

Sequence_Listing
SEQUENCE LISTING

<110> Vegenics Pty Limited
Commonwealth Scientific and Industrial Research
Organization

<120> LIGAND BINDING MOLECULES AND USES THEREOF

<130> 28967/47459A

<160> 21

<170> PatentIn version 3.5

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<211> 4195

<212> DNA

<213> Homo sapiens

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<221> CDS

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Lys	Leu	Pro 355	Val	Lys	Leu	Ala	Ala 360	Tyr	Pro	Pro	Pro	Glu 365	Phe	Gln	Trp	
Tyr 370	Lys	Asp	Gly	Lys	Ala	Leu 375	Ser	Gly	Arg	His	Ser 380	Pro	His	Ala	Leu	
Val 385	Leu	Lys	Glu	Val	Thr 390	Glu	Ala	Ser	Thr	Gly 395	Thr	Tyr	Thr	Leu	Ala 400	
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Arg	Asn	Ile	Ser	Leu	Glu	Leu	

Sequence_Listing																
405					410					415						
Val	Val	Asn	Val	Pro	Pro	Gln	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro	
			420					425					430			
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Ala	Leu	Thr	Cys	Thr	Ala	Tyr	
		435					440					445				
Gly	Val	Pro	Leu	Pro	Leu	Ser	Ile	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr	
	450					455					460					
Pro	Cys	Lys	Met	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln	
465					470					475					480	
Asp	Leu	Met	Pro	Gln	Cys	Arg	Asp	Trp	Arg	Ala	Val	Thr	Thr	Gln	Asp	
				485					490					495		
Ala	Val	Asn	Pro	Ile	Glu	Ser	Leu	Asp	Thr	Trp	Thr	Glu	Phe	Val	Glu	
			500					505					510			
Gly	Lys	Asn	Lys	Thr	Val	Ser	Lys	Leu	Val	Ile	Gln	Asn	Ala	Asn	Val	
		515					520					525				
Ser	Ala	Met	Tyr	Lys	Cys	Val	Val	Ser	Asn	Lys	Val	Gly	Gln	Asp	Glu	
	530					535					540					
Arg	Leu	Ile	Tyr	Phe	Tyr	Val	Thr	Thr	Ile	Pro	Asp	Gly	Phe	Thr	Ile	
545					550					555					560	
Glu	Ser	Lys	Pro	Ser	Glu	Glu	Leu	Leu	Glu	Gly	Gln	Pro	Val	Leu	Leu	
				565					570					575		
Ser	Cys	Gln	Ala	Asp	Ser	Tyr	Lys	Tyr	Glu	His	Leu	Arg	Trp	Tyr	Arg	
			580					585					590			
Leu	Asn	Leu	Ser	Thr	Leu	His	Asp	Ala	His	Gly	Asn	Pro	Leu	Leu	Leu	
		595					600					605				
Asp	Cys	Lys	Asn	Val	His	Leu	Phe	Ala	Thr	Pro	Leu	Ala	Ala	Ser	Leu	
	610					615					620					
Glu	Glu	Val	Ala	Pro	Gly	Ala	Arg	His	Ala	Thr	Leu	Ser	Leu	Ser	Ile	
625					630					635					640	
Pro	Arg	Val	Ala	Pro	Glu	His	Glu	Gly	His	Tyr	Val	Cys	Glu	Val	Gln	
				645					650					655		
Asp	Arg	Arg	Ser	His	Asp	Lys	His	Cys	His	Lys	Lys	Tyr	Leu	Ser	Val	
			660					665					670			
Gln	Ala	Leu	Glu	Ala	Pro	Arg	Leu	Thr	Gln	Asn	Leu	Thr	Asp	Leu	Leu	

Sequence_Listing															
675				680				685							
Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Gln	Cys	Leu	Val	Ala	Gly	Ala
690						695					700				
His	Ala	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Glu
705					710					715					720
Lys	Ser	Gly	Val	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Lys	Leu	Ser	Ile	Gln
				725					730					735	
Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Arg	Tyr	Leu	Cys	Ser	Val	Cys	Asn
			740					745					750		
Ala	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser	Val	Ala	Val	Glu	Gly	Ser
		755					760					765			
Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile	Leu	Val	Gly	Thr	Gly	Val
	770					775					780				
Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu	Leu	Ile	Phe	Cys	Asn	Met
785					790					795					800
Arg	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile
				805					810					815	
Met	Asp	Pro	Gly	Glu	Val	Pro	Leu	Glu	Glu	Gln	Cys	Glu	Tyr	Leu	Ser
			820					825					830		
Tyr	Asp	Ala	Ser	Gln	Trp	Glu	Phe	Pro	Arg	Glu	Arg	Leu	His	Leu	Gly
		835					840					845			
Arg	Val	Leu	Gly	Tyr	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Ser	Ala
	850					855					860				
Phe	Gly	Ile	His	Lys	Gly	Ser	Ser	Cys	Asp	Thr	Val	Ala	Val	Lys	Met
865					870					875					880
Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu
				885					890					895	
Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	Asn	His	Leu	Asn	Val	Val	Asn	Leu
			900					905					910		
Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gln	Gly	Pro	Leu	Met	Val	Ile	Val	Glu
		915					920					925			
Phe	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Phe	Leu	Arg	Ala	Lys	Arg	Asp
	930					935					940				
Ala	Phe	Ser	Pro	Cys	Ala	Glu	Lys	Ser	Pro	Glu	Gln	Arg	Gly	Arg	Phe

Sequence_Listing															
945	950										955	960			
Arg	Ala	Met	Val	Glu	Leu	Ala	Arg	Leu	Asp	Arg	Arg	Arg	Pro	Gly	Ser
				965					970					975	
Ser	Asp	Arg	Val	Leu	Phe	Ala	Arg	Phe	Ser	Lys	Thr	Glu	Gly	Gly	Ala
			980					985					990		
Arg	Arg	Ala	Ser	Pro	Asp	Gln	Glu	Ala	Glu	Asp	Leu	Trp	Leu	Ser	Pro
		995					1000					1005			
Leu	Thr	Met	Glu	Asp	Leu	Val	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Arg	
	1010					1015					1020				
Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	
	1025					1030					1035				
Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu	Ser	Asp	Val	Val	Lys	Ile	
	1040					1045					1050				
Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	
	1055					1060					1065				
Val	Arg	Lys	Gly	Ser	Ala	Arg	Leu	Pro	Leu	Lys	Trp	Met	Ala	Pro	
	1070					1075					1080				
Glu	Ser	Ile	Phe	Asp	Lys	Val	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	
	1085					1090					1095				
Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	
	1100					1105					1110				
Pro	Tyr	Pro	Gly	Val	Gln	Ile	Asn	Glu	Glu	Phe	Cys	Gln	Arg	Leu	
	1115					1120					1125				
Arg	Asp	Gly	Thr	Arg	Met	Arg	Ala	Pro	Glu	Leu	Ala	Thr	Pro	Ala	
	1130					1135					1140				
Ile	Arg	Arg	Ile	Met	Leu	Asn	Cys	Trp	Ser	Gly	Asp	Pro	Lys	Ala	
	1145					1150					1155				
Arg	Pro	Ala	Phe	Ser	Glu	Leu	Val	Glu	Ile	Leu	Gly	Asp	Leu	Leu	
	1160					1165					1170				
Gln	Gly	Arg	Gly	Leu	Gln	Glu	Glu	Glu	Glu	Val	Cys	Met	Ala	Pro	
	1175					1180					1185				
Arg	Ser	Ser	Gln	Ser	Ser	Glu	Glu	Gly	Ser	Phe	Ser	Gln	Val	Ser	
	1190					1195					1200				
Thr	Met	Ala	Leu	His	Ile	Ala	Gln	Ala	Asp	Ala	Glu	Asp	Ser	Pro	

