

pctfr2009051343-seq1
SEQUENCE LISTING

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<130> FR2008-072 PCT

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<170> PatentIn version 3.3

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pctfr2009051343-seq1

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pctfr2009051343-seq1

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

pctfr2009051343-seq1

atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac acc att	1104
Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile	
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cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg acc tgc	1152
Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys	
370 375 380	
atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg cag tgg	1200
Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp	
385 390 395 400	
aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg gac	1248
Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp	
405 410 415	
aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc	1296
Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser	
420 425 430	
aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat gag ggc	1344
Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly	
435 440 445	
ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt aag	1392
Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys	
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tga	1395

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<400> 16

Met Asp Ser Arg Leu Asn Leu Val Phe Leu Val Leu Ile Leu Lys Gly
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Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Phe Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
50 55 60

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

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn
85 90 95

Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Tyr Asp Tyr Asp Asp Asp Tyr Tyr Ala Met Glu
Page 12

115

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

Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
145 150 155 160

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

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

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

Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
210 215 220

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

Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
245 250 255

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
260 265 270

Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
275 280 285

Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
290 295 300

Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
305 310 315 320

Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
325 330 335

Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
340 345 350

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

Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
370 375 380

Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp

gaa gag ctc gag act aac aag gcc aca ctg gtg tgt acg atc act gat 480
Glu Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp
Page 14

pctfr2009051343-seq1

145		150	155	160	
ttc tac cca ggt gtg gtg aca gtg gac tgg aag gta gat ggt acc cct					528
Phe Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro					
		165	170	175	
gtc act cag ggt atg gag aca acc cag cct tcc aaa cag agc aac aac					576
Val Thr Gln Gly Met Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn					
		180	185	190	
aag tac atg gct agc agc tac ctg acc ctg aca gca aga gca tgg gaa					624
Lys Tyr Met Ala Ser Ser Tyr Leu Thr Leu Thr Ala Arg Ala Trp Glu					
		195	200	205	
agg cat agc agt tac agc tgc cag gtc act cat gaa ggt cac act gtg					672
Arg His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val					
		210	215	220	
gag aag agt ttg tcc cgt gct gac tgt tcc tag					705
Glu Lys Ser Leu Ser Arg Ala Asp Cys Ser					
		225	230		

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<400> 18

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

Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu
 50 55 60

Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile
 85 90 95

Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp
 100 105 110

Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 115 120 125

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

Glu Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp
 145 150 155 160

pctfr2009051343-seq1

Phe Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro
165 170 175

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

Lys Tyr Met Ala Ser Ser Tyr Leu Thr Leu Thr Ala Arg Ala Trp Glu
195 200 205

Arg His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val
210 215 220

Glu Lys Ser Leu Ser Arg Ala Asp Cys Ser
225 230

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<212> DNA
<213> Mus sp.

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<221> CDS
<222> (1)..(420)

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gtc cag tgt gat gtg cag ctg gtg gag tct ggg gga ggc tta gtg cag 96
Val Gln Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
cct gga ggg tcc cgg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45
agt aac ttt gga atg cac tgg gtt cgt cag gct cca gag aag gga ctg 192
Ser Asn Phe Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
50 55 60
gag tgg gtc gca tac att agt agt ggc agt agt acc atc tac tat gca 240
Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala
65 70 75 80
gac aca gtg aag ggc cga ttc acc atc tcc aga gac aat ccc aag aac 288
Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn
85 90 95
acc ctg ttc ctg caa atg acc agt cta agg tct gag gac acg gcc atg 336
Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110
tat tac tgt gca aga tat gat tac gac gat gat tac tat gct atg gaa 384
Tyr Tyr Cys Ala Arg Tyr Asp Tyr Asp Asp Asp Tyr Tyr Ala Met Glu
115 120 125
tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 420
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135 140

pctfr2009051343-seq1

<210> 20
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 <213> Mus sp.

<400> 20

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

Val Gln Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
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Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Asn Phe Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
 50 55 60

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

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn
 85 90 95

Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Arg Tyr Asp Tyr Asp Asp Asp Tyr Tyr Ala Met Glu
 115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

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 <212> DNA
 <213> Mus sp.

<220>
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 <222> (29)..(412)

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 Met Ala Trp Ile Ser Leu Ile Leu
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tct ctc ctg gct ctc agc tca ggg gcc att tcc cag gct gtt gtg act 100
 Ser Leu Leu Ala Leu Ser Ser Gly Ala Ile Ser Gln Ala Val Val Thr
 10 15 20

cag gaa tct gca ctc acc aca tca cct ggt gaa aca gtc aca ctc act 148
 Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr
 25 30 35 40

pctfr2009051343-seq1

tgt cgc tca agt act ggg gct gtt aca act agt aac tat gcc aac tgg	196
Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn Trp	
45 50 55	
gtc caa gaa aaa cca gat cat tta ttc act ggt cta ata ggt ggt acc	244
Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly Gly Thr	
60 65 70	
aac aac cga gct cca ggt gtt cct gcc aga ttc tca ggc tcc ctg att	292
Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile	
75 80 85	
gga gac aag gct gcc ctc acc atc aca ggg gca cag act gag gat gag	340
Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu	
90 95 100	
gca ata tat ttc tgt gct cta tgg tac agc aac cat tgg gtg ttc ggt	388
Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly	
105 110 115 120	
gga gga acc aaa ctg act gtc cta	412
Gly Gly Thr Lys Leu Thr Val Leu	
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<400> 22

Met Ala Trp Ile Ser Leu Ile Leu Ser Leu Leu Ala Leu Ser Ser Gly
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Ala Ile Ser Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser
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Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val
 35 40 45

Thr Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu
 50 55 60

Phe Thr Gly Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro
 65 70 75 80

Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile
 85 90 95

Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp
 100 105 110

Tyr Ser Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 115 120 125

<210> 23
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 <213> Mus sp.

<400> 23

Asn Phe Gly Met His
1 5

<210> 24
<211> 17
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<400> 24

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Thr Val Lys
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Gly

<210> 25
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<400> 25

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1 5 10

<210> 26
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<213> Mus sp.

<400> 26

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 27
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<213> Mus sp.

<400> 27

Gly Thr Asn Asn Arg Ala Pro
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<210> 28
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<400> 28

Ala Leu Trp Tyr Ser Asn His Trp Val
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<210> 29
<211> 321

pctfr2009051343-seq1

<212> DNA
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<220>
 <223> Humanized sequence

<220>
 <221> CDS
 <222> (1)..(321)

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

caa tct gtg agc ctg tcc tgt cgg gca agc cag tct att tcc aat tat      96
Gln Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
                               20                               25          30

ctg cac tgg tat cag caa cac cca ggc gag agc cca cgg ctc ctg atc      144
Leu His Trp Tyr Gln Gln His Pro Gly Glu Ser Pro Arg Leu Leu Ile
                               35                               40          45

aaa tac gcc tct caa tcc att tct ggc tcc aac aga cgc ttc tct ggc      192
Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ser Asn Arg Arg Phe Ser Gly
                               50                               55          60

agc ggc tcc ggc acc gat ttc att ctc agc ttt aat agc gtt cag gca      240
Ser Gly Ser Gly Thr Asp Phe Ile Leu Ser Phe Asn Ser Val Gln Ala
65                               70                               75          80

gag gat ttt ggg atg tac ttc tgt caa cag agc aac tct tgg cct ttt      288
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                               85                               90          95

acc ttc gga agc ggg act aaa ctg acc gtt ctg      321
Thr Phe Gly Ser Gly Thr Lys Leu Thr Val Leu
                               100                              105

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<210> 30
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

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<400> 30
Gln Ser Ala Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
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Gln Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
                               20                               25          30

Leu His Trp Tyr Gln Gln His Pro Gly Glu Ser Pro Arg Leu Leu Ile
                               35                               40          45

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

Ser Gly Ser Gly Thr Asp Phe Ile Leu Ser Phe Asn Ser Val Gln Ala

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65

70

75

80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
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Thr Phe Gly Ser Gly Thr Lys Leu Thr Val Leu
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 <211> 321
 <212> DNA
 <213> Artificial

<220>
 <223> Humanized sequence

<220>
 <221> CDS
 <222> (1)..(321)

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 1 5 10 15

caa tcc gtg agc ctc agc tgt agg gca tcc cag tcc att agc aac tat 96
 Gln Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
 20 25 30

ctc cac tgg tac cag cag cac cca gga gaa agc cct cgc ctg ctg ata 144
 Leu His Trp Tyr Gln Gln His Pro Gly Glu Ser Pro Arg Leu Leu Ile
 35 40 45

aaa tac gca agc cag tct att agc ggc agc aac cgg cgc ttc agc ggg 192
 Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ser Asn Arg Arg Phe Ser Gly
 50 55 60

tcc ggc tcc ggg aca gac ttt atc ctg tct ttt agc agc gtg caa gcc 240
 Ser Gly Ser Gly Thr Asp Phe Ile Leu Ser Phe Ser Ser Val Gln Ala
 65 70 75 80

gaa gac ttt ggc atg tac ttc tgc cag cag tct aac aat tgg cca ttc 288
 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Asn Trp Pro Phe
 85 90 95

acc ttc gga tcc ggc aca aag ctg acc gtg ctg 321
 Thr Phe Gly Ser Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 32
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 <212> PRT
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 <223> Synthetic Construct

<400> 32

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

pctfr2009051343-seq1

Gln Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
20 25 30

Leu His Trp Tyr Gln Gln His Pro Gly Glu Ser Pro Arg Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Asn Trp Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Thr Val Leu
100 105

