

eolf-othd-000001
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<120> Novel fish pathogenic virus

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gcggggctgg gcg	130333

<210> 2
 <211> 1047
 <212> DNA

<213> Herpes virus

<220>

<221> CDS

<222> (1)..(1047)

<400> 2

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

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atc ggt gac ctg gag gtg ggc acc aag aag tcc ttc acc gag gac ggt Ile Gly Asp Leu Glu Val Gly Thr Lys Lys Ser Phe Thr Glu Asp Gly 180 185 190	576
ttc gcc gcc gag gcc acc aag tac ttc gcc tcc gag gtg atc aaa tac Phe Ala Ala Glu Ala Thr Lys Tyr Phe Ala Ser Glu Val Ile Lys Tyr 195 200 205	624
ggg gct gac ccc acc aag gcg gtc aac ctt tcc acc gcc gat gcc cac Gly Ala Asp Pro Thr Lys Ala Val Asn Leu Ser Thr Ala Asp Ala His 210 215 220	672
ttc aga cac ctc att cat tcg ctg gag acc ggt aac agg atg acg tgg Phe Arg His Leu Ile His Ser Leu Glu Thr Gly Asn Arg Met Thr Trp 225 230 235 240	720
acc ggg ggc atg tcc gtg atc aag agc cgc gac ctc tcc ggg gtg gtc Thr Gly Gly Met Ser Val Ile Lys Ser Arg Asp Leu Ser Gly Val Val 245 250 255	768
gtg ggt ctc ggt cgc tgc tgg agt ctg ggc gcc acg gcg ccc gta acc Val Gly Leu Gly Arg Cys Trp Ser Leu Gly Ala Thr Ala Pro Val Thr 260 265 270	816
acc ctc ctc att ctc ctc ttt ttc atg ggc acc tac acg ctt ctg gct Thr Leu Leu Ile Leu Leu Phe Phe Met Gly Thr Tyr Thr Leu Leu Ala 275 280 285	864
gct aag gcc ctc atg agg aaa ccc ccc cag ccc atc cca tgt aac gtg Ala Lys Ala Leu Met Arg Lys Pro Pro Gln Pro Ile Pro Cys Asn Val 290 295 300	912
aac gaa ctc caa tcc ctg gca tgt tac aca gac tgc gat gac gga ccc Asn Glu Leu Gln Ser Leu Ala Cys Tyr Thr Asp Cys Asp Asp Gly Pro 305 310 315 320	960
tca gcg tgg gag cag acc agc ggc ctg acc gtc cca ggg ctc tcc ggt Ser Ala Trp Glu Gln Thr Ser Gly Leu Thr Val Pro Gly Leu Ser Gly 325 330 335	1008
acc cgt cac gac acg tac atg aac aga cga cac ctt tga Thr Arg His Asp Thr Tyr Met Asn Arg Arg His Leu 340 345	1047

<210> 3
 <211> 348
 <212> PRT
 <213> Herpes virus

<400> 3

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Met Glu Pro Gly Ala Glu Gly Phe Leu Gln Thr Ser Leu Gln Tyr Ile
1 5 10 15

Glu Gly Phe Ala Gly Lys Ile Ser Gly Ala Asp Ile Gly Ala Gln Met
20 25 30

Arg Arg Ala Gly Tyr His Ile Val Thr Tyr Arg Ala Ser Lys Tyr Phe
35 40 45

Ile Ala Tyr Gly Ala Leu Val Thr Leu Tyr Ile Ile Thr Thr Met Gly
50 55 60

Leu Thr Asp Val Thr Leu Asp Leu Leu Lys His Thr Tyr Pro His Arg
65 70 75 80

His Pro Pro Leu Ser Asp Thr Leu Gln Leu Gln Ser Phe Asn Ala Ala
85 90 95

Val Asp Ala Phe Ala Ile Ala Met Val Val Leu Cys Val Phe Met Leu
100 105 110

Ile Gly Ile Val Cys Ala Ser Val Met Tyr Leu Arg Lys Arg Gln Thr
115 120 125

Ile Asn Lys Leu Leu Leu Ala Thr Asn Trp Val Met Arg Gly Ser Val
130 135 140

Thr His Ile Val Phe Val Ile Ile Cys Ile Val Val Cys Leu Thr Val
145 150 155 160

Thr Val Phe Ala Ile Phe His Ile Thr Cys Val Asp Thr Asn Val Leu
165 170 175

Ile Gly Asp Leu Glu Val Gly Thr Lys Lys Ser Phe Thr Glu Asp Gly
180 185 190

Phe Ala Ala Glu Ala Thr Lys Tyr Phe Ala Ser Glu Val Ile Lys Tyr
195 200 205

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Gly Ala Asp Pro Thr Lys Ala Val Asn Leu Ser Thr Ala Asp Ala His
210 215 220

Phe Arg His Leu Ile His Ser Leu Glu Thr Gly Asn Arg Met Thr Trp
225 230 235 240

Thr Gly Gly Met Ser Val Ile Lys Ser Arg Asp Leu Ser Gly Val Val
245 250 255

Val Gly Leu Gly Arg Cys Trp Ser Leu Gly Ala Thr Ala Pro Val Thr
260 265 270

Thr Leu Leu Ile Leu Leu Phe Phe Met Gly Thr Tyr Thr Leu Leu Ala
275 280 285

Ala Lys Ala Leu Met Arg Lys Pro Pro Gln Pro Ile Pro Cys Asn Val
290 295 300

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

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

Thr Arg His Asp Thr Tyr Met Asn Arg Arg His Leu
340 345

<210> 4
<211> 849
<212> DNA
<213> Herpes virus

<220>
<221> CDS
<222> (1)..(849)