Sequence_Listing

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1205                               1210                               1215

Pro Ser  Leu Gln Arg His Ser  Leu Ala Ala Arg Tyr  Tyr Asn Trp
1220                               1225                               1230

Val Ser  Phe Pro Gly Cys Leu  Ala Arg Gly Ala Glu  Thr Arg Gly
1235                               1240                               1245

Ser Ser  Arg Met Lys Thr Phe  Glu Glu Phe Pro Met  Thr Pro Thr
1250                               1255                               1260

Thr Tyr  Lys Gly Ser Val Asp  Asn Gln Thr Asp Ser  Gly Met Val
1265                               1270                               1275

Leu Ala  Ser Glu Glu Phe Glu  Gln Ile Glu Ser Arg  His Arg Gln
1280                               1285                               1290

Glu Ser  Gly Phe Arg
1295

<210>  3
<211>  537
<212>  PRT
<213>  Homo sapiens

<400>  3

Tyr Ser Met Thr  Pro Pro Thr Leu Asn Ile Thr Glu Glu Ser His Val
1      5      10      15

Ile Asp Thr  Gly Asp Ser Leu Ser Ile Ser Cys Arg Gly Gln His Pro
20     25     30

Leu Glu Trp Ala Trp Pro Gly Ala Gln Glu Ala Pro Ala Thr Gly Asp
35     40     45

Lys Asp Ser Glu Asp Thr  Gly Val Val Arg Asp Cys Glu Gly Thr Asp
50     55     60

Ala Arg Pro Tyr Cys Lys Val Leu Leu Leu His Glu Val His Ala Gln
65     70     75     80

Asp Thr Gly Ser Tyr Val Cys Tyr Tyr Lys Tyr Ile Lys Ala Arg Ile
85     90     95

Glu Gly Thr Thr Ala Ala Ser Ser Tyr Val Phe Val Arg Asp Phe Glu
100    105    110

Gln Pro Phe Ile Asn Lys Pro Asp Thr Leu Leu Val Asn Arg Lys Asp
115    120    125

Ala Met Trp Val Pro Cys Leu Val Ser Ile Pro Gly Leu Asn Val Thr
130    135    140

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Sequence_Listing

Leu Arg Ser Gln Ser Ser Val Leu Trp Pro Asp Gly Gln Glu Val Val
 145 150 155 160
 Trp Asp Asp Arg Arg Gly Met Leu Val Ser Thr Pro Leu Leu His Asp
 165 170 175
 Ala Leu Tyr Leu Gln Cys Glu Thr Thr Trp Gly Asp Gln Asp Phe Leu
 180 185 190
 Ser Asn Pro Phe Leu Val His Ile Thr Gly Asn Glu Leu Tyr Asp Ile
 195 200 205
 Gln Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu
 210 215 220
 Val Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe
 225 230 235 240
 Asp Trp Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val Pro
 245 250 255
 Glu Arg Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu Thr
 260 265 270
 Ile His Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala
 275 280 285
 Asn Asn Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val His
 290 295 300
 Glu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 305 310 315 320
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 325 330 335
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 340 345 350
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 355 360 365
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 370 375 380
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 385 390 395 400
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 405 410 415

Sequence_Listing

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
420 425 430

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
435 440 445

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
450 455 460

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
465 470 475 480

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
485 490 495

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
500 505 510

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
515 520 525

Lys Ser Leu Ser Leu Ser Pro Gly Lys
530 535

<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 4

Pro Ile Glu Gly Arg Gly Gly Gly Gly Gly
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<210> 5
<211> 2292
<212> DNA
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<220>
<221> CDS
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<400> 5
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Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
1 5 10 15

acc cgg gcc gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc 96
Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
20 25 30

agg ctc agc ata caa aaa gac ata ctt aca att aag gct aat aca act 144

Sequence_Listing																
Arg	Leu	Ser 35	Ile	Gln	Lys	Asp	Ile 40	Leu	Thr	Ile	Lys	Ala 45	Asn	Thr	Thr	
ctt	caa	att	act	tgc	agg	gga	cag	agg	gac	ttg	gac	tgg	ctt	tgg	ccc	192
Leu	Gln	Ile	Thr	Cys	Arg	Gly 55	Gln	Arg	Asp	Leu	Asp 60	Trp	Leu	Trp	Pro	
aat	aat	cag	agt	ggc	agt	gag	caa	agg	gtg	gag	gtg	act	gag	tgc	agc	240
Asn	Asn	Gln	Ser	Gly	Ser 70	Glu	Gln	Arg	Val	Glu 75	Val	Thr	Glu	Cys	Ser 80	
gat	ggc	ctc	ttc	tgt	aag	aca	ctc	aca	att	cca	aaa	gtg	atc	gga	aat	288
Asp	Gly	Leu	Phe	Cys 85	Lys	Thr	Leu	Thr	Ile 90	Pro	Lys	Val	Ile	Gly 95	Asn	
gac	act	gga	gcc	tac	aag	tgc	ttc	tac	cgg	gaa	act	gac	ttg	gcc	tcg	336
Asp	Thr	Gly	Ala 100	Tyr	Lys	Cys	Phe	Tyr 105	Arg	Glu	Thr	Asp	Leu 110	Ala	Ser	
gtc	att	tat	gtc	tat	gtt	caa	gat	tac	aga	tct	cca	ttt	att	gct	tct	384
Val	Ile	Tyr 115	Val	Tyr	Val	Gln	Asp 120	Tyr	Arg	Ser	Pro	Phe 125	Ile	Ala	Ser	
gtt	agt	gac	caa	cat	gga	gtc	gtg	tac	att	act	gag	aac	aaa	aac	aaa	432
Val	Ser 130	Asp	Gln	His	Gly 135	Val	Val	Tyr	Ile	Thr	Glu 140	Asn	Lys	Asn	Lys	
act	gtg	gtg	att	cca	tgt	ctc	ggg	tcc	att	tca	aat	ctc	aac	gtg	tca	480
Thr	Val	Val	Ile	Pro	Cys 150	Leu	Gly	Ser	Ile	Ser 155	Asn	Leu	Asn	Val	Ser 160	
ctt	tgt	gca	aga	tac	cca	gaa	aag	aga	ttt	gtt	cct	gat	ggt	aac	aga	528
Leu	Cys	Ala	Arg	Tyr 165	Pro	Glu	Lys	Arg	Phe 170	Val	Pro	Asp	Gly	Asn 175	Arg	
att	tcc	tgg	gac	agc	aag	aag	ggc	ttt	act	att	ccc	agc	tac	atg	atc	576
Ile	Ser	Trp	Asp 180	Ser	Lys	Lys	Gly 185	Phe	Thr	Ile	Pro	Ser	Tyr 190	Met	Ile	
agc	tat	gct	ggc	atg	gtc	ttc	tgt	gaa	gca	aaa	att	aat	gat	gaa	agt	624
Ser	Tyr	Ala 195	Gly	Met	Val	Phe	Cys 200	Glu	Ala	Lys	Ile	Asn 205	Asp	Glu	Ser	
tac	cag	tct	att	atg	tac	ata	gtt	gtc	gtt	gta	ggg	tat	agg	att	tat	672
Tyr	Gln 210	Ser	Ile	Met	Tyr	Ile 215	Val	Val	Val	Val	Gly 220	Tyr	Arg	Ile	Tyr	
gat	gtg	gtt	ctg	agt	ccg	tct	cat	gga	att	gaa	cta	tct	gtt	gga	gaa	720
Asp	Val	Val	Leu	Ser	Pro 230	Ser	His	Gly	Ile	Glu 235	Leu	Ser	Val	Gly	Glu 240	
aag	ctt	gtc	tta	aat	tgt	aca	gca	aga	act	gaa	cta	aat	gtg	ggg	att	768
Lys	Leu	Val	Leu	Asn 245	Cys	Thr	Ala	Arg	Thr 250	Glu	Leu	Asn	Val	Gly 255	Ile	
gac	ttc	aac	tgg	gaa	tac	cct	tct	tcg	aag	cat	cag	cat	aag	aaa	ctt	816
Asp	Phe	Asn 260	Trp	Glu	Tyr	Pro	Ser	Ser 265	Lys	His	Gln	His	Lys 270	Lys	Leu	
gta	aac	cga	gac	cta	aaa	acc	cag	tct	ggg	agt	gag	atg	aag	aaa	ttt	864
Val	Asn	Arg 275	Asp	Leu	Lys	Thr	Gln 280	Ser	Gly	Ser	Glu	Met 285	Lys	Lys	Phe	
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Leu	Ser 290	Thr	Leu	Thr	Ile	Asp 295	Gly	Val	Thr	Arg	Ser 300	Asp	Gln	Gly	Leu	
tac	acc	tgt	gca	gca	tcc	agt	ggg	ctg	atg	acc	aag	aag	aac	agc	aca	960