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<211> 342
<212> DNA
<213> Artificial

<220>
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<220>
<221> CDS
<222> (1)..(342)

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acc ctg tcc ctc acc tgt tct ttc tcc ggc ttt agc ctg agc aca agc	96
Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser	
20 25 30	
gga atg ggc gtc agc tgg atc aga caa cca ccc ggc aag ggc ctg gag	144
Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg ctg gcc cac atc tat tgg gat gat gat aag agg tat aac cct tcc	192
Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser	
50 55 60	
ctg aaa tcc aga ctc aca att tcc aag gac acc tcc agc aac cag gtc	240
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val	
65 70 75 80	
ttc ctg aag ata acc tct gtt gat cca gtg gac acc gca act tac tac	288
Phe Leu Lys Ile Thr Ser Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr	
85 90 95	
tgc gcc cgc gac tac tat gcc agc tct ttt gac tac tgg ggg cag ggc	336
Cys Ala Arg Asp Tyr Tyr Ala Ser Ser Phe Asp Tyr Trp Gly Gln Gly	
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aca ctc	342
Thr Leu	

<210> 34
 <211> 114
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 34

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
 50 55 60

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

Phe Leu Lys Ile Thr Ser Val Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

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

Thr Leu

<210> 35
 <211> 342
 <212> DNA
 <213> Artificial

<220>
 <223> Humanized sequence

<220>
 <221> CDS
 <222> (1)..(342)

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

aca ctc agc ctg acc tgc tcc ttc agc ggc ttc tct ctg agc act tcc 96
 Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

gga ctc gga gtg agc tgg att cgc caa cct cct ggg aaa ggc ctg gag 144
 Page 23

pctfr2009051343-seq1

Gly	Leu	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu		
		35					40					45					
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Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	Tyr	Asn	Pro	Ser		
		50				55					60						
ctg	aag	tcc	aga	ctc	aca	atc	tcc	aaa	gat	aca	tcc	agc	aat	cag	gtg		240
Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Ser	Asn	Gln	Val		
		65			70					75					80		
ttt	ctg	aag	atc	acc	tcc	gtc	gat	cca	gtc	gac	acc	gcc	act	tac	tat		288
Phe	Leu	Lys	Ile	Thr	Ser	Val	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr		
				85					90					95			
tgt	gct	cgc	gat	tac	tat	gcc	agc	tcc	ttc	gac	tac	tgg	gga	cag	gga		336
Cys	Ala	Arg	Asp	Tyr	Tyr	Ala	Ser	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly		
			100					105					110				
aca	ctg																342
Thr	Leu																

<210> 36
 <211> 114
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 36

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

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

Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	Tyr	Asn	Pro	Ser		
		50				55					60						

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

Phe	Leu	Lys	Ile	Thr	Ser	Val	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr		
				85					90					95			

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

Thr Leu

<210> 37
 <211> 342

pctfr2009051343-seq1

<212> DNA
 <213> Artificial

<220>
 <223> Humanized sequence

<220>
 <221> CDS
 <222> (1)..(342)

<400> 37
 cag gtc aca ctc aaa gaa tct gga cca aca ctc gtt aaa cca act caa 48
 Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
 1 5 10 15
 aca ctc agc ctg act tgc agc ttt tct ggc ttc agc ctc tcc act agc 96
 Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 ggc ctc ggc gtg tcc tgg atc cgg cag ccc cct gga aaa ggc ctg gag 144
 Gly Leu Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg ctg gcc cac atc tat tgg gac gat gac aag cgg tac aat cca agc 192
 Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
 50 55 60
 ctg aaa tct cgg ctg acc ata tct aag gat act tct tcc aat cag gtg 240
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Gln Val
 65 70 75 80
 ttc ctg aag atc aca tct gtg gct cct gtc gac act gcc act tat tat 288
 Phe Leu Lys Ile Thr Ser Val Ala Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 tgc gca agg gat tac tac gca tcc tcc ttc gat tac tgg ggc cag gga 336
 Cys Ala Arg Asp Tyr Tyr Ala Ser Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 act ctg 342
 Thr Leu

<210> 38
 <211> 114
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 38
 Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Leu Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser

50

55

60

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

Phe Leu Lys Ile Thr Ser Val Ala Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

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

Thr Leu

<210> 39
<211> 1059
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1059)

<400> 39	ctg gag gcc tct gag gaa gtg gag ctt gag ccc tgc ctg gct ccc agc	48
	Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro Cys Leu Ala Pro Ser	
	1 5 10 15	
	ctg gag cag caa gag cag gag ctg aca gta gcc ctt ggg cag cct gtg	96
	Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala Leu Gly Gln Pro Val	
	20 25 30	
	cgg ctg tgc tgt ggg cgg gct gag cgt ggt ggc cac tgg tac aag gag	144
	Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly His Trp Tyr Lys Glu	
	35 40 45	
	ggc agt cgc ctg gca cct gct ggc cgt gta cgg ggc tgg agg ggc cgc	192
	Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg Gly Trp Arg Gly Arg	
	50 55 60	
	cta gag att gcc agc ttc cta cct gag gat gct ggc cgc tac ctc tgc	240
	Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys	
	65 70 75 80	
	ctg gca cga ggc tcc atg atc gtc ctg cag aat ctc acc ttg att aca	288
	Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn Leu Thr Leu Ile Thr	
	85 90 95	
	ggt gac tcc ttg acc tcc agc aac gat gat gag gac ccc aag tcc cat	336
	Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu Asp Pro Lys Ser His	
	100 105 110	
	agg gac ctc tcg aat agg cac agt tac ccc cag caa gca ccc tac tgg	384
	Arg Asp Leu Ser Asn Arg His Ser Tyr Pro Gln Gln Ala Pro Tyr Trp	
	115 120 125	
	aca cac ccc cag cgc atg gag aag aaa ctg cat gca gta cct gcg ggg	432
	Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly	
	130 135 140	
	aac acc gtc aag ttc cgc tgt cca gct gca ggc aac ccc acg ccc acc	480
	Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Thr Pro Thr	

pctfr2009051343-seq1

145		150		155		160										
atc	cgc	tgg	ctt	aag	gat	gga	cag	gcc	ttt	cat	ggg	gag	aac	cgc	att	528
Ile	Arg	Trp	Leu	Lys	Asp	Gly	Gln	Ala	Phe	His	Gly	Glu	Asn	Arg	Ile	
				165					170					175		
gga	ggc	att	cgg	ctg	cgc	cat	cag	cac	tgg	agt	ctc	gtg	atg	gag	agc	576
Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	Leu	Val	Met	Glu	Ser	
			180					185					190			
gtg	gtg	ccc	tcg	gac	cgc	ggc	aca	tac	acc	tgc	ctg	gta	gag	aac	gct	624
Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	Leu	Val	Glu	Asn	Ala	
		195					200					205				
gtg	ggc	agc	atc	cgt	tat	aac	tac	ctg	cta	gat	gtg	ctg	gag	cgg	tcc	672
Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	Val	Leu	Glu	Arg	Ser	
	210					215					220					
ccg	cac	cgg	ccc	atc	ctg	cag	gcc	ggg	ctc	ccg	gcc	aac	acc	aca	gcc	720
Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Thr	Thr	Ala	
225					230					235					240	
gtg	gtg	ggc	agc	gac	gtg	gag	ctg	ctg	tgc	aag	gtg	tac	agc	gat	gcc	768
Val	Val	Gly	Ser	Asp	Val	Glu	Leu	Leu	Cys	Lys	Val	Tyr	Ser	Asp	Ala	
				245					250					255		
cag	ccc	cac	atc	cag	tgg	ctg	aag	cac	atc	gtc	atc	aac	ggc	agc	agc	816
Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Val	Ile	Asn	Gly	Ser	Ser	
			260					265					270			
ttc	gga	gcc	gac	ggc	ttc	ccc	tat	gtg	caa	gtc	cta	aag	act	gca	gac	864
Phe	Gly	Ala	Asp	Gly	Phe	Pro	Tyr	Val	Gln	Val	Leu	Lys	Thr	Ala	Asp	
	275						280					285				
atc	aat	agc	tca	gag	gtg	gag	gtc	ctg	tac	ctg	cgg	aac	gtg	tca	gcc	912
Ile	Asn	Ser	Ser	Glu	Val	Glu	Val	Leu	Tyr	Leu	Arg	Asn	Val	Ser	Ala	
	290					295					300					
gag	gac	gca	ggc	gag	tac	acc	tgc	ctc	gca	ggc	aat	tcc	atc	ggc	ctc	960
Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn	Ser	Ile	Gly	Leu	
305					310					315					320	
tcc	tac	cag	tct	gcc	tgg	ctc	acg	gtg	ctg	cca	gag	gag	gac	ccc	aca	1008
Ser	Tyr	Gln	Ser	Ala	Trp	Leu	Thr	Val	Leu	Pro	Glu	Glu	Asp	Pro	Thr	
				325					330					335		
tgg	acc	gca	gca	gcg	ccc	gag	gcc	gct	agc	cat	cac	cat	cat	cat	cac	1056
Trp	Thr	Ala	Ala	Ala	Pro	Glu	Ala	Ala	Ser	His	His	His	His	His	His	
			340					345					350			
tga																1059

<210> 40
 <211> 352
 <212> PRT
 <213> Homo sapiens

<400> 40

Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro Cys Leu Ala Pro Ser
1 5 10 15

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

pctfr2009051343-seq1

Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly His Trp Tyr Lys Glu
35 40 45

Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
50 55 60

Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys
65 70 75 80

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

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

Arg Asp Leu Ser Asn Arg His Ser Tyr Pro Gln Gln Ala Pro Tyr Trp
115 120 125

Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly
130 135 140

Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Thr Pro Thr
145 150 155 160

Ile Arg Trp Leu Lys Asp Gly Gln Ala Phe His Gly Glu Asn Arg Ile
165 170 175

Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser
180 185 190

Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn Ala
195 200 205

Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp Val Leu Glu Arg Ser
210 215 220

Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Thr Thr Ala
225 230 235 240

Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys Val Tyr Ser Asp Ala
245 250 255

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

Phe Gly Ala Asp Gly Phe Pro Tyr Val Gln Val Leu Lys Thr Ala Asp
275 280 285

Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu Arg Asn Val Ser Ala
290 295 300

pctfr2009051343-seq1

Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu
305 310 315 320

Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp Pro Thr
325 330 335

Trp Thr Ala Ala Ala Pro Glu Ala Ala Ser His His His His His His
340 345 350

<210> 41
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(726)

<400> 41	
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Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro Cys Gln Ala Pro Tyr	
1 5 10 15	
tgg aca cac ccc cag cgc atg gag aag aaa ctg cat gca gta cct gcg	96
Trp Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala	
20 25 30	
ggg aac acc gtc aag ttc cgc tgt cca gct gca ggc aac ccc acg ccc	144
Gly Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Thr Pro	
35 40 45	
acc atc cgc tgg ctt aag gat gga cag gcc ttt cat ggg gag aac cgc	192
Thr Ile Arg Trp Leu Lys Asp Gly Gln Ala Phe His Gly Glu Asn Arg	
50 55 60	
att gga ggc att cgg ctg cgc cat cag cac tgg agt ctc gtg atg gag	240
Ile Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu	
65 70 75 80	
agc gtg gtg ccc tcg gac cgc ggc aca tac acc tgc ctg gta gag aac	288
Ser Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn	
85 90 95	
gct gtg ggc agc atc cgt tat aac tac ctg cta gat gtg ctg gag cgg	336
Ala Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp Val Leu Glu Arg	
100 105 110	
tcc ccg cac cgg ccc atc ctg cag gcc ggg ctc ccg gcc aac acc aca	384
Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Thr Thr	
115 120 125	
gcc gtg gtg ggc agc gac gtg gag ctg ctg tgc aag gtg tac agc gat	432
Ala Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys Val Tyr Ser Asp	
130 135 140	
gcc cag ccc cac atc cag tgg ctg aag cac atc gtc atc aac ggc agc	480
Ala Gln Pro His Ile Gln Trp Leu Lys His Ile Val Ile Asn Gly Ser	
145 150 155 160	
agc ttc gga gcc gac ggt ttc ccc tat gtg caa gtc cta aag act gca	528
Ser Phe Gly Ala Asp Gly Phe Pro Tyr Val Gln Val Leu Lys Thr Ala	
165 170 175	
gac atc aat agc tca gag gtg gag gtc ctg tac ctg cgg aac gtg tca	576

pctfr2009051343-seq1

Asp	Ile	Asn	Ser	Ser	Glu	Val	Glu	Val	Leu	Tyr	Leu	Arg	Asn	Val	Ser		
		180					185						190				
gcc	gag	gac	gca	ggc	gag	tac	acc	tgc	ctc	gca	ggc	aat	tcc	atc	ggc		624
Ala	Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn	Ser	Ile	Gly		
		195					200					205					
ctc	tcc	tac	cag	tct	gcc	tgg	ctc	acg	gtg	ctg	cca	gag	gag	gac	ccc		672
Leu	Ser	Tyr	Gln	Ser	Ala	Trp	Leu	Thr	Val	Leu	Pro	Glu	Glu	Asp	Pro		
	210					215					220						
aca	tgg	acc	gca	gca	gcg	ccc	gag	gcc	gct	agc	cat	cac	cat	cat	cat		720
Thr	Trp	Thr	Ala	Ala	Ala	Pro	Glu	Ala	Ala	Ser	His	His	His	His	His		
	225				230					235					240		
cac	tga																726
His																	

<210> 42
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 42

Leu	Glu	Ala	Ser	Glu	Glu	Val	Glu	Leu	Glu	Pro	Cys	Gln	Ala	Pro	Tyr		
1				5					10					15			
Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	Ala	Val	Pro	Ala		
			20					25					30				
Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	Asn	Pro	Thr	Pro		
	35						40					45					
Thr	Ile	Arg	Trp	Leu	Lys	Asp	Gly	Gln	Ala	Phe	His	Gly	Glu	Asn	Arg		
	50					55					60						
Ile	Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	Leu	Val	Met	Glu		
	65				70				75					80			
Ser	Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	Leu	Val	Glu	Asn		
				85					90					95			
Ala	Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	Val	Leu	Glu	Arg		
			100					105					110				
Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Thr	Thr		
		115					120					125					
Ala	Val	Val	Gly	Ser	Asp	Val	Glu	Leu	Leu	Cys	Lys	Val	Tyr	Ser	Asp		
	130					135					140						
Ala	Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Val	Ile	Asn	Gly	Ser		
	145				150					155				160			
Ser	Phe	Gly	Ala	Asp	Gly	Phe	Pro	Tyr	Val	Gln	Val	Leu	Lys	Thr	Ala		

pctfr2009051343-seq1

165

170

175

Asp Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu Arg Asn Val Ser
 180 185 190

Ala Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly
 195 200 205

Leu Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp Pro
 210 215 220

Thr Trp Thr Ala Ala Ala Pro Glu Ala Ala Ser His His His His His
 225 230 235 240

His

<210> 43
 <211> 1059
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(1059)

<400> 43
 ctt gag gcc tct gag gaa atg gag cag gag ccc tgc cta gcc cca atc 48
 Leu Glu Ala Ser Glu Glu Met Glu Gln Glu Pro Cys Leu Ala Pro Ile
 1 5 10 15
 ctg gag cag caa gag cag gtg ttg acg gtg gcc ctg ggg cag cct gtg 96
 Leu Glu Gln Gln Glu Gln Val Leu Thr Val Ala Leu Gly Gln Pro Val
 20 25 30
 agg ctg tgc tgt ggg cgc acc gag cgt ggt cgt cac tgg tac aaa gag 144
 Arg Leu Cys Cys Gly Arg Thr Glu Arg Gly Arg His Trp Tyr Lys Glu
 35 40 45
 ggc agc cgc cta gca tct gct ggg cga gta cgg ggt tgg aga ggc cgc 192
 Gly Ser Arg Leu Ala Ser Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
 50 55 60
 ctg gag atc gcc agc ttc ctt cct gag gat gct ggc cga tac ctc tgc 240
 Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys
 65 70 75 80
 ctg gcc cgt ggc tcc atg acc gtc gta cac aat ctt acg ttg ctt atg 288
 Leu Ala Arg Gly Ser Met Thr Val Val His Asn Leu Thr Leu Leu Met
 85 90 95
 gat gac tcc tta acc tcc atc agt aat gat gaa gac ccc aag aca ctc 336
 Asp Asp Ser Leu Thr Ser Ile Ser Asn Asp Glu Asp Pro Lys Thr Leu
 100 105 110
 agc agc tcc tcg agt ggt cat gtc tac cca cag caa gca ccc tac tgg 384
 Ser Ser Ser Ser Ser Gly His Val Tyr Pro Gln Gln Ala Pro Tyr Trp
 115 120 125
 aca cac ccc caa cgc atg gag aag aaa ctg cat gca gtg cct gcc ggg 432
 Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly

pctfr2009051343-seq1

130	135	140	
aat act gtc aaa ttc cgc tgt cca gct gca ggg aac ccc atg cct acc			480
Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Met Pro Thr			
145	150	155	160
atc cac tgg ctc aag gat gga cag gcc ttc cac ggg gag aat cgt att			528
Ile His Trp Leu Lys Asp Gly Gln Ala Phe His Gly Glu Asn Arg Ile			
	165	170	175
gga ggc att cgg ctg cgc cac caa cac tgg agc ctg gtg atg gaa agt			576
Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser			
	180	185	190
gtg gta ccc tcg gac cgt ggc aca tac aca tgc ctt gtg gag aac tct			624
Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn Ser			
	195	200	205
ctg ggt agc att cgc tac agc tat ctc ctg gat gtg ctg gag cgg tcc			672
Leu Gly Ser Ile Arg Tyr Ser Tyr Leu Leu Asp Val Leu Glu Arg Ser			
	210	215	220
ccg cac cgg ccc atc ctg cag gcg ggg ctc cca gcc aac acc aca gct			720
Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Thr Thr Ala			
	225	230	240
gtg gtg ggc agc gac gtg gag cta ctc tgc aag gtg tac agc gac gcc			768
Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys Val Tyr Ser Asp Ala			
	245	250	255
cag ccc cac ata cag tgg ctg aaa cac gtc gtc atc aac ggc agc agc			816
Gln Pro His Ile Gln Trp Leu Lys His Val Val Ile Asn Gly Ser Ser			
	260	265	270
ttc ggc gcc gac ggt ttc ccc tac gta caa gtc ctg aag aca aca gac			864
Phe Gly Ala Asp Gly Phe Pro Tyr Val Gln Val Leu Lys Thr Thr Asp			
	275	280	285
atc aat agc tcg gag gta gag gtc ttg tat ctg agg aac gtg tcc gct			912
Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu Arg Asn Val Ser Ala			
	290	295	300
gag gat gca gga gag tat acc tgt ctg gcg ggc aac tcc atc ggc ctt			960
Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu			
	305	310	315
tcc tac cag tca gcg tgg ctc acg gtg ctg cca gag gaa gac ctc acg			1008
Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp Leu Thr			
	325	330	335
tgg aca aca gca acc cct gag gcc gct agc cat cac cat cat cat cac			1056
Trp Thr Thr Ala Thr Pro Glu Ala Ala Ser His His His His His His			
	340	345	350
tga			1059
<210> 44			
<211> 352			
<212> PRT			
<213> Mus sp.			
<400> 44			
Leu Glu Ala Ser Glu Glu Met Glu Gln Glu Pro Cys Leu Ala Pro Ile			
1	5	10	15

pctfr2009051343-seq1

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

Arg Leu Cys Cys Gly Arg Thr Glu Arg Gly Arg His Trp Tyr Lys Glu
 35 40 45

Gly Ser Arg Leu Ala Ser Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
 50 55 60

Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys
 65 70 75 80

Leu Ala Arg Gly Ser Met Thr Val Val His Asn Leu Thr Leu Leu Met
 85 90 95

Asp Asp Ser Leu Thr Ser Ile Ser Asn Asp Glu Asp Pro Lys Thr Leu
 100 105 110

Ser Ser Ser Ser Ser Gly His Val Tyr Pro Gln Gln Ala Pro Tyr Trp
 115 120 125

Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly
 130 135 140

Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Met Pro Thr
 145 150 155 160

Ile His Trp Leu Lys Asp Gly Gln Ala Phe His Gly Glu Asn Arg Ile
 165 170 175

Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser
 180 185 190

Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn Ser
 195 200 205

Leu Gly Ser Ile Arg Tyr Ser Tyr Leu Leu Asp Val Leu Glu Arg Ser
 210 215 220

Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Thr Thr Ala
 225 230 235 240

Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys Val Tyr Ser Asp Ala
 245 250 255

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

Phe Gly Ala Asp Gly Phe Pro Tyr Val Gln Val Leu Lys Thr Thr Asp
 275 280 285

pctfr2009051343-seq1

Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu Arg Asn Val Ser Ala
290 295 300

Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu
305 310 315 320

Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp Leu Thr
325 330 335

Trp Thr Thr Ala Thr Pro Glu Ala Ala Ser His His His His His His
340 345 350

<210> 45
<211> 1773
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1773)

<400> 45	
agg ccg tcc ccg acc ttg cct gaa caa gcc cag ccc tgg gga gcc cct	48
Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln Pro Trp Gly Ala Pro	
1 5 10 15	
gtg gaa gtg gag tcc ttc ctg gtc cac ccc ggt gac ctg ctg cag ctt	96
Val Glu Val Glu Ser Phe Leu Val His Pro Gly Asp Leu Leu Gln Leu	
20 25 30	
cgc tgt cgg ctg cgg gac gat gtg cag agc atc aac tgg ctg cgg gac	144
Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile Asn Trp Leu Arg Asp	
35 40 45	
ggg gtg cag ctg gcg gaa agc aac cgc acc cgc atc aca ggg gag gag	192
Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg Ile Thr Gly Glu Glu	
50 55 60	
gtg gag gtg cag gac tcc gtg ccc gca gac tcc ggc ctc tat gct tgc	240
Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser Gly Leu Tyr Ala Cys	
65 70 75 80	
gta acc agc agc ccc tcg ggc agt gac acc acc tac ttc tcc gtc aat	288
Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr Tyr Phe Ser Val Asn	
85 90 95	
gtt tca gat gct ctc ccc tcc tcg gag gat gat gat gat gat gat gac	336
Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Asp Asp	
100 105 110	
tcc tct tca gag gag aaa gaa aca gat aac acc aaa cca aac cgt atg	384
Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Arg Met	
115 120 125	
ccc gta gct cca tat tgg aca tcc cca gaa aag atg gaa aag aaa ttg	432
Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys Met Glu Lys Lys Leu	
130 135 140	
cat gca gtg ccg gct gcc aag aca gtg aag ttc aaa tgc cct tcc agt	480
His Ala Val Pro Ala Ala Lys Thr Val Lys Phe Lys Cys Pro Ser Ser	
145 150 155 160	
ggg acc cca aac ccc aca ctg cgc tgg ttg aaa aat ggc aaa gaa ttc	528

pctfr2009051343-seq1

Gly	Thr	Pro	Asn	Pro 165	Thr	Leu	Arg	Trp	Leu 170	Lys	Asn	Gly	Lys	Glu 175	Phe	
aaa Lys	cct Pro	gac Asp	cac His 180	aga Arg	att Ile	gga Gly	ggc Gly	tac Tyr 185	aag Lys	gtc Val	cgt Arg	tat Tyr	gcc Ala 190	acc Thr	tgg Trp	576
agc Ser	atc Ile	ata Ile 195	atg Met	gac Asp	tct Ser	gtg Val	gtg Val 200	ccc Pro	tct Ser	gac Asp	aag Lys	ggc Gly 205	aac Asn	tac Tyr	acc Thr	624
tgc Cys	att Ile 210	gtg Val	gag Glu	aat Asn	gag Glu	tac Tyr 215	ggc Gly	agc Ser	atc Ile	aac Asn	cac His 220	aca Thr	tac Tyr	cag Gln	ctg Leu	672
gat Asp 225	gtc Val	gtg Val	gag Glu	cgg Arg	tcc Ser 230	cct Pro	cac His	cgg Arg	ccc Pro	atc Ile 235	ctg Leu	caa Gln	gca Ala	ggg Gly	ttg Leu 240	720
ccc Pro	gcc Ala	aac Asn	aaa Lys	aca Thr 245	gtg Val	gcc Ala	ctg Leu	ggt Gly	agc Ser 250	aac Asn	gtg Val	gag Glu	ttc Phe	atg Met 255	tgt Cys	768
aag Lys	gtg Val	tac Tyr	agt Ser 260	gac Asp	ccg Pro	cag Gln	ccg Pro	cac His 265	atc Ile	cag Gln	tgg Trp	cta Leu	aag Lys 270	cac His	atc Ile	816
gag Glu	gtg Val	aat Asn 275	ggg Gly	agc Ser	aag Lys	att Ile	ggc Gly 280	cca Pro	gac Asp	aac Asn	ctg Leu	cct Pro 285	tat Tyr	gtc Val	cag Gln	864
atc Ile 290	ttg Leu	aag Lys	act Thr	gct Ala	gga Gly	gtt Val 295	aat Asn	acc Thr	acc Thr	gac Asp	aaa Lys 300	gag Glu	atg Met	gag Glu	gtg Val	912
ctt Leu 305	cac His	tta Leu	aga Arg	aat Asn	gtc Val 310	tcc Ser	ttt Phe	gag Glu	gac Asp	gca Ala 315	ggg Gly	gag Glu	tat Tyr	acg Thr	tgc Cys 320	960
ttg Leu	gcg Ala	ggt Gly	aac Asn	tct Ser 325	atc Ile	gga Gly	ctc Leu	tcc Ser	cat His 330	cac His	tct Ser	gca Ala	tgg Trp	ttg Leu 335	acc Thr	1008
gtt Val	ctg Leu	gaa Glu	gcc Ala 340	ctg Leu	gaa Glu	gag Glu	agg Arg	ccg Pro 345	gca Ala	gtg Val	atg Met	acc Thr	tcg Ser 350	ccc Pro	ctg Leu	1056
tac Tyr	ctg Leu	gag Glu 355	ata Ile	gcg Ala	cta Leu	gag Glu	ccc Pro 360	aaa Lys	tct Ser	tgt Cys	gac Asp	aaa Lys 365	act Thr	cac His	aca Thr	1104
tgc Cys	cca Pro 370	ccg Pro	tgc Cys	cca Pro	gca Ala	cct Pro 375	gaa Glu	ctc Leu	ctg Leu	ggg Gly	gga Gly 380	ccg Pro	tca Ser	gtc Val	ttc Phe	1152
ctc Leu 385	ttc Phe	ccc Pro	cca Pro	aaa Lys	ccc Pro 390	aag Lys	gac Asp	acc Thr	ctc Leu	atg Met 395	atc Ile	tcc Ser	cgg Arg	acc Thr	cct Pro 400	1200
gag Glu	gtc Val	aca Thr	tgc Cys	gtg Val 405	gtg Val	gtg Val	gac Asp	gtg Val	agc Ser 410	cac His	gaa Glu	gac Asp	cct Pro	gag Glu 415	gtc Val	1248
aag Lys	ttc Phe	aac Asn	tgg Trp 420	tac Tyr	gtg Val	gac Asp	ggc Gly	gtg Val 425	gag Glu	gtg Val	cat His	aat Asn	gcc Ala 430	aag Lys	aca Thr	1296
aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	1344

pctfr2009051343-seq1

Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val		
		435					440					445					
ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	1392	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys		
		450				455					460						
aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	1440	
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser		
		465			470					475					480		
aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	1488	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro		
				485					490					495			
tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	1536	
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val		
			500					505					510				
aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	1584	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly		
		515					520					525					
cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	1632	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp		
		530				535					540						
ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	1680	
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp		
				550						555					560		
cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	1728	
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
				565					570					575			
aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	tga		1773	
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys				
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<210> 46
 <211> 590
 <212> PRT
 <213> Homo sapiens