<400> 4
atg gcg ttc ccg aaa atc gaa gtt gca gtt ttc ccg ggg ttc gag agg 48
Met Ala Phe Pro Lys Ile Glu Val Ala Val Phe Pro Gly Phe Glu Arg
1 5 10 15

gtc ccc gcg gtg aga cta ccc cga gtg gcc acc gag ggc tcg gcc ggg 96

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Val	Pro	Ala	Val	Arg	Leu	Pro	Arg	Val	Ala	Thr	Glu	Gly	Ser	Ala	Gly		
			20					25					30				
ttg	gac	ctg	tct	ccc	tgt	cgc	tcg	tac	ttg	tgc	aag	gag	ggc	gag	ccc		144
Leu	Asp	Leu	Ser	Pro	Cys	Arg	Ser	Tyr	Leu	Cys	Lys	Glu	Gly	Glu	Pro		
		35					40					45					
atc	aag	ctg	gac	acg	ggc	ctc	gcc	atc	gcg	att	ccc	acc	ggg	tac	gtc		192
Ile	Lys	Leu	Asp	Thr	Gly	Leu	Ala	Ile	Ala	Ile	Pro	Thr	Gly	Tyr	Val		
	50					55					60						
ggg	ctg	atc	ctc	ccg	agg	tcg	agc	atg	atg	cac	gcc	ttc	acc	acc	acc		240
Gly	Leu	Ile	Leu	Pro	Arg	Ser	Ser	Met	Met	His	Ala	Phe	Thr	Thr	Thr		
65					70					75					80		
ggg	gtg	ctc	gac	tcg	gac	tac	cgc	ggc	cac	gtg	aaa	ctg	ctg	atc	aac		288
Gly	Val	Leu	Asp	Ser	Asp	Tyr	Arg	Gly	His	Val	Lys	Leu	Leu	Ile	Asn		
				85				90						95			
ccc	ctc	acc	gac	ttt	tgt	tgt	gag	ggc	ggg	gta	cct	ata	gcc	caa	ctg		336
Pro	Leu	Thr	Asp	Phe	Cys	Cys	Glu	Gly	Gly	Val	Pro	Ile	Ala	Gln	Leu		
				100				105					110				
gtg	gtt	atc	ccc	tgc	atc	aac	tgg	gcc	atc	cac	gtc	ccg	ttc	tcg	acc		384
Val	Val	Ile	Pro	Cys	Ile	Asn	Trp	Ala	Ile	His	Val	Pro	Phe	Ser	Thr		
		115					120					125					
atg	gga	aag	acc	tcc	cgg	ggc	acg	ggg	ggc	ttc	ggg	tcg	acc	tcc	gtc		432
Met	Gly	Lys	Thr	Ser	Arg	Gly	Thr	Gly	Gly	Phe	Gly	Ser	Thr	Ser	Val		
	130					135					140						
tcc	ccc	acg	acg	ccc	agc	ccc	gcg	ccc	agc	ccc	gcg	ccc	agc	ccc	gcg		480
Ser	Pro	Thr	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Ala		
145					150					155					160		
ccc	agc	ccc	gcg	ccc	agc	ccc	gcg	ccc	agc	ccc	gcg	ccc	agc	ccc	gcg		528
Pro	Ser	Pro	Ala	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Ala		
				165				170						175			
ccc	cgc	cca	gcc	ccg	cgc	cca	gcc	ccg	cgc	cca	gcc	ccg	cgc	cca	gcc		576
Pro	Arg	Pro	Ala	Pro	Arg	Pro	Ala	Pro	Arg	Pro	Ala	Pro	Arg	Pro	Ala		
			180					185						190			
ccg	cgc	cca	gcc	ccg	cgc	cca	gcc	ccg	cgc	cct	tgt	acc	atg	gac	cgg		624
Pro	Arg	Pro	Ala	Pro	Arg	Pro	Ala	Pro	Arg	Pro	Cys	Thr	Met	Asp	Arg		
		195					200					205					
gcg	tcg	cgg	gac	ctc	cgc	cac	ctc	cca	ggg	gcc	gcg	tcc	agg	ggg	gcg		672
Ala	Ser	Arg	Asp	Leu	Arg	His	Leu	Pro	Gly	Ala	Ala	Ser	Arg	Gly	Ala		
	210					215					220						
cag	tgc	ctc	ccc	ccg	cgt	ccc	ggg	gac	agt	acc	tcg	ggc	tct	ccg	acg		720

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Gln Cys Leu Pro Pro Arg Pro Gly Asp Ser Thr Ser Gly Ser Pro Thr
225 230 235 240

tgt cgt acg cgc cgc ggt ctg cgg ccg cgg ccg agc agc ccc tct tcc 768
Cys Arg Thr Arg Arg Gly Leu Arg Pro Arg Pro Ser Ser Pro Ser Ser
245 250 255

aat tcc ccg ggc ttc gca acc ccg tgc ccg aac cgg aac ccg agc ccg 816
Asn Ser Pro Gly Phe Ala Thr Pro Cys Pro Asn Arg Asn Pro Ser Pro
260 265 270

aga tca tgg agc aaa agc cga ttt cca cca tga 849
Arg Ser Trp Ser Lys Ser Arg Phe Pro Pro
275 280