Sequence_Listing																
Tyr 305	Thr	Cys	Ala	Ala	Ser 310	Ser	Gly	Leu	Met	Thr 315	Lys	Lys	Asn	Ser	Thr 320	
ttt	gtc	agg	gtc	cat	gaa	aaa	cct	ttt	gtt	gct	ttt	gga	agt	ggc	atg	1008
Phe	Val	Arg	Val	His 325	Glu	Lys	Pro	Phe	Val 330	Ala	Phe	Gly	Ser	Gly 335	Met	
gaa	tct	ctg	gtg	gaa	gcc	acg	gtg	ggg	gag	cgt	gtc	aga	atc	cct	gcg	1056
Glu	Ser	Leu	Val 340	Glu	Ala	Thr	Val	Gly 345	Glu	Arg	Val	Arg	Ile 350	Pro	Ala	
aag	tac	ctt	ggt	tac	cca	ccc	cca	gaa	ata	aaa	tgg	tat	aaa	aat	gga	1104
Lys	Tyr	Leu 355	Gly	Tyr	Pro	Pro	Pro 360	Glu	Ile	Lys	Trp	Tyr 365	Lys	Asn	Gly	
ata	ccc	ctt	gag	tcc	aat	cac	aca	att	aaa	gcg	ggg	cat	gta	ctg	acg	1152
Ile	Pro 370	Leu	Glu	Ser	Asn	His 375	Thr	Ile	Lys	Ala	Gly 380	His	Val	Leu	Thr	
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Ile	Met	Glu	Val	Ser	Glu 390	Arg	Asp	Thr	Gly	Asn 395	Tyr	Thr	Val	Ile	Leu 400	
acc	aat	ccc	att	tca	aag	gag	aag	cag	agc	cat	gtg	gtc	tct	ctg	gtt	1248
Thr	Asn	Pro	Ile	Ser 405	Lys	Glu	Lys	Gln	Ser 410	His	Val	Val	Ser	Leu 415	Val	
gtg	tat	gtc	cca	ccc	cag	att	ggg	gag	aaa	tct	cta	atc	tct	cct	gtg	1296
Val	Tyr	Val	Pro 420	Pro	Gln	Ile	Gly	Glu 425	Lys	Ser	Leu	Ile	Ser 430	Pro	Val	
gat	tcc	tac	cag	tac	ggc	acc	act	caa	acg	ctg	aca	tgt	acg	gtc	tat	1344
Asp	Ser	Tyr 435	Gln	Tyr	Gly	Thr	Thr 440	Gln	Thr	Leu	Thr	Cys 445	Thr	Val	Tyr	
gcc	att	cct	ccc	ccg	cat	cac	atc	cac	tgg	tat	tgg	cag	ttg	gag	gaa	1392
Ala	Ile 450	Pro	Pro	Pro	His	His 455	Ile	His	Trp	Tyr	Trp 460	Gln	Leu	Glu	Glu	
gag	tgc	gcc	aac	gag	ccc	agc	caa	gct	gtc	tca	gtg	aca	aac	cca	tac	1440
Glu	Cys	Ala	Asn	Glu	Pro 470	Ser	Gln	Ala	Val	Ser 475	Val	Thr	Asn	Pro	Tyr 480	
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Pro	Cys	Glu	Glu 485	Trp	Arg	Ser	Val	Glu	Asp 490	Phe	Gln	Gly	Gly	Asn 495	Lys	
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Ile	Glu	Val	Asn 500	Lys	Asn	Gln	Phe	Ala 505	Leu	Ile	Glu	Gly	Lys 510	Asn	Lys	
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Thr	Val	Ser 515	Thr	Leu	Val	Ile	Gln 520	Ala	Ala	Asn	Val	Ser 525	Ala	Leu	Tyr	
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Lys	Cys 530	Glu	Ala	Val	Asn	Lys 535	Val	Gly	Arg	Gly	Glu 540	Arg	Val	Ile	Ser	
ttc	cac	gtg	acc	agg	ggg	cct	gaa	att	act	ttg	caa	cct	gac	atg	cag	1680
Phe	His	Val	Thr	Arg	Gly 550	Pro	Glu	Ile	Thr	Leu 555	Gln	Pro	Asp	Met	Gln 560	
ccc	act	gag	cag	gag	agc	gtg	tct	ttg	tgg	tgc	act	gca	gac	aga	tct	1728
Pro	Thr	Glu	Gln	Glu 565	Ser	Val	Ser	Leu	Trp 570	Cys	Thr	Ala	Asp	Arg 575	Ser	
acg	ttt	gag	aac	ctc	aca	tgg	tac	aag	ctt	ggc	cca	cag	cct	ctg	cca	1776

