc ccg ccc gag tgc ccc gag tgc ctg cat gac ctt atg tgc	1488
Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys	
485 490 495	
cag tgc tgg cgg agg gac cct gag gag cgg ccc act ttc gag tac ctg	1536
Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu	

500 505 510

cag gcc cag ctg ctc cct gct tgt gtg ttg gag gtc gct gag tag 1581

Gln Ala Gln Leu Leu Pro Ala Cys Val Leu Glu Val Ala Glu

515 520 525

$\langle 210 \rangle$	4
$\langle 211 \rangle$	526
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Rous sarcoma virus

 $\langle 400 \rangle$ 4

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg
1 5 10 15

Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser

20 25 30

Gln Thr Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser
35 40 45

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

Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala
65 70 75 80

Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Trp Ile
85 90 95

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

Asn	Thr	Glu	Gly	Asn	Trp	Trp	Leu	Ala	His	Ser	Leu	Thr	Thr	Gly	Gln
		115					120					125			

Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Ser	Asp	Ser	Ile	Gln
	130						135					140			

Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Thr	Arg	Arg	Glu	Ser	Glu	Arg
145						150				155					160

Leu	Leu	Leu	Asn	Pro	Glu	Asn	Pro	Arg	Gly	Thr	Phe	Leu	Val	Arg	Glu
				165					170					175	

Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Cys	Leu	Ser	Val	Ser	Asp	Phe	Asp
			180					185					190		

Asn	Ala	Lys	Gly	Leu	Asn	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp
		195						200				205			

Ser	Gly	Gly	Phe	Tyr	Ile	Thr	Ser	Arg	Thr	Gln	Phe	Ser	Ser	Leu	Gln
	210							215				220			

Gln	Leu	Val	Ala	Tyr	Tyr	Ser	Lys	His	Ala	Asp	Gly	Leu	Cys	His	Arg
225						230				235					240

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

Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys
260 265 270

Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
275 280 285

Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
290 295 300

Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
305 310 315 320

Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
325 330 335

Val Ile Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
340 345 350

Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
355 360 365

Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
370 375 380

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
385 390 395 400

Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
405 410 415

Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
420 425 430

Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
435 440 445

Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
450 455 460

Gly Met Gly Asn Gly Glu Val Leu Asp Arg Val Glu Arg Gly Tyr Arg
465 470 475 480

Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys
485 490 495

Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu
500 505 510

Gln Ala Gln Leu Leu Pro Ala Cys Val Leu Glu Val Ala Glu
515 520 525

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- <212> DNA
- <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(912)

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1 5 10 15

tat ggg aca gtg tac aag gcc cgt gat ccc cac agt ggc cac ttt gtg 96
Tyr Gly Thr Val Tyr Lys Ala Arg Asp Pro His Ser Gly His Phe Val
20 25 30

gcc ctc aag agt gtg aga gtc ccc aat gga gga gga ggt gga gga ggc 144
Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
35 40 45

ctt ccc atc agc aca gtt cgt gag gtg gct tta ctg agg cga ctg gag 192
Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60

gct ttt gag cat ccc aat gtt gtc cgg ctg atg gac gtc tgt gcc aca 240
Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

tcc cga act gac cgg gag atc aag gta acc ctg gtg ttt gag cat gta 288
Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95

gac cag gac cta agg aca tat ctg gac aag gca ccc cca cca ggc ttg 336
Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110

cca gcc gaa acg atc aag gat ctg atg cgc cag ttt cta aga ggc cta 384
Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125

gat ttc ctt cat gcc aat tgc atc gtt cac cga gat ctg aag cca gag 432

Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu	
130 135 140	
aac att ctg gtg aca agt ggt gga aca gtc aag ctg gct gac ttt ggc	480
Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly	
145 150 155 160	
ctg gcc aga atc tac agc tac cag atg gca ctt aca ccc gtg gtt gtt	528
Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val	
165 170 175	
aca ctc tgg tac cga gct ccc gaa gtt ctt ctg cag tcc aca tat gca	576
Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala	
180 185 190	
aca cct gtg gac atg tgg agt gtt ggc tgt atc ttt gca gag atg ttt	624
Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe	
195 200 205	
cgt cga aag cct ctc ttc tgt gga aac tct gaa gcc gac cag ttg ggc	672
Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly	
210 215 220	
aaa atc ttt gac ctg att ggg ctg cct cca gag gat gac tgg cct cga	720
Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg	
225 230 235 240	
gat gta tcc ctg ccc cgt gga gcc ttt ccc ccc aga ggg ccc cgc cca	768
Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro	
245 250 255	
gtg cag tcg gtg gta cct gag atg gag gag tcg gga gca cag ctg ctg	816
Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu	
260 265 270	
ctg gaa atg ctg act ttt aac cca cac aag cga atc tct gcc ttt cga	864
Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg	
275 280 285	