<210> 5
<211> 282
<212> PRT
<213> Herpes virus

<400> 5

Met Ala Phe Pro Lys Ile Glu Val Ala Val Phe Pro Gly Phe Glu Arg
1 5 10 15

Val Pro Ala Val Arg Leu Pro Arg Val Ala Thr Glu Gly Ser Ala Gly
20 25 30

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

Ile Lys Leu Asp Thr Gly Leu Ala Ile Ala Ile Pro Thr Gly Tyr Val
50 55 60

Gly Leu Ile Leu Pro Arg Ser Ser Met Met His Ala Phe Thr Thr Thr
65 70 75 80

Gly Val Leu Asp Ser Asp Tyr Arg Gly His Val Lys Leu Leu Ile Asn
85 90 95

Pro Leu Thr Asp Phe Cys Cys Glu Gly Gly Val Pro Ile Ala Gln Leu
100 105 110

Val Val Ile Pro Cys Ile Asn Trp Ala Ile His Val Pro Phe Ser Thr

115

120

125

Met Gly Lys Thr Ser Arg Gly Thr Gly Gly Phe Gly Ser Thr Ser Val
 130 135 140

Ser Pro Thr Thr Pro Ser Pro Ala Pro Ser Pro Ala Pro Ser Pro Ala
 145 150 155 160

Pro Ser Pro Ala Pro Ser Pro Ala Pro Ser Pro Ala Pro Ser Pro Ala
 165 170 175

Pro Arg Pro Ala Pro Arg Pro Ala Pro Arg Pro Ala Pro Arg Pro Ala
 180 185 190

Pro Arg Pro Ala Pro Arg Pro Ala Pro Arg Pro Cys Thr Met Asp Arg
 195 200 205

Ala Ser Arg Asp Leu Arg His Leu Pro Gly Ala Ala Ser Arg Gly Ala
 210 215 220

Gln Cys Leu Pro Pro Arg Pro Gly Asp Ser Thr Ser Gly Ser Pro Thr
 225 230 235 240

Cys Arg Thr Arg Arg Gly Leu Arg Pro Arg Pro Ser Ser Pro Ser Ser
 245 250 255

Asn Ser Pro Gly Phe Ala Thr Pro Cys Pro Asn Arg Asn Pro Ser Pro
 260 265 270

Arg Ser Trp Ser Lys Ser Arg Phe Pro Pro
 275 280

<210> 6
 <211> 984
 <212> DNA
 <213> Herpes virus

<220>
 <221> CDS
 <222> (1)..(984)

<400> 6
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Met Phe Ser Val Ser Lys Leu Leu Ala Thr Val Ser Ala Asp Ser Thr
1 5 10 15

ttg aac agg gtc gtc atc tct acc gct cgt ccc gcg cct tct gtt ctg 96
Leu Asn Arg Val Val Ile Ser Thr Ala Arg Pro Ala Pro Ser Val Leu
20 25 30

agc gtc cag ggt cat aaa tat acg gat tat gaa ttg ggg gac ggg ttc 144
Ser Val Gln Gly His Lys Tyr Thr Asp Tyr Glu Leu Gly Asp Gly Phe
35 40 45

tac aaa aac att aac ctg tac gtc gat gac gca aaa ctc atg gca cgg 192
Tyr Lys Asn Ile Asn Leu Tyr Val Asp Asp Ala Lys Leu Met Ala Arg
50 55 60

aaa gag gaa aat gct cgc cta ctc aag gat ctc aaa gat cct ctg aag 240
Lys Glu Glu Asn Ala Arg Leu Leu Lys Asp Leu Lys Asp Pro Leu Lys
65 70 75 80

cgg gcc atg aag gtt tgg gaa ttg ggg ggg gac gcg gtg gac cgc atg 288
Arg Ala Met Lys Val Trp Glu Leu Gly Gly Asp Ala Val Asp Arg Met
85 90 95

gaa cga gat ttg aaa cgg atg tgt gtc gat ccc acg ctc ccg aaa cta 336
Glu Arg Asp Leu Lys Arg Met Cys Val Asp Pro Thr Leu Pro Lys Leu
100 105 110

acc cga ttt acc gac atg atc aaa tcg gtt ttc agg atc atg gag gac 384
Thr Arg Phe Thr Asp Met Ile Lys Ser Val Phe Arg Ile Met Glu Asp
115 120 125

agg ggc ggg atg aga tta gag cct ttt cag att gag ctg atg cga ggc 432
Arg Gly Gly Met Arg Leu Glu Pro Phe Gln Ile Glu Leu Met Arg Gly
130 135 140

ttt ttc atc ggg ctc gcc ccg aat caa ttc ggg gac gac cta ttc aaa 480
Phe Phe Ile Gly Leu Ala Pro Asn Gln Phe Gly Asp Asp Leu Phe Lys
145 150 155 160

tac aaa cac atc ctt ttg gat ctg gtt ggg ttg gcc acc ccg gaa att 528
Tyr Lys His Ile Leu Leu Asp Leu Val Gly Leu Ala Thr Pro Glu Ile
165 170 175

gta gcc ttc aat cct ctg tgt cct tcg aaa att aca tcg gag ctc atc 576
Val Ala Phe Asn Pro Leu Cys Pro Ser Lys Ile Thr Ser Glu Leu Ile
180 185 190

gac tcc aca atg gcg ggt tac gct aaa aat tat act ctg gcc ctg gcg 624
Asp Ser Thr Met Ala Gly Tyr Ala Lys Asn Tyr Thr Leu Ala Leu Ala