Sequence_Listing																	
Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Pro	Gln	Pro	Leu	Pro		
			580					585					590				
atc	cat	gtg	gga	gag	ttg	ccc	aca	cct	gtt	tgc	aag	aac	ttg	gat	act	1824	
Ile	His	Val	Gly	Glu	Leu	Pro	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Thr		
		595					600					605					
ctt	tgg	aaa	ttg	aat	gcc	acc	atg	ttc	tct	aat	agc	aca	aat	gac	att	1872	
Leu	Trp	Lys	Leu	Asn	Ala	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile		
	610					615					620						
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Leu	Ile	Met	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr		
625					630					635					640		
gtc	tgc	ctt	gct	caa	gac	agg	aag	acc	aag	aaa	aga	cat	tgc	gtg	gtc	1968	
Val	Cys	Leu	Ala	Gln	Asp	Arg	Lys	Thr	Lys	Lys	Arg	His	Cys	Val	Val		
				645					650					655			
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Arg	Gln	Leu	Thr	Val	Leu	Glu	Arg	Val	Ala	Pro	Thr	Ile	Thr	Gly	Asn		
			660					665					670				
ctg	gag	aat	cag	acg	aca	agt	att	ggg	gaa	agc	atc	gaa	gtc	tca	tgc	2064	
Leu	Glu	Asn	Gln	Thr	Thr	Ser	Ile	Gly	Glu	Ser	Ile	Glu	Val	Ser	Cys		
		675					680					685					
acg	gca	tct	ggg	aat	ccc	cct	cca	cag	atc	atg	tgg	ttt	aaa	gat	aat	2112	
Thr	Ala	Ser	Gly	Asn	Pro	Pro	Pro	Gln	Ile	Met	Trp	Phe	Lys	Asp	Asn		
	690					695					700						
gag	acc	ctt	gta	gaa	gac	tca	ggc	att	gta	ttg	aag	gat	ggg	aac	cgg	2160	
Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Lys	Asp	Gly	Asn	Arg		
705					710					715					720		
aac	ctc	act	atc	cgc	aga	gtg	agg	aag	gag	gac	gaa	ggc	ctc	tac	acc	2208	
Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Glu	Gly	Leu	Tyr	Thr		
				725					730					735			
tgc	cag	gca	tgc	agt	gtt	ctt	ggc	tgt	gca	aaa	gtg	gag	gca	ttt	ttc	2256	
Cys	Gln	Ala	Cys	Ser	Val	Leu	Gly	Cys	Ala	Lys	Val	Glu	Ala	Phe	Phe		
			740				745						750				
ata	ata	gaa	ggg	gcc	cag	gaa	aag	acg	aac	ttg	gaa					2292	
Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	Leu	Glu						
		755					760										

<210> 6
 <211> 764
 <212> PRT
 <213> Homo sapiens

 <400> 6

Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
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20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
Page 16

Sequence_Listing

50		55		60											
Asn 65	Asn	Gln	Ser	Gly	Ser 70	Glu	Gln	Arg	Val	Glu 75	Val	Thr	Glu	Cys	Ser 80
Asp	Gly	Leu	Phe	Cys 85	Lys	Thr	Leu	Thr	Ile 90	Pro	Lys	Val	Ile	Gly 95	Asn
Asp	Thr	Gly	Ala 100	Tyr	Lys	Cys	Phe	Tyr 105	Arg	Glu	Thr	Asp	Leu 110	Ala	Ser
Val	Ile	Tyr 115	Val	Tyr	Val	Gln	Asp 120	Tyr	Arg	Ser	Pro	Phe 125	Ile	Ala	Ser
Val	Ser 130	Asp	Gln	His	Gly	Val 135	Val	Tyr	Ile	Thr	Glu 140	Asn	Lys	Asn	Lys
Thr 145	Val	Val	Ile	Pro	Cys 150	Leu	Gly	Ser	Ile	Ser 155	Asn	Leu	Asn	Val	Ser 160
Leu	Cys	Ala	Arg	Tyr 165	Pro	Glu	Lys	Arg	Phe 170	Val	Pro	Asp	Gly	Asn 175	Arg
Ile	Ser	Trp	Asp 180	Ser	Lys	Lys	Gly	Phe 185	Thr	Ile	Pro	Ser	Tyr 190	Met	Ile
Ser	Tyr	Ala 195	Gly	Met	Val	Phe	Cys 200	Glu	Ala	Lys	Ile	Asn 205	Asp	Glu	Ser
Tyr	Gln 210	Ser	Ile	Met	Tyr	Ile 215	Val	Val	Val	Val	Gly 220	Tyr	Arg	Ile	Tyr
Asp 225	Val	Val	Leu	Ser	Pro 230	Ser	His	Gly	Ile	Glu 235	Leu	Ser	Val	Gly	Glu 240
Lys	Leu	Val	Leu	Asn 245	Cys	Thr	Ala	Arg	Thr 250	Glu	Leu	Asn	Val	Gly 255	Ile
Asp	Phe	Asn	Trp 260	Glu	Tyr	Pro	Ser	Ser 265	Lys	His	Gln	His	Lys 270	Lys	Leu
Val	Asn	Arg 275	Asp	Leu	Lys	Thr	Gln 280	Ser	Gly	Ser	Glu	Met 285	Lys	Lys	Phe
Leu	Ser 290	Thr	Leu	Thr	Ile	Asp 295	Gly	Val	Thr	Arg	Ser 300	Asp	Gln	Gly	Leu
Tyr 305	Thr	Cys	Ala	Ala	Ser 310	Ser	Gly	Leu	Met	Thr 315	Lys	Lys	Asn	Ser	Thr 320
Phe	Val	Arg	Val	His	Glu	Lys	Pro	Phe	Val	Ala	Phe	Gly	Ser	Gly	Met

Sequence_Listing																	
325						330						335					
Glu	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Glu	Arg	Val	Arg	Ile	Pro	Ala		
			340					345					350				
Lys	Tyr	Leu	Gly	Tyr	Pro	Pro	Pro	Glu	Ile	Lys	Trp	Tyr	Lys	Asn	Gly		
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Ile	Pro	Leu	Glu	Ser	Asn	His	Thr	Ile	Lys	Ala	Gly	His	Val	Leu	Thr		
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Ile	Met	Glu	Val	Ser	Glu	Arg	Asp	Thr	Gly	Asn	Tyr	Thr	Val	Ile	Leu		
385					390					395					400		
Thr	Asn	Pro	Ile	Ser	Lys	Glu	Lys	Gln	Ser	His	Val	Val	Ser	Leu	Val		
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Val	Tyr	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ser	Leu	Ile	Ser	Pro	Val		
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Asp	Ser	Tyr	Gln	Tyr	Gly	Thr	Thr	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr		
		435					440					445					
Ala	Ile	Pro	Pro	Pro	His	His	Ile	His	Trp	Tyr	Trp	Gln	Leu	Glu	Glu		
	450					455					460						
Glu	Cys	Ala	Asn	Glu	Pro	Ser	Gln	Ala	Val	Ser	Val	Thr	Asn	Pro	Tyr		
465					470					475					480		
Pro	Cys	Glu	Glu	Trp	Arg	Ser	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys		
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Ile	Glu	Val	Asn	Lys	Asn	Gln	Phe	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys		
			500					505					510				
Thr	Val	Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr		
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Lys	Cys	Glu	Ala	Val	Asn	Lys	Val	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser		
	530					535					540						
Phe	His	Val	Thr	Arg	Gly	Pro	Glu	Ile	Thr	Leu	Gln	Pro	Asp	Met	Gln		
545					550					555					560		
Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Trp	Cys	Thr	Ala	Asp	Arg	Ser		
				565					570					575			
Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Pro	Gln	Pro	Leu	Pro		
			580					585					590				
Ile	His	Val	Gly	Glu	Leu	Pro	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Thr		