<400> 46

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Val	Glu	Val	Glu	Ser	Phe	Leu	Val	His	Pro	Gly	Asp	Leu	Leu	Gln	Leu
			20					25					30		
Arg	Cys	Arg	Leu	Arg	Asp	Asp	Val	Gln	Ser	Ile	Asn	Trp	Leu	Arg	Asp
		35					40					45			
Gly	Val	Gln	Leu	Ala	Glu	Ser	Asn	Arg	Thr	Arg	Ile	Thr	Gly	Glu	Glu
	50					55					60				
Val	Glu	Val	Gln	Asp	Ser	Val	Pro	Ala	Asp	Ser	Gly	Leu	Tyr	Ala	Cys
65					70					75					80
Val	Thr	Ser	Ser	Pro	Ser	Gly	Ser	Asp	Thr	Thr	Tyr	Phe	Ser	Val	Asn

Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Asp Asp
 100 105 110
 Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Arg Met
 115 120 125
 Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys Met Glu Lys Lys Leu
 130 135 140
 His Ala Val Pro Ala Ala Lys Thr Val Lys Phe Lys Cys Pro Ser Ser
 145 150 155 160
 Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys Asn Gly Lys Glu Phe
 165 170 175
 Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val Arg Tyr Ala Thr Trp
 180 185 190
 Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr
 195 200 205
 Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr Gln Leu
 210 215 220
 Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu
 225 230 235 240
 Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn Val Glu Phe Met Cys
 245 250 255
 Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln Trp Leu Lys His Ile
 260 265 270
 Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn Leu Pro Tyr Val Gln
 275 280 285
 Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp Lys Glu Met Glu Val
 290 295 300
 Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala Gly Glu Tyr Thr Cys
 305 310 315 320
 Leu Ala Gly Asn Ser Ile Gly Leu Ser His His Ser Ala Trp Leu Thr
 325 330 335
 Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val Met Thr Ser Pro Leu
 340 345 350
 Tyr Leu Glu Ile Ala Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr

355

pctfr2009051343-seq1
360 365

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
370 375 380

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
385 390 395 400

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
405 410 415

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
420 425 430

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
435 440 445

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
450 455 460

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
465 470 475 480

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
485 490 495

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
500 505 510

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
515 520 525

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
530 535 540

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
545 550 555 560

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585 590

<210> 47
<211> 1773
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1773)

pctfr2009051343-seq1

<400> 47
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 Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
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cca cca acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gca 96
 Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

cca ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg 144
 Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val
 35 40 45

atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac aat agg aca 192
 Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr
 50 55 60

gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg cct aga gac 240
 Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp
 65 70 75 80

tcc ggc ctc tat gct tgt act gcc agt agg act gta gac agt gaa act 288
 Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr
 85 90 95

tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc gga gat gat 336
 Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

gag gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac 384
 Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

aac aag aga gca cca tac tgg acc aac aca gaa aag atg gaa aag cgg 432
 Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc tgc cca gcc 480
 Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac ggg aag gag 528
 Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

ttt aag cag gag cat cgc att gga ggc tac aag gta cga aac cag cac 576
 Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag gga aat tat 624
 Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
 195 200 205

acc tgt gtg gtg gag aat gaa tac ggg tcc atc aat cac acg tac cac 672
 Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
 210 215 220

ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc caa gcc gga 720
 Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
 225 230 235 240

ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta gag ttt gtc 768
 Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
 245 250 255

tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg atc aag cac 816
 Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His

pctfr2009051343-seq1

260	265	270	
gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg ccc tac ctc Val Glu Lys Asn Gly Ser Lys Tyr 280 Gly Pro Asp Gly Leu 285 Pro Tyr Leu			864
aag gtt ctc aag gcc gcc ggt gtt aac acc acg gac aaa gag att gag Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu			912
gtt ctc tat att cgg aat gta act ttt gag gac gct ggg gaa tat acg Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr			960
tgc ttg gcg ggt aat tct att ggg ata tcc ttt cac tct gca tgg ttg Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu			1008
aca gtt ctg cca gcg cct gga aga gaa aag gag att aca gct tcc cca Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro			1056
gac tac ctg tca gcg cta gag ccc aaa tct tgt gac aaa act cac aca Asp Tyr Leu Ser Ala Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr			1104
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc Cys Pro Pro Cys Pro Ala Pro 375 Glu Leu Leu Gly 380 Pro Ser Val Phe			1152
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct Leu Phe Pro Pro Lys Pro 390 Lys Asp Thr Met Ile Ser Arg Thr Pro			1200
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val			1248
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca Lys Phe Asn Trp Tyr Val Asp Gly Val 425 Glu Val His Asn Ala Lys Thr			1296
aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val			1344
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys			1392
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc Lys Val Ser Asn Lys Ala 470 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser			1440
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro			1488
tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val			1536
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly			1584
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp			1632

pctfr2009051343-seq1

530	535	540	
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg			1680
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp			
545	550	555	560
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac			1728
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His			
	565	570	575
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga			1773
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
	580	585	590

<210> 48
 <211> 590
 <212> PRT
 <213> Homo sapiens

<400> 48

Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
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Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
 20 25 30

Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val
 35 40 45

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

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

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

Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
 100 105 110

Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
 115 120 125

Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
 130 135 140

Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
 145 150 155 160

Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
 165 170 175

Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
 180 185 190

pctfr2009051343-seq1

Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
195 200 205

Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
210 215 220

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

Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
245 250 255

Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
260 265 270

Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu
275 280 285

Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
290 295 300

Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305 310 315 320

Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
325 330 335

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

Asp Tyr Leu Ser Ala Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr
355 360 365

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
370 375 380

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
385 390 395 400

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
405 410 415

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
420 425 430

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
435 440 445

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
450 455 460

pctfr2009051343-seq1

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
465 470 475 480

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
485 490 495

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
500 505 510

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
515 520 525

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
530 535 540

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
545 550 555 560

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
565 570 575

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585 590

<210> 49
<211> 2403
<212> DNA
<213> Rattus sp.

<220>
<221> CDS
<222> (1)..(2403)

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ttc tcc ctt gag gcc tct gag gaa atg gaa cag gag ccc tgc cca gcc	96
Phe Ser Leu 20 Glu Ala Ser Glu Glu Met 25 Glu Gln Glu Pro 30 Cys Pro Ala	
cca atc tcg gag cag caa gag cag gtg ttg act gtg gcc ctt ggg cag	144
Pro Ile Ser 35 Glu Gln Gln Glu Gln Val 40 Leu Thr Val 45 Ala Leu Gly Gln	
cct gtg cgg cta tgc tgt ggc cgc act gag cgt ggt cgt cat tgg tac	192
Pro Val 50 Arg Leu Cys Cys 55 Gly Arg Thr Glu Arg 60 Gly Arg His Trp Tyr	
aag gag ggc agc cgt tta gca tct gct ggg aga gta cgg ggc tgg aga	240
Lys Glu Gly Ser Arg 70 Leu Ala Ser Ala Gly 75 Arg Val Arg Gly Trp Arg 80	
ggc cgc ctg gag atc gcc agc ttc ctt cct gag gat gct ggc cgg tac	288
Gly Arg Leu Glu 85 Ile Ala Ser Phe Leu 90 Pro Glu Asp Ala Gly Arg Tyr 95	

pctfr2009051343-seq1

ctc	tgc	ctg	gcc	cgt	ggc	tcc	atg	act	gtc	gta	cac	aat	ctt	act	ttg	336
Leu	Cys	Leu	Ala	Arg	Gly	Ser	Met	Thr	Val	Val	His	Asn	Leu	Thr	Leu	
			100					105					110			
att	atg	gat	gac	tcc	tta	ccc	tcc	atc	aat	aac	gag	gac	ccc	aag	acc	384
Ile	Met	Asp	Asp	Ser	Leu	Pro	Ser	Ile	Asn	Asn	Glu	Asp	Pro	Lys	Thr	
		115					120					125				
ctc	agc	agc	tcc	tcg	agt	ggg	cac	tcc	tac	ctg	cag	caa	gca	cct	tac	432
Leu	Ser	Ser	Ser	Ser	Ser	Gly	His	Ser	Tyr	Leu	Gln	Gln	Ala	Pro	Tyr	
	130					135					140					
tgg	aca	cac	ccc	caa	cgc	atg	gag	aag	aaa	ctg	cac	gcg	gta	cct	gcc	480
Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	Ala	Val	Pro	Ala	
145					150					155					160	
ggg	aac	act	gtc	aaa	ttc	cgc	tgt	cca	gct	gca	ggg	aac	ccc	atg	ccc	528
Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	Asn	Pro	Met	Pro	
				165					170					175		
acc	atc	cac	tgg	ctc	aag	aac	gga	cag	gcc	ttc	cac	gga	gag	aat	cgt	576
Thr	Ile	His	Trp	Leu	Lys	Asn	Gly	Gln	Ala	Phe	His	Gly	Glu	Asn	Arg	
			180					185					190			
atc	gga	ggc	att	cgg	ctg	cgt	cac	caa	cac	tgg	agc	ctc	gtg	atg	gag	624
Ile	Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	Leu	Val	Met	Glu	
		195					200					205				
agc	gtg	gtg	ccc	tca	gac	cgt	ggc	acg	tac	acg	tgt	ctt	gtg	gag	aac	672
Ser	Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	Leu	Val	Glu	Asn	
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pctfr2009051343-seq1