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195	200	205	
cct agg cag tgc ggt aag acg acc atc atg acg atc ctc atg ggc gcg Pro Arg Gln Cys Gly Lys Thr Thr Ile Met Thr Ile Leu Met Gly Ala 210 215 220			672
ctc atc acg tat ctg gac att gag atc gta gtc cag ggg cag aac aag Leu Ile Thr Tyr Leu Asp Ile Glu Ile Val Val Gln Gly Gln Asn Lys 225 230 235 240			720
gtt ctg tgc aaa agc ctg tac gac cgg atc gag cca atc att cat gag Val Leu Cys Lys Ser Leu Tyr Asp Arg Ile Glu Pro Ile Ile His Glu 245 250 255			768
atc caa cac gct ccg tgg tac ccc ccc gaa aat cgt ttc atc gcg atc Ile Gln His Ala Pro Trp Tyr Pro Pro Glu Asn Arg Phe Ile Ala Ile 260 265 270			816
cgc gga act acg gag acc cga gaa ttc ctc tac aat ccg agc tac aag Arg Gly Thr Thr Glu Thr Arg Glu Phe Leu Tyr Asn Pro Ser Tyr Lys 275 280 285			864
gga tct acc aac gta cac ttt ctg tcc tcg agt cca aac gtg agt aac Gly Ser Thr Asn Val His Phe Leu Ser Ser Ser Pro Asn Val Ser Asn 290 295 300			912
cat gta cta cgt tgt ggt aaa aag tct ttc ttg cat gac cgt gta ctt His Val Leu Arg Cys Gly Lys Lys Ser Phe Leu His Asp Arg Val Leu 305 310 315 320			960
cac gga ggg cga ggt tgc gga tag His Gly Gly Arg Gly Cys Gly 325			984

<210> 7
 <211> 327
 <212> PRT
 <213> Herpes virus

<400> 7

Met Phe Ser Val Ser Lys Leu Leu Ala Thr Val Ser Ala Asp Ser Thr
1 5 10 15

Leu Asn Arg Val Val Ile Ser Thr Ala Arg Pro Ala Pro Ser Val Leu
20 25 30

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

Tyr Lys Asn Ile Asn Leu Tyr Val Asp Asp Ala Lys Leu Met Ala Arg
50 55 60

Lys Glu Glu Asn Ala Arg Leu Leu Lys Asp Leu Lys Asp Pro Leu Lys
65 70 75 80

Arg Ala Met Lys Val Trp Glu Leu Gly Gly Asp Ala Val Asp Arg Met
85 90 95

Glu Arg Asp Leu Lys Arg Met Cys Val Asp Pro Thr Leu Pro Lys Leu
100 105 110

Thr Arg Phe Thr Asp Met Ile Lys Ser Val Phe Arg Ile Met Glu Asp
115 120 125

Arg Gly Gly Met Arg Leu Glu Pro Phe Gln Ile Glu Leu Met Arg Gly
130 135 140

Phe Phe Ile Gly Leu Ala Pro Asn Gln Phe Gly Asp Asp Leu Phe Lys
145 150 155 160

Tyr Lys His Ile Leu Leu Asp Leu Val Gly Leu Ala Thr Pro Glu Ile
165 170 175

Val Ala Phe Asn Pro Leu Cys Pro Ser Lys Ile Thr Ser Glu Leu Ile
180 185 190

Asp Ser Thr Met Ala Gly Tyr Ala Lys Asn Tyr Thr Leu Ala Leu Ala
195 200 205

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

Leu Ile Thr Tyr Leu Asp Ile Glu Ile Val Val Gln Gly Gln Asn Lys
225 230 235 240

Val Leu Cys Lys Ser Leu Tyr Asp Arg Ile Glu Pro Ile Ile His Glu
245 250 255

Ile Gln His Ala Pro Trp Tyr Pro Pro Glu Asn Arg Phe Ile Ala Ile
260 265 270

Arg Gly Thr Thr Glu Thr Arg Glu Phe Leu Tyr Asn Pro Ser Tyr Lys
275 280 285

Gly Ser Thr Asn Val His Phe Leu Ser Ser Ser Pro Asn Val Ser Asn
290 295 300

His Val Leu Arg Cys Gly Lys Lys Ser Phe Leu His Asp Arg Val Leu
305 310 315 320

His Gly Gly Arg Gly Cys Gly
325

<210> 8
<211> 2979
<212> DNA
<213> Herpes virus

<220>
<221> CDS
<222> (1)..(2979)

<400> 8
atg gat ccc ggc tgt gac ctt gcc aag ttg acc cac ctg ttt ccc gcg 48
Met Asp Pro Gly Cys Asp Leu Ala Lys Leu Thr His Leu Phe Pro Ala
1 5 10 15
cag cga tcg ctg aga ccc gag gag agc gaa acg cta aca ccc ctc ttc 96
Gln Arg Ser Leu Arg Pro Glu Glu Ser Glu Thr Leu Thr Pro Leu Phe
20 25 30
ttt tct tct gtc cgc cat gtt tcg cgt aat ggg gaa gat gtt ttg ctc 144
Phe Ser Ser Val Arg His Val Ser Arg Asn Gly Glu Asp Val Leu Leu
35 40 45
atc cac gtg ctc aac ctg cgt tcg aag gag acg ggg tgc atc atg gtc 192
Ile His Val Leu Asn Leu Arg Ser Lys Glu Thr Gly Cys Ile Met Val
50 55 60
aaa tca ctg gct ttt ctc gca gtg gtt ccg gag gtc gcc ctg tct tcc 240
Lys Ser Leu Ala Phe Leu Ala Val Val Pro Glu Val Ala Leu Ser Ser
65 70 75 80