Sequence_Listing

595	600	605
Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile		
610	615	620
Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr		
625	630	635
Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val		
645	650	655
Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn		
660	665	670
Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys		
675	680	685
Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn		
690	695	700
Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg		
705	710	715
Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr		
725	730	735
Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe		
740	745	750
Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu		
755	760	

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic linker

<400> 7

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<210> 8
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic linker

<400> 8

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
Page 19

sequence = 15

<400> 9

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<220>  
<221> CDS  
<222> (250)..(4266)
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Sequence_Listing																
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ttt Phe	att Ile	agt Ser	gat Asp 130	aca Thr	ggt Gly	aga Arg	cct Pro	ttc Phe 135	gta Val	gag Glu	atg Met	tac Tyr	agt Ser 140	gaa Glu	atc Ile	675
ccc Pro	gaa Glu	att Ile 145	ata Ile	cac His	atg Met	act Thr	gaa Glu 150	gga Gly	agg Arg	gag Glu	ctc Leu	gtc Val 155	att Ile	ccc Pro	tgc Cys	723
cgg Arg	gtt Val 160	acg Thr	tca Ser	cct Pro	aac Asn	atc Ile 165	act Thr	gtt Val	act Thr	tta Leu	aaa Lys 170	aag Lys	ttt Phe	cca Pro	ctt Leu	771
gac Asp 175	act Thr	ttg Leu	atc Ile	cct Pro	gat Asp 180	gga Gly	aaa Lys	cgc Arg	ata Ile	atc Ile 185	tgg Trp	gac Asp	agt Ser	aga Arg	aag Lys 190	819
ggc Gly	ttc Phe	atc Ile	ata Ile	tca Ser 195	aat Asn	gca Ala	acg Thr	tac Tyr	aaa Lys 200	gaa Glu	ata Ile	ggg Gly	ctt Leu	ctg Leu 205	acc Thr	867
tgt Cys	gaa Glu	gca Ala	aca Thr 210	gtc Val	aat Asn	ggg Gly	cat His	ttg Leu 215	tat Tyr	aag Lys	aca Thr	aac Asn	tat Tyr 220	ctc Leu	aca Thr	915
cat His	cga Arg	caa Gln 225	acc Thr	aat Asn	aca Thr	atc Ile	ata Ile 230	gat Asp	gtc Val	caa Gln	ata Ile	agc Ser 235	aca Thr	cca Pro	cgc Arg	963
cca Pro 240	gtc Val	aaa Lys	tta Leu	ctt Leu	aga Arg	ggc Gly 245	cat His	act Thr	ctt Leu	gtc Val	ctc Leu 250	aat Asn	tgt Cys	act Thr	gct Ala	1011
acc Thr 255	act Thr	ccc Pro	ttg Leu	aac Asn	acg Thr 260	aga Arg	gtt Val	caa Gln	atg Met	acc Thr 265	tgg Trp	agt Ser	tac Tyr	cct Pro	gat Asp 270	1059
gaa Glu	aaa Lys	aat Asn	aag Lys	aga Arg 275	gct Ala	tcc Ser	gta Val	agg Arg	cga Arg 280	cga Arg	att Ile	gac Asp	caa Gln	agc Ser 285	aat Asn	1107
tcc Ser	cat His	gcc Ala	aac Asn 290	ata Ile	ttc Phe	tac Tyr	agt Ser	gtt Val 295	ctt Leu	act Thr	att Ile	gac Asp	aaa Lys 300	atg Met	cag Gln	1155
aac Asn	aaa Lys	gac Asp 305	aaa Lys	gga Gly	ctt Leu	tat Tyr	act Thr 310	tgt Cys	cgt Arg	gta Val	agg Arg	agt Ser 315	gga Gly	cca Pro	tca Ser	1203
ttc Phe 320	aaa Lys	tct Ser	gtt Val	aac Asn	acc Thr	tca Ser 325	gtg Val	cat His	ata Ile	tat Tyr	gat Asp 330	aaa Lys	gca Ala	ttc Phe	atc Ile	1251
act Thr 335	gtg Val	aaa Lys	cat His	cga Arg	aaa Lys 340	cag Gln	cag Gln	gtg Val	ctt Leu	gaa Glu 345	acc Thr	gta Val	gct Ala	ggc Gly	aag Lys 350	1299
cgg Arg	tct Ser	tac Tyr	cgg Arg	ctc Leu 355	tct Ser	atg Met	aaa Lys	gtg Val	aag Lys 360	gca Ala	ttt Phe	ccc Pro	tcg Ser	ccg Pro 365	gaa Glu	1347
gtt Val	gta Val	tgg Trp	tta Leu 370	aaa Lys	gat Asp	ggg Gly	tta Leu	cct Pro 375	gcg Ala	act Thr	gag Glu	aaa Lys	tct Ser 380	gct Ala	cgc Arg	1395