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pctfr2009051343-seq1

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Ala Ser Ser Thr Cys Ser Ser Ser Asp Ser Val Phe Ser His Asp Pro	
770 775 780	
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Pro Val Arg Leu Cys Cys Gly Arg Thr Glu Arg Gly Arg His Trp Tyr
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Lys Glu Gly Ser Arg Leu Ala Ser Ala Gly Arg Val Arg Gly Trp Arg
Page 46

pctfr2009051343-seq1

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Ile Met Asp Asp Ser Leu Pro Ser Ile Asn Asn Glu Asp Pro Lys Thr			
	115	120	125
Leu Ser Ser Ser Ser Ser Gly His Ser Tyr Leu Gln Gln Ala Pro Tyr			
	130	135	140
Trp Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala			
	145	150	155
Gly Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Met Pro			
	165	170	175
Thr Ile His Trp Leu Lys Asn Gly Gln Ala Phe His Gly Glu Asn Arg			
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Ile Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu			
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Ser Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn			
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345

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Thr Val Ala Val Lys Met Leu Lys Asp Asn Ala Ser Asp Lys Asp Leu
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Tyr Val Ile Val Glu Tyr Ala Ala Lys Gly Asn Leu Arg Glu Phe Leu
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Ser Ser Glu Gly Pro Leu Ser Phe Pro Ala Leu Val Ser Cys Ala Tyr
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Gln Val Ala Arg Gly Met Gln Tyr Leu Glu Ser Arg Lys Cys Ile His
 595 600 605

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asp Val Met
 Page 48

610 615 620

Lys Ile Ala Asp Phe Gly Leu Ala Arg Gly Val His His Ile Asp Tyr
625 630 635 640

Tyr Lys Lys Thr Ser Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
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Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
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Phe Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
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Pro Gly Ile Pro Val Glu Glu Leu Phe Ser Leu Leu Arg Glu Gly His
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725 730 735

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pctfr2009051343-seq1

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Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala Leu Gly Gln Pro Val
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cgg ctg tgc tgt ggg cgg gct gag cgt ggt ggc cac tgg tac aag gag 144
Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly His Trp Tyr Lys Glu
35 40 45

ggc agt cgc ctg gca cct gct ggc cgt gta cgg ggc tgg agg ggc cgc 192
Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
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cta gag att gcc agc ttc cta cct gag gat gct ggc cgc tac ctc tgc 240
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Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn Leu Thr Leu Ile Thr
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ggt gac tcc ttg acc tcc agc aac gat gat gag gac ccc aag tcc cat 336
Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu Asp Pro Lys Ser His
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agg gac ctc tcg aat agg cac agt tac ccc cag caa gca ccc tac tgg 384
Arg Asp Leu Ser Asn Arg His Ser Tyr Pro Gln Gln Ala Pro Tyr Trp
115 120 125

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Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly
130 135 140

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Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser
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Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn Ala
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pctfr2009051343-seq1

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Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
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Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys
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Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn Leu Thr Leu Ile Thr
 Page 53

Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu Asp Pro Lys Ser His
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 Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser
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 Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp Val Leu Glu Arg Ser
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 Gln Pro His Ile Gln Trp Leu Lys His Ile Val Ile Asn Gly Ser Ser
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 275 280 285
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pctfr2009051343-seq1

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Gly Glu Asn Arg Ile Gly Gly Ile Arg Leu Arg His Gln His Trp Ser
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Val Leu

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Arg Val Thr Ile Ser Cys Ser Gly Gly Tyr Ser Asn Met Gly Ser Asn	
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Tyr Ala His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu	
35 40 45	
atc tat aac aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct	192
Ile Tyr Asn Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser	
50 55 60	
ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cgg	240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg	
65 70 75 80	

pctfr2009051343-seq1

tcc gag gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg	288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu	
85 90 95	
agt ggt ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag	336
Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln	
100 105 110	
ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag	384
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu	
115 120 125	
ctt caa gcc aac aag gcc aca ctg gtg tgt ctg atc agt gac ttc tac	432
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr	
130 135 140	
ccg gga gct gtg aca gtg gcc tgg aag gca gat ggc agc ccc gtc aag	480
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys	
145 150 155 160	
gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag tac	528
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr	
165 170 175	
gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc cac	576
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His	
180 185 190	
aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag	624
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys	
195 200 205	
aca gtg gcc cct aca gaa tgt tca	648
Thr Val Ala Pro Thr Glu Cys Ser	
210 215	

<210> 72
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 72

Gln Ser Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln	
1 5 10 15	
Arg Val Thr Ile Ser Cys Ser Gly Gly Tyr Ser Asn Met Gly Ser Asn	
20 25 30	
Tyr Ala His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu	
35 40 45	
Ile Tyr Asn Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser	
50 55 60	
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg	
65 70 75 80	
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu	
85 90 95	

pctfr2009051343-seq1

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 73
<211> 9
<212> PRT
<213> Homo sapiens

<400> 73

Ser Asn Met Gly Ser Asn Tyr Ala His
1 5

<210> 74
<211> 5
<212> PRT
<213> Homo sapiens

<400> 74

Tyr Asn Asn Asn Gln
1 5

<210> 75
<211> 8
<212> PRT
<213> Homo sapiens

<400> 75

Ala Trp Asp Asp Ser Leu Ser Gly
1 5

<210> 76
<211> 411

pctfr2009051343-seq1

<212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(411)

<400> 76
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 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc tct cct tac 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
 20 25 30
 tgg atg ggt tgg gtt cgc caa gct cct ggt aaa ggt ttg gag tgg gtt 144
 Trp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tct gtt atc tgg cct tct ggt ggc act act gat tat gct gac tcc gtt 192
 Ser Val Ile Trp Pro Ser Gly Gly Thr Thr Asp Tyr Ala Asp Ser Val
 50 55 60
 aaa ggt cgc ttc act atc tct aga gac aac tct aag aat act ctc tac 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ttg cag atg aac agc tta agg gct gag gac acg gcc gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gtc cat cca gct ggc cac aac gac cac tgg ggc cag gga acc 336
 Ala Arg Val His Pro Ala Gly His Asn Asp His Trp Gly Gln Gly Thr
 100 105 110
 ctg gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccg 384
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 cta gca ccc tcc tcc aag agc acc tct 411
 Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135

<210> 77
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 77
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Tyr
 20 25 30
 Trp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Trp Pro Ser Gly Gly Thr Thr Asp Tyr Ala Asp Ser Val
 50 55 60

pctfr2009051343-seq1

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

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

Ala Arg Val His Pro Ala Gly His Asn Asp His Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135

<210> 78
<211> 9
<212> PRT
<213> Homo sapiens

<400> 78

Phe Thr Phe Ser Pro Tyr Trp Met Gly
1 5

<210> 79
<211> 10
<212> PRT
<213> Homo sapiens

<400> 79

Val Ile Trp Pro Ser Gly Gly Thr Thr Asp
1 5 10

<210> 80
<211> 10
<212> PRT
<213> Homo sapiens

<400> 80

Arg Val His Pro Ala Gly His Asn Asp His
1 5 10

<210> 81
<211> 645
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(645)

<400> 81
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Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Leu Ser Pro
1 5 10 15

48

pctfr2009051343-seq1

ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt att aac aga	96
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Asn Arg	
20 25 30	
aac tta ggc tgg tac cag cag aag cct ggc cag gct ccc agg ctc ctc	144
Asn Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gcg tcc acc agg gcc act ggt atc cca gcc agg ttc act	192
Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Thr	
50 55 60	
ggc agt ggc tct ggc aca gag ttc tct ctc acc atc agc agc ctg cag	240
Gly Ser Gly Ser Gly Thr Glu Phe Ser Leu Thr Ile Ser Ser Leu Gln	
65 70 75 80	
tct gaa gat tat gca att tat tat tgt cag cag tat gat aac tgg ccg	288
Ser Glu Asp Tyr Ala Ile Tyr Tyr Cys Gln Gln Tyr Asp Asn Trp Pro	
85 90 95	
atc atc ttc ggc caa ggc aca cga ctg gag att aaa gga act gtg gct	336
Ile Ile Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Thr Val Ala	
100 105 110	
gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct	384
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser	
115 120 125	
gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag	432
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu	
130 135 140	
gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc	480
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser	
145 150 155 160	
cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc	528
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu	
165 170 175	
agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc	576
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val	
180 185 190	
tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag	624
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys	
195 200 205	
agc ttc aac agg gga gag tgt	645
Ser Phe Asn Arg Gly Glu Cys	
210 215	

<210> 82
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 82

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

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Asn Arg
 20 25 30

pctfr2009051343-seq1

Asn Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Thr
50 55 60

Gly Ser Gly Ser Gly Thr Glu Phe Ser Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

Ser Glu Asp Tyr Ala Ile Tyr Tyr Cys Gln Gln Tyr Asp Asn Trp Pro
85 90 95

Ile Ile Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 83
<211> 7
<212> PRT
<213> Homo sapiens

<400> 83

Ser Ile Asn Arg Asn Leu Gly
1 5

<210> 84
<211> 5
<212> PRT
<213> Homo sapiens

<400> 84

Tyr Gly Ala Ser Thr

1

5

<210> 85
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 85

Gln Tyr Asp Asn Trp Pro
 1 5

<210> 86
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(411)