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

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cgc aag gag ctc atc gtc tac tac aat gag aag ctg ttg cag cac ccc Arg Lys Glu Leu Ile Val Tyr Tyr Asn Glu Lys Leu Leu Gln His Pro 290 295 300	912
ctc gag gag ata ccc gtg gct cat ctg gga ctg gac tgg gac cgc atc Leu Glu Glu Ile Pro Val Ala His Leu Gly Leu Asp Trp Asp Arg Ile 305 310 315 320	960
gtc ttc aag gcg tgc aaa aac gag ttc tac atg ctc atg cac ttt atc Val Phe Lys Ala Cys Lys Asn Glu Phe Tyr Met Leu Met His Phe Ile 325 330 335	1008
aac aag ttg aag agc tcg gtg gat gtg ctg tac gtg ttc aac gcg cag Asn Lys Leu Lys Ser Ser Val Asp Val Leu Tyr Val Phe Asn Ala Gln 340 345 350	1056
ttt gac ata aag gtc atc tgc cag cga ttg gcc tat tac gcc ttc gag Phe Asp Ile Lys Val Ile Cys Gln Arg Leu Ala Tyr Tyr Ala Phe Glu 355 360 365	1104
gga agg aga ccc ggc tgc tgc aaa tgc cac gct gag att tct cgg gag Gly Arg Arg Pro Gly Cys Cys Lys Cys His Ala Glu Ile Ser Arg Glu 370 375 380	1152
tac ggc gat gcc ctc atg gaa aag tgg gag ctg ttc cta tcg cgc aaa Tyr Gly Asp Ala Leu Met Glu Lys Trp Glu Leu Phe Leu Ser Arg Lys 385 390 395 400	1200
ccg cag ctg gtc aag ggg gag att ctg atg ggc agc gag atc ctc cag Pro Gln Leu Val Lys Gly Glu Ile Leu Met Gly Ser Glu Ile Leu Gln 405 410 415	1248
gcc cag tac ctc aag atg cta cgg ggg gtg agc agc ctt ctg gca gct Ala Gln Tyr Leu Lys Met Leu Arg Gly Val Ser Ser Leu Leu Ala Ala 420 425 430	1296
ccc ggg ggc gga aac gtg ggg ctg ata aag aag aaa ctg gag atg tac Pro Gly Gly Gly Asn Val Gly Leu Ile Lys Lys Lys Leu Glu Met Tyr 435 440 445	1344
aag cag ggg aag gac acc gtc cag aat ttc aag act gtg gga ttc ggc Lys Gln Gly Lys Asp Thr Val Gln Asn Phe Lys Thr Val Gly Phe Gly 450 455 460	1392
tgc gac atc atc gat atg atg tac gtg tgc aag cgc aag gag tac gag Cys Asp Ile Ile Asp Met Met Tyr Val Cys Lys Arg Lys Glu Tyr Glu 465 470 475 480	1440
acg ccc tcg ggg tcg gga gcc ctc aac gac gtg gcc aag ttg atc atc Thr Pro Ser Gly Ser Gly Ala Leu Asn Asp Val Ala Lys Leu Ile Ile 485 490 495	1488

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cag atg tac agg ccc aag aag cta gcc gcg aag acg gtg aag ctg ggg Gln Met Tyr Arg Pro Lys Lys Leu Ala Ala Lys Thr Val Lys Leu Gly 500 505 510	1536
gac gtg gag tac cga aaa atg gac gag tac tac cgg tac ggg ggg acc Asp Val Glu Tyr Arg Lys Met Asp Glu Tyr Tyr Arg Tyr Gly Gly Thr 515 520 525	1584
aag ctg gcg gaa tgc ctg gtc tac aat ctg atc gac tcc cag ctg gtc Lys Leu Ala Glu Cys Leu Val Tyr Asn Leu Ile Asp Ser Gln Leu Val 530 535 540	1632
gtg aga atg gcc aaa ttt ctg aag ccg gtg gag gaa tac att ttc agg Val Arg Met Ala Lys Phe Leu Lys Pro Val Glu Glu Tyr Ile Phe Arg 545 550 555 560	1680
caa ctc gcc tgt tac aac ctg gat gtg gcg gcg cac acc cga ggg gtg Gln Leu Ala Cys Tyr Asn Leu Asp Val Ala Ala His Thr Arg Gly Val 565 570 575	1728
atg aat ttt tcg ggg ttt att caa tcc acc aag gtg gtc gag gtc tcc Met Asn Phe Ser Gly Phe Ile Gln Ser Thr Lys Val Val Glu Val Ser 580 585 590	1776
agg aac aag gcg cgg ctg gac gcg ggg atc gtg ctg gcc acc ggg aac Arg Asn Lys Ala Arg Leu Asp Ala Gly Ile Val Leu Ala Thr Gly Asn 595 600 605	1824
ctc tcc gac tcc ctc ttc acc ccc gag aca att ccg cga aga gga ggg Leu Ser Asp Ser Leu Phe Thr Pro Glu Thr Ile Pro Arg Arg Gly Gly 610 615 620	1872
ttc gtg gcc aac ccc ctg acg ggt ctc ttc ttc gcc cag ccg acc cag Phe Val Ala Asn Pro Leu Thr Gly Leu Phe Phe Ala Gln Pro Thr Gln 625 630 635 640	1920
tgt ctt gag atg tgc ctc gac ttc acc agc ctg tac ccc agc atc atg Cys Leu Glu Met Cys Leu Asp Phe Thr Ser Leu Tyr Pro Ser Ile Met 645 650 655	1968
tgc gac ctc aac att tcc ccc gaa acg atc gtc gat ctg gac aag gcc Cys Asp Leu Asn Ile Ser Pro Glu Thr Ile Val Asp Leu Asp Lys Ala 660 665 670	2016
gag aag att gaa gat ttt gtc ggg tac gac tgg tcc cag atc cag ggc Glu Lys Ile Glu Asp Phe Val Gly Tyr Asp Trp Ser Gln Ile Gln Gly 675 680 685	2064
ggc ttc aag aag atg acc ctc gtc ctc tca gtc gat cgc agc gac ccc Gly Phe Lys Lys Met Thr Leu Val Leu Ser Val Asp Arg Ser Asp Pro 690 695 700	2112