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 290 295 300

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 <212> PRT
 <213> Homo sapiens

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Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
 35 40 45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
 50 55 60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
 85 90 95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu

100	105	110
Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu		
115	120	125
Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu		
130	135	140
Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly		
145	150	155
		160
Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val		
165	170	175
Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala		
180	185	190
Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe		
195	200	205
Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly		
210	215	220
Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg		
225	230	235
		240
Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro		
245	250	255

Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
260 265 270

Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
275 280 285

Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
290 295 300

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<220>
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<210> 8
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthetic DNA

<400> 8
ctcactagcc atctggagta g 21

<210> 9

<211> 3633
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 9

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gcg ctc tgc ccg gcg agt cgg gct ctg gag gaa aag aaa gtt tgc caa	96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln	
20 25 30	

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt	144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe	
35 40 45	

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat	192
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn	
50 55 60	

ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag	240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys	
65 70 75 80	

acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg	288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val	
85 90 95	

gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac	336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr	
100 105 110	

tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat	384
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn	
115 120 125	
aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg	432
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu	
130 135 140	
cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag	480
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu	
145 150 155 160	
agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg	528
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met	
165 170 175	
tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca	576
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro	
180 185 190	
agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag	624
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln	
195 200 205	
aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc tgc cgt	672
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg	
210 215 220	
ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc	720
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys	
225 230 235 240	
aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac	768
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp	
245 250 255	
gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc	816
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro	

260	265	270	
acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt			864
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly			
275	280	285	
gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac			912
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His			
290	295	300	
ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa			960
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu			
305	310	315	320
gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg			1008
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val			
325	330	335	
tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat			1056
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn			
340	345	350	
gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat			1104
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp			
355	360	365	
ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act			1152
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr			
370	375	380	
cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa			1200
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu			
385	390	395	400
atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac			1248
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp			
405	410	415	

ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa	1296
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln	
420 425 430	
cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg	1344
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu	
435 440 445	
gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca	1392
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser	
450 455 460	
gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg	1440
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu	
465 470 475 480	
ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa	1488
Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu	
485 490 495	
aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc	1536
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro	
500 505 510	
gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cgg aat	1584
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn	
515 520 525	
gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt	1632
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly	
530 535 540	
gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca	1680
Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro	
545 550 555 560	
gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca	1728
Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro	

565	570	575	
gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc			1776
Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val			
580	585	590	
aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg			1824
Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp			
595	600	605	
aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc			1872
Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys			
610	615	620	
acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt cca acg aat ggg			1920
Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly			
625	630	635	640
cct aag atc ccg tcc atc gcc act ggg atg gtg ggg gcc ctc ctc ttg			1968
Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu			
645	650	655	
ctg ctg gtg gtg gcc ctg ggg atc ggc ctc ttc atg cga agg cgc cac			2016
Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His			
660	665	670	
atc gtt cgg aag cgc acg ctg cgg agg ctg ctg cag gag agg gag ctt			2064
Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu			
675	680	685	
gtg gag cct ctt aca ccc agt gga gaa gct ccc aac caa gct ctc ttg			2112
Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu			
690	695	700	
agg atc ttg aag gaa act gaa ttc aaa aag atc aaa gtg ctg ggc tcc			2160
Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser			
705	710	715	720

ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc cca gaa ggt gag	2208
Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu	
725 730 735	
aaa gtt aaa att ccc gtc gct atc aag gaa tta aga gaa gca aca tct	2256
Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser	
740 745 750	
ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac gtg atg gcc agc	2304
Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser	
755 760 765	
gtg gac aac ccc cac gtg tgc cgc ctg ctg ggc atc tgc ctc acc tcc	2352
Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser	
770 775 780	
acc gtg cag ctc atc atg cag ctc atg ccc ttc ggc tgc ctc ctg gac	2400
Thr Val Gln Leu Ile Met Gln Leu Met Pro Phe Gly Cys Leu Leu Asp	
785 790 795 800	
tat gtc cgg gaa cac aaa gac aat att ggc tcc cag tac ctg ctc aac	2448
Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn	
805 810 815	
tgg tgt gtg cag atc gca aag ggc atg aac tac ttg gag gac cgt cgc	2496
Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg	
820 825 830	
ttg gtg cac cgc gac ctg gca gcc agg aac gta ctg gtg aaa aca ccg	2544
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro	
835 840 845	
cag cat gtc aag atc aca gat ttt ggg cgg gcc aaa ctg ctg ggt gcg	2592
Gln His Val Lys Ile Thr Asp Phe Gly Arg Ala Lys Leu Leu Gly Ala	
850 855 860	
gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg cct atc aag tgg	2640
Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp	

865	870	875	880	
atg gca ttg gaa tca att tta cac aga atc tat acc cac cag agt gat				2688
Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp				
	885	890	895	
gtc tgg agc tac ggg gtg acc gtt tgg gag ttg atg acc ttt gga tcc				2736
Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser				
	900	905	910	
aag cca tat gac gga atc cct gcc agc gag atc tcc tcc atc ctg gag				2784
Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu				
	915	920	925	
aaa gga gaa cgc ctc cct cag cca ccc ata tgt acc atc gat gtc tac				2832
Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr				
	930	935	940	
atg atc atg gtc aag tgc tgg atg ata gac gca gat agt cgc cca aag				2880
Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys				
945	950	955	960	
ttc cgt gag ttg atc atc gaa ttc tcc aaa atg gcc cga gac ccc cag				2928
Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln				
	965	970	975	
cgc tac ctt gtc att cag ggg gat gaa aga atg cat ttg cca agt cct				2976
Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro				
	980	985	990	
aca gac tcc aac ttc tac cgt gcc ctg atg gat gaa gaa gac atg gac				3024
Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp				
	995	1000	1005	
gac gtg gtg gat gcc gac gag tac ctc atc cca cag cag ggc ttc				3069
Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe				
1010	1015	1020		

ttc agc	agc ccc tcc acg tca	cgg act ccc ctc ctg	agc tct ctg	3114
Phe Ser	Ser Pro Ser Thr Ser	Arg Thr Pro Leu Leu	Ser Ser Leu	
1025	1030	1035		
agt gca	acc agc aac aat tcc	acc gtg gct tgc att	gat aga aat	3159
Ser Ala	Thr Ser Asn Asn Ser	Thr Val Ala Cys Ile	Asp Arg Asn	
1040	1045	1050		
ggg ctg	caa agc tgt ccc atc	aag gaa gac agc ttc	ttg cag cga	3204
Gly Leu	Gln Ser Cys Pro Ile	Lys Glu Asp Ser Phe	Leu Gln Arg	
1055	1060	1065		
tac agc	tca gac ccc aca ggc	gcc ttg act gag gac	agc ata gac	3249
Tyr Ser	Ser Asp Pro Thr Gly	Ala Leu Thr Glu Asp	Ser Ile Asp	
1070	1075	1080		
gac acc	ttc ctc cca gtg cct	gaa tac ata aac cag	tcc gtt ccc	3294
Asp Thr	Phe Leu Pro Val Pro	Glu Tyr Ile Asn Gln	Ser Val Pro	
1085	1090	1095		
aaa agg	ccc gct ggc tct gtg	cag aat cct gtc tat	cac aat cag	3339
Lys Arg	Pro Ala Gly Ser Val	Gln Asn Pro Val Tyr	His Asn Gln	
1100	1105	1110		
cct ctg	aac ccc gcg ccc agc	aga gac cca cac tac	cag gac ccc	3384
Pro Leu	Asn Pro Ala Pro Ser	Arg Asp Pro His Tyr	Gln Asp Pro	
1115	1120	1125		
cac agc	act gca gtg ggc aac	ccc gag tat ctc aac	act gtc cag	3429
His Ser	Thr Ala Val Gly Asn	Pro Glu Tyr Leu Asn	Thr Val Gln	
1130	1135	1140		
ccc acc	tgt gtc aac agc aca	ttc gac agc cct gcc	cac tgg gcc	3474
Pro Thr	Cys Val Asn Ser Thr	Phe Asp Ser Pro Ala	His Trp Ala	
1145	1150	1155		
cag aaa	ggc agc cac caa att	agc ctg gac aac cct	gac tac cag	3519
Gln Lys	Gly Ser His Gln Ile	Ser Leu Asp Asn Pro	Asp Tyr Gln	