<400> 86
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 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc tct cgt tac 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30
 ttt atg aag tgg gtt cgc caa gct cct ggt aaa ggt ttg gag tgg gtt 144
 Phe Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tct tgg atc tct cct tct ggt ggc ctt act gag tat gct gac tcc gtt 192
 Ser Trp Ile Ser Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val
 50 55 60
 aaa ggt cgc ttc act atc tct aga gac aac tct aag aat act ctc tac 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ttg cag atg aac agc tta agg gct gag gac acg gcc gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcc aga gcc tca tac ggt gcc tgg ctg gac tac tgg ggc cag ggc acc 336
 Ala Arg Ala Ser Tyr Gly Ala Trp Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 ctg gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccg 384
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 cta gca ccc tcc tcc aag agc acc tct 411
 Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135

<210> 87
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 87

pctfr2009051343-seq1

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

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

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

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

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

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

Ala Arg Ala Ser Tyr Gly Ala Trp Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135

<210> 88
<211> 9
<212> PRT
<213> Homo sapiens

<400> 88

Phe Thr Phe Ser Arg Tyr Phe Met Lys
1 5

<210> 89
<211> 10
<212> PRT
<213> Homo sapiens

<400> 89

Trp Ile Ser Pro Ser Gly Gly Leu Thr Glu
1 5 10

<210> 90
<211> 10
<212> PRT
<213> Homo sapiens

<400> 90

Arg Ala Ser Tyr Gly Ala Trp Leu Asp Tyr
1 5 10

pctfr2009051343-seq1

<210> 91
 <211> 651
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(651)

<400> 91
 cag agc gtc ttg act cag cca ccc tca gcg tct ggg acc ccc ggc cag 48
 Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15
 ggg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat 96
 Gly Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 agt gtt aac tgg tac cag cag ctc cca gga gcg gcc ccc aaa ctc ctc 144
 Ser Val Asn Trp Tyr Gln Gln Leu Pro Gly Ala Ala Pro Lys Leu Leu
 35 40 45
 atc tat agt aac aat ctg cgg ccc tca ggg gtc cct gcc cga ttc tct 192
 Ile Tyr Ser Asn Asn Leu Arg Pro Ser Gly Val Pro Ala Arg Phe Ser
 50 55 60
 ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggc ctc cgg 240
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
 65 70 75 80
 tct gag gat gag gct gat tat tac tgt gca gcc tgg gat gac ggc ctg 288
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Gly Leu
 85 90 95
 gat gcc tat gtg gtg ttc ggc gga ggg acc aaa ctg acc gtc ctg ggt 336
 Asp Ala Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110
 cag ccc aag gcc aac ccc act gtc act ctg ttc ccg ccc tcc tct gag 384
 Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125
 gag ctc caa gcc aac aag gcc aca cta gtg tgt ctg atc agt gac ttc 432
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140
 tac ccg gga gct gtg aca gtg gcc tgg aag gca gat ggc agc ccc gtc 480
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
 145 150 155 160
 aag gcg gga gtg gag acc acc aaa ccc tcc aaa cag agc aac aac aag 528
 Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175
 tac gcg gcc agc agc tac ctg agc ctg acg ccc gag cag tgg aag tcc 576
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190
 cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag 624
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205
 aag aca gtg gcc cct gca gaa tgc tct 651
 Lys Thr Val Ala Pro Ala Glu Cys Ser
 210 215

pctfr2009051343-seq1

<210> 92
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 92

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

Gly Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30

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

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

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

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Gly Leu
 85 90 95

Asp Ala Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110

Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140

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

Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205

Lys Thr Val Ala Pro Ala Glu Cys Ser
 210 215

<210> 93
 <211> 9
 <212> PRT

<213> Homo sapiens

<400> 93

Ser Asn Ile Gly Ser Asn Ser Val Asn
 1 5

<210> 94

<211> 5

<212> PRT

<213> Homo sapiens

<400> 94

Tyr Ser Asn Asn Leu
 1 5

<210> 95

<211> 9

<212> PRT

<213> Homo sapiens

<400> 95

Ala Trp Asp Asp Gly Leu Asp Ala Tyr
 1 5

<210> 96

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(414)

<400> 96	
gaa gtt caa ttg tta gag tct ggt ggc ggt ctt gtt cag cct ggt ggt	48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc tct act tac	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr	
20 25 30	
tgg atg gct tgg gtt cgc caa gct cct ggt aaa ggt ttg gag tgg gtt	144
Trp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tct gtt atc ggt cct tct ggt ggc atg act gtt tat gct gac tcc gtt	192
Ser Val Ile Gly Pro Ser Gly Gly Met Thr Val Tyr Ala Asp Ser Val	
50 55 60	
aaa ggt cgc ttc act atc tct aga gac aac tct aag aat act ctc tac	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ttg cag atg aac agc tta agg gct gag gac acg gcc gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca cgg att aat agt ggg agc tcc cac ttt gac tac tgg ggc cag gga	336
Ala Arg Ile Asn Ser Gly Ser Ser His Phe Asp Tyr Trp Gly Gln Gly	
100 105 110	

pctfr2009051343-seq1

acc ctg gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc 384
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

ccg cta gca ccc tcc tcc aag agc acc tct 414
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135

<210> 97
<211> 138
<212> PRT
<213> Homo sapiens

<400> 97

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

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

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

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

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

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

Ala Arg Ile Asn Ser Gly Ser Ser His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135

<210> 98
<211> 9
<212> PRT
<213> Homo sapiens

<400> 98

Phe Thr Phe Ser Thr Tyr Trp Met Ala
1 5

<210> 99
<211> 10
<212> PRT
<213> Homo sapiens

pctfr2009051343-seq1

<400> 99

Val Ile Gly Pro Ser Gly Gly Met Thr Val
 1 5 10

<210> 100

<211> 11

<212> PRT

<213> Homo sapiens

<400> 100

Arg Ile Asn Ser Gly Ser Ser His Phe Asp Tyr
 1 5 10

<210> 101

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(651)

<400> 101

cag tac gaa ttg act cag cca ccc tca gcg tct ggg acc ccc ggg cag 48
 Gln Tyr Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15

agg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga agc aat 96
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30

att gta cac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc 144
 Ile Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45

ata tat ggt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct 192
 Ile Tyr Gly Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

gtc tcc aag tct ggc tcc tca gcc tcc ctg gcc atc agt ggg ctc cag 240
 Val Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

tct gag gat gag gct gat tat tac tgt gca tca tgg gat gac agc ctg 288
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Ser Leu
 85 90 95

aaa gcc ttt tat gtc ttc gga act ggg acc aag gtc acc gtc cta ggt 336
 Lys Ala Phe Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
 100 105 110

cag ccc aag gcc aac ccc act gtc act ctg ttc ccg ccc tcc tct gag 384
 Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125

gag ctc caa gcc aac aag gcc aca cta gtg tgt ctg atc agt gac ttc 432
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140

tac ccg gga gct gtg aca gtg gcc tgg aag gca gat ggc agc ccc gtc 480
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
 145 150 155 160

pctfr2009051343-seq1

aag gcg gga gtg gag acc acc aaa ccc tcc aaa cag agc aac aac aag 528
 Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175

tac gcg gcc agc agc tac ctg agc ctg acg ccc gag cag tgg aag tcc 576
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190

cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag 624
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205

aag aca gtg gcc cct aca gaa tgt tca 651
 Lys Thr Val Ala Pro Thr Glu Cys Ser
 210 215

<210> 102
 <211> 217
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 20 25 30

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 35 40 45

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

Val Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Ser Leu
 85 90

Lys Ala Phe Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
 100 105 110

Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140

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

Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175

pctfr2009051343-seq1

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
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His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

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<400> 103

Ser Asn Ile Gly Ser Asn Ile Val His
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tct tta cgt ctt tct tgc gct gct tcc gga ttc act ttc tct cat tac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
20 25 30

tgg atg ggt tgg gtt cgc caa gct cct ggt aaa ggt ttg gag tgg gtt 144
Trp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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pctfr2009051343-seq1

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Ser Val Ile Ser Pro Ser Gly Gly Leu Thr Ile Tyr Ala Asp Ser Val	
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aaa ggt cgc ttc act atc tct aga gac aac tct aag aat act ctc tac	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ttg cag atg aac agc tta agg gct gag gac acg gcc gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca cgg agc agt ggc tgg gct ctg gat gct ttt gat atc tgg ggc caa	336
Ala Arg Ser Ser Gly Trp Ala Leu Asp Ala Phe Asp Ile Trp Gly Gln	
100 105 110	
ggg aca atg gtc acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc	384
Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val	
115 120 125	
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Trp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Val Ile Ser Pro Ser Gly Gly Leu Thr Ile Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Ser Ser Gly Trp Ala Leu Asp Ala Phe Asp Ile Trp Gly Gln	
100 105 110	
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 1 5

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Val Ile Ser Pro Ser Gly Gly Leu Thr Ile
 1 5 10