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gaa aat cca aaa ctg gtg cgc cac ttt tct gac acc tcg gga tcc ctc	2160
Glu Asn Pro Lys Leu Val Arg His Phe Ser Asp Thr Ser Gly Ser Leu	
705 710 715 720	
tcc cgg tat ctg gcc ctc agg gcc cat cac aag cgg gag atg aag gct	2208
Ser Arg Tyr Leu Ala Leu Arg Ala His His Lys Arg Glu Met Lys Ala	
725 730 735	
aac aag gag gat ccg tta gcc cac ggg tat cac gat cgc ctc cag aac	2256
Asn Lys Glu Asp Pro Leu Ala His Gly Tyr His Asp Arg Leu Gln Asn	
740 745 750	
gag atg aaa atc tgc gca aac acc cac tac gga gtt tcg gac cac acg	2304
Glu Met Lys Ile Cys Ala Asn Thr His Tyr Gly Val Ser Asp His Thr	
755 760 765	
tgc tca ctc atg atc acc acc cag ggt cag cac aag atc aaa cac gtc	2352
Cys Ser Leu Met Ile Thr Thr Gln Gly Gln His Lys Ile Lys His Val	
770 775 780	
aac gcc ttc atc tcc agg ctc aac aga gac ggg gta tcc ctg ttt ccc	2400
Asn Ala Phe Ile Ser Arg Leu Asn Arg Asp Gly Val Ser Leu Phe Pro	
785 790 795 800	
aac tac gga gac acg gac agc acg atg ttt ttt ccc ccc cac gat aga	2448
Asn Tyr Gly Asp Thr Asp Ser Thr Met Phe Phe Pro Pro His Asp Arg	
805 810 815	
acg gag agg ccg gtc ccc gac acc gcg cga gtc ttc tgg gat aaa gtg	2496
Thr Glu Arg Pro Val Pro Asp Thr Ala Arg Val Phe Trp Asp Lys Val	
820 825 830	
atg aac aag gcc acc gcg gtg gtc gag acc ggt gac tct cgc gcc gtg	2544
Met Asn Lys Ala Thr Ala Val Val Glu Thr Gly Asp Ser Arg Ala Val	
835 840 845	
gaa gcg ggt gaa gat tgt ttt ccc ccc gag ctg aaa gac cac ata gtg	2592
Glu Ala Gly Glu Asp Cys Phe Pro Pro Glu Leu Lys Asp His Ile Val	
850 855 860	
cgc aag atg aga cgg gac ata gtg gac cac atc aag aca aag ttc aag	2640
Arg Lys Met Arg Arg Asp Ile Val Asp His Ile Lys Thr Lys Phe Lys	
865 870 875 880	
agc acc gac atc ttt gtc aac acg ttc ctg gag gag gcc gcc gtt gtg	2688
Ser Thr Asp Ile Phe Val Asn Thr Phe Leu Glu Glu Ala Ala Val Val	
885 890 895	
ctc ttt gat gac atg gtg tcc aaa ctg gtc ctc cac acc agg aag ggg	2736
Leu Phe Asp Asp Met Val Ser Lys Leu Val Leu His Thr Arg Lys Gly	
900 905 910	

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act gcc acc ccg gtc aag gac gag ggg cga aac acg tgg acg atc act 2784
Thr Ala Thr Pro Val Lys Asp Glu Gly Arg Asn Thr Trp Thr Ile Thr
915 920 925

gac ccc gtc acg gga aag gaa atg gac tgc acc aca ccc ttc aga aag 2832
Asp Pro Val Thr Gly Lys Glu Met Asp Cys Thr Thr Pro Phe Arg Lys
930 935 940

ggt ctc atc tgc aag ctg gag tac gag aac gca tcc tcc atc ggc tgt 2880
Gly Leu Ile Cys Lys Leu Glu Tyr Glu Asn Ala Ser Ser Ile Gly Cys
945 950 955 960

cac gtc gca aaa aaa atg gtg agt atc ccc ccc ctt ttt ttt ttc ccc 2928
His Val Ala Lys Lys Met Val Ser Ile Pro Pro Leu Phe Phe Phe Pro
965 970 975

cac aac cca cta ccc gtc cca agt gag tat cta acc acc ggt ttt ttt 2976
His Asn Pro Leu Pro Val Pro Ser Glu Tyr Leu Thr Thr Gly Phe Phe
980 985 990