Sequence_Listing																
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Tyr	Leu	Thr	Arg	Gly	Tyr	Ser	Leu	Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	
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gat	gca	ggg	aat	tat	aca	atc	ttg	ctg	agc	ata	aaa	cag	tca	aat	gtg	1491
Asp	Ala	Gly	Asn	Tyr	Thr	Ile	Leu	Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	
	400					405					410					
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Phe	Lys	Asn	Leu	Thr	Ala	Thr	Leu	Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	
415					420					425					430	
tac	gaa	aag	gcc	gtg	tca	tcg	ttt	cca	gac	ccg	gct	ctc	tac	cca	ctg	1587
Tyr	Glu	Lys	Ala	Val	Ser	Ser	Phe	Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	
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ggc	agc	aga	caa	atc	ctg	act	tgt	acc	gca	tat	ggg	atc	cct	caa	cct	1635
Gly	Ser	Arg	Gln	Ile	Leu	Thr	Cys	Thr	Ala	Tyr	Gly	Ile	Pro	Gln	Pro	
			450					455					460			
aca	atc	aag	tgg	ttc	tgg	cac	ccc	tgt	aac	cat	aat	cat	tcc	gaa	gca	1683
Thr	Ile	Lys	Trp	Phe	Trp	His	Pro	Cys	Asn	His	Asn	His	Ser	Glu	Ala	
		465					470					475				
agg	tgt	gac	ttt	tgt	tcc	aat	aat	gaa	gag	tcc	ttt	atc	ctg	gat	gct	1731
Arg	Cys	Asp	Phe	Cys	Ser	Asn	Asn	Glu	Glu	Ser	Phe	Ile	Leu	Asp	Ala	
	480					485					490					
gac	agc	aac	atg	gga	aac	aga	att	gag	agc	atc	act	cag	cgc	atg	gca	1779
Asp	Ser	Asn	Met	Gly	Asn	Arg	Ile	Glu	Ser	Ile	Thr	Gln	Arg	Met	Ala	
495					500					505					510	
ata	ata	gaa	gga	aag	aat	aag	atg	gct	agc	acc	ttg	gtt	gtg	gct	gac	1827
Ile	Ile	Glu	Gly	Lys	Asn	Lys	Met	Ala	Ser	Thr	Leu	Val	Val	Ala	Asp	
				515					520					525		
tct	aga	att	tct	gga	atc	tac	att	tgc	ata	gct	tcc	aat	aaa	gtt	ggg	1875
Ser	Arg	Ile	Ser	Gly	Ile	Tyr	Ile	Cys	Ile	Ala	Ser	Asn	Lys	Val	Gly	
			530					535					540			
act	gtg	gga	aga	aac	ata	agc	ttt	tat	atc	aca	gat	gtg	cca	aat	ggg	1923
Thr	Val	Gly	Arg	Asn	Ile	Ser	Phe	Tyr	Ile	Thr	Asp	Val	Pro	Asn	Gly	
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Phe	His	Val	Asn	Leu	Glu	Lys	Met	Pro	Thr	Glu	Gly	Glu	Asp	Leu	Lys	
	560					565					570					
ctg	tct	tgc	aca	gtt	aac	aag	ttc	tta	tac	aga	gac	gtt	act	tgg	att	2019
Leu	Ser	Cys	Thr	Val	Asn	Lys	Phe	Leu	Tyr	Arg	Asp	Val	Thr	Trp	Ile	
575					580					585					590	
tta	ctg	cgg	aca	gtt	aat	aac	aga	aca	atg	cac	tac	agt	att	agc	aag	2067
Leu	Leu	Arg	Thr	Val	Asn	Asn	Arg	Thr	Met	His	Tyr	Ser	Ile	Ser	Lys	
				595					600					605		
caa	aaa	atg	gcc	atc	act	aag	gag	cac	tcc	atc	act	ctt	aat	ctt	acc	2115
Gln	Lys	Met	Ala	Ile	Thr	Lys	Glu	His	Ser	Ile	Thr	Leu	Asn	Leu	Thr	
			610					615					620			
atc	atg	aat	gtt	tcc	ctg	caa	gat	tca	ggc	acc	tat	gcc	tgc	aga	gcc	2163
Ile	Met	Asn	Val	Ser	Leu	Gln	Asp	Ser	Gly	Thr	Tyr	Ala	Cys	Arg	Ala	
		625					630					635				
agg	aat	gta	tac	aca	ggg	gaa	gaa	atc	ctc	cag	aag	aaa	gaa	att	aca	2211
Arg	Asn	Val	Tyr	Thr	Gly	Glu	Glu	Ile	Leu	Gln	Lys	Lys	Glu	Ile	Thr	
	640					645					650					

Sequence_Listing																
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aca Thr	gtg Val	gcc Ala	atc Ile	agc Ser 675	agt Ser	tcc Ser	acc Thr	act Thr	tta Leu 680	gac Asp	tgt Cys	cat His	gct Ala	aat Asn 685	ggg Gly	2307
gtc Val	ccc Pro	gag Glu	cct Pro 690	cag Gln	atc Ile	act Thr	tgg Trp	ttt Phe 695	aaa Lys	aac Asn	aac Asn	cac His	aaa Lys 700	ata Ile	caa Gln	2355
caa Gln	gag Glu	cct Pro 705	gga Gly	att Ile	att Ile	tta Leu	gga Gly 710	cca Pro	gga Gly	agc Ser	agc Ser	acg Thr 715	ctg Leu	ttt Phe	att Ile	2403
gaa Glu 720	aga Arg	gtc Val	aca Thr	gaa Glu	gag Glu	gat Asp 725	gaa Glu	ggg Gly	gtc Val	tat Tyr	cac His 730	tgc Cys	aaa Lys	gcc Ala	acc Thr	2451
aac Asn 735	cag Gln	aag Lys	ggc Gly	tct Ser	gtg Val 740	gaa Glu	agt Ser	tca Ser	gca Ala	tac Tyr 745	ctc Leu	act Thr	gtt Val	caa Gln	gga Gly 750	2499
acc Thr	tcg Ser	gac Asp	aag Lys	tct Ser 755	aat Asn	ctg Leu	gag Glu	ctg Leu	atc Ile 760	act Thr	cta Leu	aca Thr	tgc Cys	acc Thr 765	tgt Cys	2547
gtg Val	gct Ala	gcg Ala	act Thr 770	ctc Leu	ttc Phe	tgg Trp	ctc Leu	cta Leu 775	tta Leu	acc Thr	ctc Leu	ctt Leu	atc Ile 780	cga Arg	aaa Lys	2595
atg Met	aaa Lys	agg Arg 785	tct Ser	tct Ser	tct Ser	gaa Glu	ata Ile 790	aag Lys	act Thr	gac Asp	tac Tyr	cta Leu 795	tca Ser	att Ile	ata Ile	2643
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tat Tyr 815	gat Asp	gcc Ala	agc Ser	aag Lys	tgg Trp 820	gag Glu	ttt Phe	gcc Ala	cgg Arg	gag Glu 825	aga Arg	ctt Leu	aaa Lys	ctg Leu	ggc Gly 830	2739
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ctg Leu	aaa Lys	gag Glu 865	ggg Gly	gcc Ala	acg Thr	gcc Ala	agc Ser 870	gag Glu	tac Tyr	aaa Lys	gct Ala	ctg Leu 875	atg Met	act Thr	gag Glu	2883
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ctg Leu 895	gga Gly	gcc Ala	tgc Cys	acc Thr	aag Lys 900	caa Gln	gga Gly	ggg Gly	cct Pro	ctg Leu 905	atg Met	gtg Val	att Ile	gtt Val	gaa Glu 910	2979
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Sequence Listing																
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gaa Glu	aaa Lys	atg Met 945	gag Glu	cca Pro	ggc Gly	ctg Leu	gaa Glu 950	caa Gln	ggc Gly	aag Lys	aaa Lys	cca Pro 955	aga Arg	cta Leu	gat Asp	3123
agc Ser	gtc Val 960	acc Thr	agc Ser	agc Ser	gaa Glu	agc Ser 965	ttt Phe	gcg Ala	agc Ser	tcc Ser	ggc Gly 970	ttt Phe	cag Gln	gaa Glu	gat Asp	3171
aaa Lys 975	agt Ser	ctg Leu	agt Ser	gat Asp	gtt Val 980	gag Glu	gaa Glu	gag Glu	gag Glu	gat Asp 985	tct Ser	gac Asp	ggt Gly	ttc Phe	tac Tyr 990	3219
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gcc Ala	aga Arg	ggc Gly	atg Met 1010	gag Glu	ttc Phe	ctg Leu	tct Ser	tcc Ser 1015	aga Arg	aag Lys	tgc Cys	att Ile	cat His 1020	cgg Arg		3312
gac Asp	ctg Leu	gca Ala	gcg Ala 1025	aga Arg	aac Asn	att Ile	ctt Leu	tta Leu 1030	tct Ser	gag Glu	aac Asn	aac Asn	gtg Val 1035	gtg Val		3357
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gat Asp	tat Tyr	gtg Val	aga Arg 1055	aaa Lys	gga Gly	gat Asp	act Thr	cga Arg 1060	ctt Leu	cct Pro	ctg Leu	aaa Lys	tgg Trp 1065	atg Met		3447
gct Ala	ccc Pro	gaa Glu	tct Ser 1070	atc Ile	ttt Phe	gac Asp	aaa Lys	atc Ile 1075	tac Tyr	agc Ser	acc Thr	aag Lys	agc Ser 1080	gac Asp		3492
gtg Val	tgg Trp	tct Ser	tac Tyr 1085	gga Gly	gta Val	ttg Leu	ctg Leu	tgg Trp 1090	gaa Glu	atc Ile	ttc Phe	tcc Ser	tta Leu 1095	ggt Gly		3537
ggg Gly	tct Ser	cca Pro	tac Tyr 1100	cca Pro	gga Gly	gta Val	caa Gln	atg Met 1105	gat Asp	gag Glu	gac Asp	ttt Phe	tgc Cys 1110	agt Ser		3582
cgc Arg	ctg Leu	agg Arg	gaa Glu 1115	ggc Gly	atg Met	agg Arg	atg Met	aga Arg 1120	gct Ala	cct Pro	gag Glu	tac Tyr	tct Ser 1125	act Thr		3627
cct Pro	gaa Glu	atc Ile	tat Tyr 1130	cag Gln	atc Ile	atg Met	ctg Leu	gac Asp 1135	tgc Cys	tgg Trp	cac His	aga Arg	gac Asp 1140	cca Pro		3672
aaa Lys	gaa Glu	agg Arg	cca Pro 1145	aga Arg	ttt Phe	gca Ala	gaa Glu	ctt Leu 1150	gtg Val	gaa Glu	aaa Lys	cta Leu	ggt Gly 1155	gat Asp		3717
ttg Leu	ctt Leu	caa Gln	gca Ala 1160	aat Asn	gta Val	caa Gln	cag Gln	gat Asp 1165	ggt Gly	aaa Lys	gac Asp	tac Tyr	atc Ile 1170	cca Pro		3762
atc Ile	aat Asn	gcc Ala	ata Ile 1175	ctg Leu	aca Thr	gga Gly	aat Asn	agt Ser 1180	ggg Gly	ttt Phe	aca Thr	tac Tyr	tca Ser 1185	act Thr		3807