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cct cca gtc ttg tcc ctg gag gcc tct gag gaa gtg gag ctt gag ccc	96
Pro Pro Val Leu Ser Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro	
20 25 30	
tgc ctg gct ccc agc ctg gag cag caa gag cag gag ctg aca gta gcc	144
Cys Leu Ala Pro Ser Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala	
35 40 45	
ctt ggg cag cct gtg cgg ctg tgc tgt ggg cgg gct gag cgt ggt ggc	192
Leu Gly Gln Pro Val Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly	
50 55 60	
cac tgg tac aag gag ggc agt cgc ctg gca cct gct ggc cgt gta cgg	240
His Trp Tyr Lys Glu Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg	
65 70 75 80	
ggc tgg agg ggc cgc cta gag att gcc agc ttc cta cct gag gat gct	288
Gly Trp Arg Gly Arg Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala	
85 90 95	

pctfr2009051343-seq1

ggc cgc tac ctc tgc ctg gca cga ggc tcc atg atc gtc ctg cag aat Gly Arg Tyr Leu Cys Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn 100 105 110	336
ctc acc ttg att aca ggt gac tcc ttg acc tcc agc aac gat gat gag Leu Thr Leu Ile Thr Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu 115 120 125	384
gac ccc aag tcc cat agg gac ctc tcg aat agg cac agt tac ccc cag Asp Pro Lys Ser His Arg Asp Leu Ser Asn Arg His Ser Tyr Pro Gln 130 135 140	432
caa gca ccc tac tgg aca cac ccc cag cgc atg gag aag aaa ctg cat Gln Ala Pro Tyr Trp Thr His Pro Gln Arg Met Glu Lys Lys Leu His 145 150 155 160	480
gca gta cct gcg ggg aac acc gtc aag ttc cgc tgt cca gct gca ggc Ala Val Pro Ala Gly Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly 165 170 175	528
aac ccc acg aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc Asn Pro Thr Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu 180 185 190	576
ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr 195 200 205	624
ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val 210 215 220	672
agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val 225 230 235 240	720
gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser 245 250 255	768
acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu 260 265 270	816
aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala 275 280 285	864
ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro 290 295 300	912
cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln 305 310 315 320	960
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala 325 330 335	1008
gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr 340 345 350	1056
cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu 355 360 365	1104

pctfr2009051343-seq1

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Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	
	370					375					380					
gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	1200
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	
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ctg	tct	ccg	ggt	tga												1215
Leu	Ser	Pro	Gly													

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			20					25					30			
Cys	Leu	Ala	Pro	Ser	Leu	Glu	Gln	Gln	Glu	Gln	Glu	Leu	Thr	Val	Ala	
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Leu	Gly	Gln	Pro	Val	Arg	Leu	Cys	Cys	Gly	Arg	Ala	Glu	Arg	Gly	Gly	
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His	Trp	Tyr	Lys	Glu	Gly	Ser	Arg	Leu	Ala	Pro	Ala	Gly	Arg	Val	Arg	
	65				70					75					80	
Gly	Trp	Arg	Gly	Arg	Leu	Glu	Ile	Ala	Ser	Phe	Leu	Pro	Glu	Asp	Ala	
				85					90					95		
Gly	Arg	Tyr	Leu	Cys	Leu	Ala	Arg	Gly	Ser	Met	Ile	Val	Leu	Gln	Asn	
			100					105					110			
Leu	Thr	Leu	Ile	Thr	Gly	Asp	Ser	Leu	Thr	Ser	Ser	Asn	Asp	Asp	Glu	
		115					120					125				
Asp	Pro	Lys	Ser	His	Arg	Asp	Leu	Ser	Asn	Arg	His	Ser	Tyr	Pro	Gln	
	130					135					140					
Gln	Ala	Pro	Tyr	Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	
	145				150					155					160	
Ala	Val	Pro	Ala	Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	
				165					170					175		
Asn	Pro	Thr	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	
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pctfr2009051343-seq1

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 195 200 205
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 210 215 220
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 225 230 235 240
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 245 250 255
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 260 265 270
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 275 280 285
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 290 295 300
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 305 310 315 320
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 325 330 335
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 340 345 350
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 355 360 365
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
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 Leu Ser Pro Gly

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<400> 113

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Met	Arg	Leu	Leu	Leu	Ala	Leu	Leu	Gly	Val	Leu	Leu	Ser	Val	Pro	Gly	
1				5				10					15			
cct	cca	gtc	tgg	tcc	ctg	gag	gcc	tct	gag	gaa	gtg	gag	ctt	gag	ccc	96
Pro	Pro	Val	Leu	Ser	Leu	Glu	Ala	Ser	Glu	Glu	Val	Glu	Leu	Glu	Pro	
			20					25					30			
caa	gca	ccc	tac	tgg	aca	cac	ccc	cag	cgc	atg	gag	aag	aaa	ctg	cat	144
Gln	Ala	Pro	Tyr	Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	
		35					40				45					
gca	gta	cct	gcg	ggg	aac	acc	gtc	aag	ttc	cgc	tgt	cca	gct	gca	ggc	192
Ala	Val	Pro	Ala	Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	
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Asn	Pro	Thr	Pro	Thr	Ile	Arg	Trp	Leu	Lys	Asp	Gly	Gln	Ala	Phe	His	
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Gly	Glu	Asn	Arg	Ile	Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	
				85					90					95		
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Leu	Val	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	
			100					105					110			
ctg	gta	gag	aac	gct	gtg	ggc	agc	atc	cgt	tat	aac	tac	ctg	cta	gat	384
Leu	Val	Glu	Asn	Ala	Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	
		115					120					125				
gtg	ctg	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	432
Val	Leu	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
	130					135					140					
ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	480
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
145					150					155					160	
atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	528
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
				165					170					175		
cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	576
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
			180					185					190			
gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	624
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
		195					200					205				
tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	672
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
	210					215					220					
ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	720
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
225					230					235					240	
atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	768
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
				245					250					255		
gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	816
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
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pctfr2009051343-seq1

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Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
	290					295					300					
ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	960
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	
305					310					315					320	
gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	1008
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	
				325					330					335		
atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	1056
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	
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tct	ccg	ggg	tga													1068
Ser	Pro	Gly														
		355														

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<400> 114

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			20					25					30			
Gln	Ala	Pro	Tyr	Trp	Thr	His	Pro	Gln	Arg	Met	Glu	Lys	Lys	Leu	His	
		35					40					45				
Ala	Val	Pro	Ala	Gly	Asn	Thr	Val	Lys	Phe	Arg	Cys	Pro	Ala	Ala	Gly	
	50					55					60					
Asn	Pro	Thr	Pro	Thr	Ile	Arg	Trp	Leu	Lys	Asp	Gly	Gln	Ala	Phe	His	
65					70					75				80		
Gly	Glu	Asn	Arg	Ile	Gly	Gly	Ile	Arg	Leu	Arg	His	Gln	His	Trp	Ser	
				85					90					95		
Leu	Val	Met	Glu	Ser	Val	Val	Pro	Ser	Asp	Arg	Gly	Thr	Tyr	Thr	Cys	
			100					105					110			
Leu	Val	Glu	Asn	Ala	Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	
		115					120					125				
Val	Leu	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
						135					140					

pctfr2009051343-seq1

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
145 150 155 160

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
165 170 175

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
180 185 190

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
195 200 205

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
210 215 220

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
225 230 235 240

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
245 250 255

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
260 265 270

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
275 280 285

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
290 295 300

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
305 310 315 320

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
325 330 335

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
340 345 350

Ser Pro Gly
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<222> (1)..(1188)

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Page 78

pctfr2009051343-seq1

Met	Arg	Leu	Leu	Leu	Ala	Leu	Leu	Gly	Val	Leu	Leu	Ser	Val	Pro	Gly		
1				5				10					15				
cct	cca	gtc	ttg	tcc	ctg	gag	gcc	tct	gag	gaa	gtg	gag	ctt	gag	ccc		96
Pro	Pro	Val	Leu	Ser	Leu	Glu	Ala	Ser	Glu	Glu	Val	Glu	Leu	Glu	Pro		
			20					25					30				
aac	gct	gtg	ggc	agc	atc	cgt	tat	aac	tac	ctg	cta	gat	gtg	ctg	gag		144
Asn	Ala	Val	Gly	Ser	Ile	Arg	Tyr	Asn	Tyr	Leu	Leu	Asp	Val	Leu	Glu		
		35					40					45					
cgg	tcc	ccg	cac	cgg	ccc	atc	ctg	cag	gcc	ggg	ctc	ccg	gcc	aac	acc		192
Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Thr		
		50				55					60						
aca	gcc	gtg	gtg	ggc	agc	gac	gtg	gag	ctg	ctg	tgc	aag	gtg	tac	agc		240
Thr	Ala	Val	Val	Gly	Ser	Asp	Val	Glu	Leu	Leu	Cys	Lys	Val	Tyr	Ser		
		65			70				75						80		
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Ser	Ser	Phe	Gly	Ala	Asp	Gly	Phe	Pro	Tyr	Val	Gln	Val	Leu	Lys	Thr		
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Ala	Asp	Ile	Asn	Ser	Ser	Glu	Val	Glu	Val	Leu	Tyr	Leu	Arg	Asn	Val		
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tca	gcc	gag	gac	gca	ggc	gag	tac	acc	tgc	ctc	gca	ggc	aat	tcc	atc		432
Ser	Ala	Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn	Ser	Ile		
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Gly	Leu	Ser	Tyr	Gln	Ser	Ala	Trp	Leu	Thr	Val	Leu	Pro	Glu	Glu	Asp		
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ccc	aca	tgg	acc	gca	gca	gcg	ccc	gag	gcc	aaa	act	cac	aca	tgc	cca		528
Pro	Thr	Trp	Thr	Ala	Ala	Ala	Pro	Glu	Ala	Lys	Thr	His	Thr	Cys	Pro		
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ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc		576
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe		
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Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val		
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aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc		672
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe		
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aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg		720
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro		
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cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc		768
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr		
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gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc		816
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val		
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pctfr2009051343-seq1

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

115

Ser Ala Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile
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Gly Leu Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp
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Pro Thr Trp Thr Ala Ala Ala Pro Glu Ala Lys Thr His Thr Cys Pro
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Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
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Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
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Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
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Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
Page 81

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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
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Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
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Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
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pctfr2009051343-seq1

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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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