tga 2979

<210> 9
<211> 992
<212> PRT
<213> Herpes virus

<400> 9

Met Asp Pro Gly Cys Asp Leu Ala Lys Leu Thr His Leu Phe Pro Ala
1 5 10 15

Gln Arg Ser Leu Arg Pro Glu Glu Ser Glu Thr Leu Thr Pro Leu Phe
20 25 30

Phe Ser Ser Val Arg His Val Ser Arg Asn Gly Glu Asp Val Leu Leu
35 40 45

Ile His Val Leu Asn Leu Arg Ser Lys Glu Thr Gly Cys Ile Met Val
50 55 60

Lys Ser Leu Ala Phe Leu Ala Val Val Pro Glu Val Ala Leu Ser Ser
65 70 75 80

Val Ala Phe Asn Ala Leu Val Ala Glu Ser Ala Pro His Phe His His

Asp Tyr Thr Val Phe Asn Gly Asp Leu Lys Lys His Met Arg Gly Arg
 100 105 110

Leu Phe Val Phe His Ser Met Glu Ala Arg Arg Leu Phe Ile Lys Arg
 115 120 125

Gly Asn Thr Ile Leu Asn Arg Ile Gly Glu Asn Val Tyr Thr Tyr Gly
 130 135 140

Asp His Arg Ser Thr Tyr Glu Gly Asn Thr Val Ala Leu Tyr Asn Asn
 145 150 155 160

Leu Met Cys Ser His Val Tyr His Val Arg Leu Lys Gly Gly Ser Glu
 165 170 175

Ile Tyr Glu Pro Trp Asp Phe Val Tyr Asp Ala Ala Val Asp Ser Arg
 180 185 190

Trp Ala Met Asn Leu Gly Glu Ile Thr Lys Tyr Cys Lys Arg Glu Gly
 195 200 205

Ala Phe Asp Ile Glu Thr Leu Val His Glu Val Ser Leu Asp Pro Asp
 210 215 220

Met Val Cys Arg Ala Phe Glu Lys Ser Tyr Phe Lys Asp Ala Asp Asp
 225 230 235 240

Ala Arg Glu Leu Leu Ala Gly Leu Arg Ser Lys Gly Val Ala Gly Ile
 245 250 255

Pro Thr Ser Pro Phe Val Gly Leu Thr Gln Lys Leu His Glu Ile Thr
 260 265 270

Ser Ile Ser Leu Val Val Cys Asn Tyr His Lys Pro Lys Asp Gly Pro
 275 280 285

Arg Lys Glu Leu Ile Val Tyr Tyr Asn Glu Lys Leu Leu Gln His Pro

290

295

300

Leu Glu Glu Ile Pro Val Ala His Leu Gly Leu Asp Trp Asp Arg Ile
 305 310 315 320

Val Phe Lys Ala Cys Lys Asn Glu Phe Tyr Met Leu Met His Phe Ile
 325 330 335

Asn Lys Leu Lys Ser Ser Val Asp Val Leu Tyr Val Phe Asn Ala Gln
 340 345 350

Phe Asp Ile Lys Val Ile Cys Gln Arg Leu Ala Tyr Tyr Ala Phe Glu
 355 360 365

Gly Arg Arg Pro Gly Cys Cys Lys Cys His Ala Glu Ile Ser Arg Glu
 370 375 380

Tyr Gly Asp Ala Leu Met Glu Lys Trp Glu Leu Phe Leu Ser Arg Lys
 385 390 395 400

Pro Gln Leu Val Lys Gly Glu Ile Leu Met Gly Ser Glu Ile Leu Gln
 405 410 415

Ala Gln Tyr Leu Lys Met Leu Arg Gly Val Ser Ser Leu Leu Ala Ala
 420 425 430

Pro Gly Gly Gly Asn Val Gly Leu Ile Lys Lys Lys Leu Glu Met Tyr
 435 440 445

Lys Gln Gly Lys Asp Thr Val Gln Asn Phe Lys Thr Val Gly Phe Gly
 450 455 460

Cys Asp Ile Ile Asp Met Met Tyr Val Cys Lys Arg Lys Glu Tyr Glu
 465 470 475 480

Thr Pro Ser Gly Ser Gly Ala Leu Asn Asp Val Ala Lys Leu Ile Ile
 485 490 495

Gln Met Tyr Arg Pro Lys Lys Leu Ala Ala Lys Thr Val Lys Leu Gly

500

505

510

Asp Val Glu Tyr Arg Lys Met Asp Glu Tyr Tyr Arg Tyr Gly Gly Thr
 515 520 525

Lys Leu Ala Glu Cys Leu Val Tyr Asn Leu Ile Asp Ser Gln Leu Val
 530 535 540

Val Arg Met Ala Lys Phe Leu Lys Pro Val Glu Glu Tyr Ile Phe Arg
 545 550 555 560

Gln Leu Ala Cys Tyr Asn Leu Asp Val Ala Ala His Thr Arg Gly Val
 565 570 575

Met Asn Phe Ser Gly Phe Ile Gln Ser Thr Lys Val Val Glu Val Ser
 580 585 590

Arg Asn Lys Ala Arg Leu Asp Ala Gly Ile Val Leu Ala Thr Gly Asn
 595 600 605

Leu Ser Asp Ser Leu Phe Thr Pro Glu Thr Ile Pro Arg Arg Gly Gly
 610 615 620

Phe Val Ala Asn Pro Leu Thr Gly Leu Phe Phe Ala Gln Pro Thr Gln
 625 630 635 640

Cys Leu Glu Met Cys Leu Asp Phe Thr Ser Leu Tyr Pro Ser Ile Met
 645 650 655

Cys Asp Leu Asn Ile Ser Pro Glu Thr Ile Val Asp Leu Asp Lys Ala
 660 665 670

Glu Lys Ile Glu Asp Phe Val Gly Tyr Asp Trp Ser Gln Ile Gln Gly
 675 680 685

Gly Phe Lys Lys Met Thr Leu Val Leu Ser Val Asp Arg Ser Asp Pro
 690 695 700

Glu Asn Pro Lys Leu Val Arg His Phe Ser Asp Thr Ser Gly Ser Leu

705 710 715 720

Asn Lys Glu Asp Pro Leu Ala His Gly Tyr His Asp Arg Leu Gln Asn
740 745 750

Glu Met Lys Ile Cys Ala Asn Thr His Tyr Gly Val Ser Asp His Thr
755 760 765

Cys Ser Leu Met Ile Thr Thr Gln Gly Gln His Lys Ile Lys His Val