Sequence_Listing															
cct	gcc	ttc	tct	gag	gac	ttc	ttc	aag	gaa	agt	att	tca	gct	ccg	3852
Pro	Ala	Phe	Ser	Glu	Asp	Phe	Phe	Lys	Glu	Ser	Ile	Ser	Ala	Pro	
			1190					1195					1200		
aag	ttt	aat	tca	gga	agc	tct	gat	gat	gtc	aga	tat	gta	aat	gct	3897
Lys	Phe	Asn	Ser	Gly	Ser	Ser	Asp	Asp	Val	Arg	Tyr	Val	Asn	Ala	
			1205					1210					1215		
ttc	aag	ttc	atg	agc	ctg	gaa	aga	atc	aaa	acc	ttt	gaa	gaa	ctt	3942
Phe	Lys	Phe	Met	Ser	Leu	Glu	Arg	Ile	Lys	Thr	Phe	Glu	Glu	Leu	
			1220					1225					1230		
tta	ccg	aat	gcc	acc	tcc	atg	ttt	gat	gac	tac	cag	ggc	gac	agc	3987
Leu	Pro	Asn	Ala	Thr	Ser	Met	Phe	Asp	Asp	Tyr	Gln	Gly	Asp	Ser	
			1235					1240					1245		
agc	act	ctg	ttg	gcc	tct	ccc	atg	ctg	aag	cgc	ttc	acc	tgg	act	4032
Ser	Thr	Leu	Leu	Ala	Ser	Pro	Met	Leu	Lys	Arg	Phe	Thr	Trp	Thr	
			1250					1255					1260		
gac	agc	aaa	ccc	aag	gcc	tcg	ctc	aag	att	gac	ttg	aga	gta	acc	4077
Asp	Ser	Lys	Pro	Lys	Ala	Ser	Leu	Lys	Ile	Asp	Leu	Arg	Val	Thr	
			1265					1270					1275		
agt	aaa	agt	aag	gag	tcg	ggg	ctg	tct	gat	gtc	agc	agg	ccc	agt	4122
Ser	Lys	Ser	Lys	Glu	Ser	Gly	Leu	Ser	Asp	Val	Ser	Arg	Pro	Ser	
			1280					1285					1290		
ttc	tgc	cat	tcc	agc	tgt	ggg	cac	gtc	agc	gaa	ggc	aag	cgc	agg	4167
Phe	Cys	His	Ser	Ser	Cys	Gly	His	Val	Ser	Glu	Gly	Lys	Arg	Arg	
			1295					1300					1305		
ttc	acc	tac	gac	cac	gct	gag	ctg	gaa	agg	aaa	atc	gcg	tgc	tgc	4212
Phe	Thr	Tyr	Asp	His	Ala	Glu	Leu	Glu	Arg	Lys	Ile	Ala	Cys	Cys	
			1310					1315					1320		
tcc	ccg	ccc	cca	gac	tac	aac	tcg	gtg	gtc	ctg	tac	tcc	acc	cca	4257
Ser	Pro	Pro	Pro	Asp	Tyr	Asn	Ser	Val	Val	Leu	Tyr	Ser	Thr	Pro	
			1325					1330					1335		
ccc	atc	tag	agtttgacac	gaagccttat	ttctagaagc	acatgtgtat									4306
Pro	Ile														
ttataccccc	aggaaactag	cttttgccag	tattatgcat	atataagttt	acacctttat										4366
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aacaagaatg	taactccaga	tagagaaata	gtgacaagtg	aagaacacta	ctgctaaatc										4486
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cccgccacct	cagggcacgc	aggaccagtt	tgattgagga	gctgcactga	tcacccaatg										4606
catcacgtac	cccactgggc	cagccctgca	gccccaaaacc	cagggcaaca	agcccgttag										4666
ccccagggga	tactggctg	gcctgagcaa	catctcggga	gtcctctagc	aggcctaaga										4726
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gccatttcag	tggcttccca	gctctgaccc	ttctacattt	gagggcccag	ccaggagcag										4906
atggacagcg	atgaggggac	attttctgga	ttctgggagg	caagaaaagg	acaaatatct										4966
tttttgaac	taaagcaaat	tttagacctt	tacctatgga	agtggttcta	tgtccattct										5026