1160	1165	1170	
cag gac ttc ttt ccc aag gaa gcc aag cca aat ggc atc ttt aag			3564
Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys			
1175	1180	1185	
ggc tcc aca gct gaa aat gca gaa tac cta agg gtc gcg cca caa			3609
Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln			
1190	1195	1200	
agc agt gaa ttt att gga gca tga			3633
Ser Ser Glu Phe Ile Gly Ala			
1205	1210		

 $\langle 400 \rangle$ 10

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly	Lys	Ser	Pro	Ser	Asp	Cys	Cys	His	Asn	Gln	Cys	Ala	Ala	Gly	Cys
225					230					235					240

Thr	Gly	Pro	Arg	Glu	Ser	Asp	Cys	Leu	Val	Cys	Arg	Lys	Phe	Arg	Asp
				245					250					255	

Glu	Ala	Thr	Cys	Lys	Asp	Thr	Cys	Pro	Pro	Leu	Met	Leu	Tyr	Asn	Pro
			260					265						270	

Thr	Thr	Tyr	Gln	Met	Asp	Val	Asn	Pro	Glu	Gly	Lys	Tyr	Ser	Phe	Gly
		275					280					285			

Ala	Thr	Cys	Val	Lys	Lys	Cys	Pro	Arg	Asn	Tyr	Val	Val	Thr	Asp	His
	290					295					300				

Gly	Ser	Cys	Val	Arg	Ala	Cys	Gly	Ala	Asp	Ser	Tyr	Glu	Met	Glu	Glu
305						310				315					320

Asp	Gly	Val	Arg	Lys	Cys	Lys	Lys	Cys	Glu	Gly	Pro	Cys	Arg	Lys	Val
				325					330					335	

Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn
			340					345						350	

Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp
		355						360				365			

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

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

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Met Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Arg Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Glu	Arg	Met	His	Leu	Pro	Ser	Pro
			980					985					990		

Thr	Asp	Ser	Asn	Phe	Tyr	Arg	Ala	Leu	Met	Asp	Glu	Glu	Asp	Met	Asp
		995					1000					1005			

Asp	Val	Val	Asp	Ala	Asp	Glu	Tyr	Leu	Ile	Pro	Gln	Gln	Gly	Phe
	1010					1015					1020			

Phe	Ser	Ser	Pro	Ser	Thr	Ser	Arg	Thr	Pro	Leu	Leu	Ser	Ser	Leu
	1025					1030					1035			

Ser	Ala	Thr	Ser	Asn	Asn	Ser	Thr	Val	Ala	Cys	Ile	Asp	Arg	Asn
	1040					1045					1050			

Gly	Leu	Gln	Ser	Cys	Pro	Ile	Lys	Glu	Asp	Ser	Phe	Leu	Gln	Arg
	1055					1060					1065			

Tyr	Ser	Ser	Asp	Pro	Thr	Gly	Ala	Leu	Thr	Glu	Asp	Ser	Ile	Asp
	1070					1075					1080			

Asp	Thr	Phe	Leu	Pro	Val	Pro	Glu	Tyr	Ile	Asn	Gln	Ser	Val	Pro
	1085					1090					1095			

Lys	Arg	Pro	Ala	Gly	Ser	Val	Gln	Asn	Pro	Val	Tyr	His	Asn	Gln
	1100					1105					1110			

Pro	Leu	Asn	Pro	Ala	Pro	Ser	Arg	Asp	Pro	His	Tyr	Gln	Asp	Pro
	1115					1120					1125			

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

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

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

Ser Ser Glu Phe Ile Gly Ala
1205 1210