Sequence_Listing

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cattcgtggc atgttttgat ttgtagcact gagggaggca ctcaactctg agcccatact 5086
tttggtcct ctagtaagat gcactgaaaa ctagccaga gtaggtgtg ctccaggcca 5146
tgatggcctt acactgaaaa tgcacattc tattttgggt attaatatat agtccagaca 5206
cttaactcaa tttcttggtt ttattctggt ttgcacagtt agttgtgaaa gaaagctgag 5266
aagaatgaaa atgcagtcct gaggagagtt ttctccatat caaacgagg gctgatggag 5326
gaaaaaggtc aataagggtc aggaagacc ccgtctctat accaaccaaa ccaattcacc 5386
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tgaaacttgc ctgggggtctg agcatgatgg gaataggag acagggtagg aaagggcgcc 5686
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<210> 11
<211> 1338
<212> PRT
<213> Homo sapiens

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<400> 11

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Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1          5          10          15

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```

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
          20          25          30

```

```

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
          35          40          45

```

```

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
          50          55          60

```

```

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65          70          75          80

```

```

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
          85          90          95

```

```

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
          100          105          110

```

```

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
          115          120          125

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Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
          130          135          140

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Sequence_Listing

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
180 185 190

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

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
245 250 255

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

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
290 295 300

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

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
325 330 335

Lys His Arg Lys Gln Gln Val Leu Glu Thr Val Ala Gly Lys Arg Ser
340 345 350

Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
355 360 365

Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
370 375 380

Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
385 390 395 400

Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
405 410 415

Sequence_Listing

Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
 420 425 430
 Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser
 435 440 445
 Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
 450 455 460
 Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
 465 470 475 480
 Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
 485 490 495
 Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
 500 505 510
 Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
 515 520 525
 Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
 530 535 540
 Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His
 545 550 555 560
 Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
 565 570 575
 Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
 580 585 590
 Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
 595 600 605
 Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
 610 615 620
 Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
 625 630 635 640
 Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
 645 650 655
 Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
 660 665 670
 Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
 675 680 685

Sequence_Listing

Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
 690 695 700
 Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
 705 710 715
 Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
 725 730 735
 Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
 740 745 750
 Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys Val Ala
 755 760 765
 Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu Ile Arg Lys Met Lys
 770 775 780
 Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Leu Ser Ile Ile Met Asp
 785 790 795 800
 Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro Tyr Asp
 805 810 815
 Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly Lys Ser
 820 825 830
 Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala Phe Gly
 835 840 845
 Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys
 850 855 860
 Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Leu Met Thr Glu Leu Lys
 865 870 875 880
 Ile Leu Thr His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly
 885 890 895
 Ala Cys Thr Lys Gln Gly Gly Pro Leu Met Val Ile Val Glu Tyr Cys
 900 905 910
 Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys Ser Lys Arg Asp Leu Phe
 915 920 925
 Phe Leu Asn Lys Asp Ala Ala Leu His Met Glu Pro Lys Lys Glu Lys
 930 935 940
 Met Glu Pro Gly Leu Glu Gln Gly Lys Lys Pro Arg Leu Asp Ser Val
 945 950 955 960

Sequence_Listing

Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Phe Gln Glu Asp Lys Ser
 965 970 975
 Leu Ser Asp Val Glu Glu Glu Glu Asp Ser Asp Gly Phe Tyr Lys Glu
 980 985 990
 Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr Ser Phe Gln Val Ala Arg
 995 1000 1005
 Gly Met Glu Phe Leu Ser Ser Arg Lys Cys Ile His Arg Asp Leu
 1010 1015 1020
 Ala Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn Val Val Lys Ile
 1025 1030 1035
 Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn Pro Asp Tyr
 1040 1045 1050
 Val Arg Lys Gly Asp Thr Arg Leu Pro Leu Lys Trp Met Ala Pro
 1055 1060 1065
 Glu Ser Ile Phe Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val Trp
 1070 1075 1080
 Ser Tyr Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser
 1085 1090 1095
 Pro Tyr Pro Gly Val Gln Met Asp Glu Asp Phe Cys Ser Arg Leu
 1100 1105 1110
 Arg Glu Gly Met Arg Met Arg Ala Pro Glu Tyr Ser Thr Pro Glu
 1115 1120 1125
 Ile Tyr Gln Ile Met Leu Asp Cys Trp His Arg Asp Pro Lys Glu
 1130 1135 1140
 Arg Pro Arg Phe Ala Glu Leu Val Glu Lys Leu Gly Asp Leu Leu
 1145 1150 1155
 Gln Ala Asn Val Gln Gln Asp Gly Lys Asp Tyr Ile Pro Ile Asn
 1160 1165 1170
 Ala Ile Leu Thr Gly Asn Ser Gly Phe Thr Tyr Ser Thr Pro Ala
 1175 1180 1185
 Phe Ser Glu Asp Phe Phe Lys Glu Ser Ile Ser Ala Pro Lys Phe
 1190 1195 1200
 Asn Ser Gly Ser Ser Asp Asp Val Arg Tyr Val Asn Ala Phe Lys
 1205 1210 1215

Sequence_Listing

Phe Met Ser Leu Glu Arg Ile Lys Thr Phe Glu Glu Leu Leu Pro
1220 1225 1230

Asn Ala Thr Ser Met Phe Asp Asp Tyr Gln Gly Asp Ser Ser Thr
1235 1240 1245

Leu Leu Ala Ser Pro Met Leu Lys Arg Phe Thr Trp Thr Asp Ser
1250 1255 1260

Lys Pro Lys Ala Ser Leu Lys Ile Asp Leu Arg Val Thr Ser Lys
1265 1270 1275

Ser Lys Glu Ser Gly Leu Ser Asp Val Ser Arg Pro Ser Phe Cys
1280 1285 1290

His Ser Ser Cys Gly His Val Ser Glu Gly Lys Arg Arg Phe Thr
1295 1300 1305

Tyr Asp His Ala Glu Leu Glu Arg Lys Ile Ala Cys Cys Ser Pro
1310 1315 1320

Pro Pro Asp Tyr Asn Ser Val Val Leu Tyr Ser Thr Pro Pro Ile
1325 1330 1335

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<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 12
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37

<210> 13
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<220>
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<400> 13
gtgtgactcc tccgtgatct gcaaggtcgg gggggtc

37

<210> 14
<211> 39
<212> DNA
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<400> 14
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39

Sequence_Listing

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<212> DNA
<213> Artificial Sequence

<220>
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<400> 15
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39

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<400> 16
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35

<210> 17
<211> 35
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<220>
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gcgagcgcag cgtgacttgg aggccgggga tggac
35

<210> 18
<211> 37
<212> DNA
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<223> Synthetic primer

<400> 18
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37

<210> 19
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 19
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37

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

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Sequence_Listing

<223> Synthetic primer

<400> 20

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38

<210> 21

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 21

aggtcgtgct ggctgacctg gtggatggtc aggatgct

38