770 775 780

Asn Ala Phe Ile Ser Arg Leu Asn Arg Asp Gly Val Ser Leu Phe Pro
785 790 795 800

Asn Tyr Gly Asp Thr Asp Ser Thr Met Phe Phe Pro Pro His Asp Arg
805 810 815

Thr Glu Arg Pro Val Pro Asp Thr Ala Arg Val Phe Trp Asp Lys Val
820 825 830

Met Asn Lys Ala Thr Ala Val Val Glu Thr Gly Asp Ser Arg Ala Val
835 840 845

Glu Ala Gly Glu Asp Cys Phe Pro Pro Glu Leu Lys Asp His Ile Val
850 855 860

Arg Lys Met Arg Arg Asp Ile Val Asp His Ile Lys Thr Lys Phe Lys
865 870 875 880

Ser Thr Asp Ile Phe Val Asn Thr Phe Leu Glu Glu Ala Ala Val Val
885 890 895

Leu Phe Asp Asp Met Val Ser Lys Leu Val Leu His Thr Arg Lys Gly
900 905 910

Thr Ala Thr Pro Val Lys Asp Glu Gly Arg Asn Thr Trp Thr Ile Thr

915

920

925

Asp Pro Val Thr Gly Lys Glu Met Asp Cys Thr Thr Pro Phe Arg Lys
 930 935 940

Gly Leu Ile Cys Lys Leu Glu Tyr Glu Asn Ala Ser Ser Ile Gly Cys
 945 950 955 960

His Val Ala Lys Lys Met Val Ser Ile Pro Pro Leu Phe Phe Phe Pro
 965 970 975

His Asn Pro Leu Pro Val Pro Ser Glu Tyr Leu Thr Thr Gly Phe Phe
 980 985 990

<210> 10
 <211> 3909
 <212> DNA
 <213> Herpes virus

<220>
 <221> CDS
 <222> (1)..(3909)

<400> 10
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 ggg atc att ttc gtt ctt tcg ctg gtc gcg tgt atc gag tgt gcg gaa 96
 Gly Ile Ile Phe Val Leu Ser Leu Val Ala Cys Ile Glu Cys Ala Glu
 20 25 30
 aag att aag tat gtc tat cac gcc aac tcg gct cag atc tca acc tgc 144
 Lys Ile Lys Tyr Val Tyr His Ala Asn Ser Ala Gln Ile Ser Thr Cys
 35 40 45
 tca tac tcg gaa ctc aac gga gtg ccc att cct cca aat aat cga gtg 192
 Ser Tyr Ser Glu Leu Asn Gly Val Pro Ile Pro Pro Asn Asn Arg Val
 50 55 60
 gtg ggc cga cag tac gtc tgc acc tcc acg ggg gca cag ctc cgc gag 240
 Val Gly Arg Gln Tyr Val Cys Thr Ser Thr Gly Ala Gln Leu Arg Glu
 65 70 75 80
 gag ggt cgc ctg agt tcc acg ggc gac ggc gtg tgc cag tac tac tgc 288
 Glu Gly Arg Leu Ser Ser Thr Gly Asp Gly Val Cys Gln Tyr Tyr Cys

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85			90			95														
ccc	aac	acg	gac	cgg	ttg	acg	ctc	aac	ggc	atc	acg	acc	ttc	acg	ggt					
Pro	Asn	Thr	Asp	Arg	Leu	Thr	Leu	Asn	Gly	Ile	Thr	Thr	Phe	Thr	Gly					336
			100					105					110							
cgc	gac	act	atg	gag	acg	acc	ctc	ctc	aac	ccc	ttc	gtg	tac	gag	ccc					
Arg	Asp	Thr	Met	Glu	Thr	Thr	Leu	Leu	Asn	Pro	Phe	Val	Tyr	Glu	Pro					384
		115					120					125								
ccc	act	gac	tgt	ata	gcg	gtg	acg	tac	cag	tgt	gac	gcg	gtc	atc	aat					
Pro	Thr	Asp	Cys	Ile	Ala	Val	Thr	Tyr	Gln	Cys	Asp	Ala	Val	Ile	Asn					432
		130				135					140									
gac	cgc	cta	ccg	atc	aac	gaa	ctt	tcc	atc	aaa	ctc	cac	ggt	tcg	ccc					
Asp	Arg	Leu	Pro	Ile	Asn	Glu	Leu	Ser	Ile	Lys	Leu	His	Gly	Ser	Pro					480
					150					155					160					
cag	ctc	aag	aac	gcc	gtc	ttc	gga	cac	ggg	tgc	acc	acg	act	aat	cac					
Gln	Leu	Lys	Asn	Ala	Val	Phe	Gly	His	Gly	Cys	Thr	Thr	Thr	Asn	His					528
				165					170					175						
agt	cgc	agc	acg	gag	tgc	gcc	gtc	gca	aaa	ttg	ctg	cac	atc	atc	cgc					
Ser	Arg	Ser	Thr	Glu	Cys	Ala	Val	Ala	Lys	Leu	Leu	His	Ile	Ile	Arg					576
			180					185					190							
aac	ggg	ggg	atc	ccc	gaa	gat	tgg	atg	gtg	acc	gcc	gta	cgt	ggg	gaa					
Asn	Gly	Gly	Ile	Pro	Glu	Asp	Trp	Met	Val	Thr	Ala	Val	Arg	Gly	Glu					624
		195				200					205									
tat	gcc	tgc	ctc	cta	ggg	tat	atc	ggc	tcg	gga	agg	att	tcc	att	cac					
Tyr	Ala	Cys	Leu	Leu	Gly	Tyr	Ile	Gly	Ser	Gly	Arg	Ile	Ser	Ile	His					672
	210				215					220										
tcg	gcc	tgc	tgg	atc	caa	ctc	ggc	gca	aac	tgt	tac	aaa	tcc	ttc	ggg					
Ser	Ala	Cys	Trp	Ile	Gln	Leu	Gly	Ala	Asn	Cys	Tyr	Lys	Ser	Phe	Gly					720
	225				230				235					240						
aaa	acc	gaa	ctg	tgc	atc	aat	gat	cgc	ccc	aag	gtc	gca	ggc	atc	acg					
Lys	Thr	Glu	Leu	Cys	Ile	Asn	Asp	Arg	Pro	Lys	Val	Ala	Gly	Ile	Thr					768
			245					250					255							
gac	ttt	caa	aac	acc	ccg	tcc	gac	cgt	aaa	aag	aac	ctg	aga	tgc	ttc					
Asp	Phe	Gln	Asn	Thr	Pro	Ser	Asp	Arg	Lys	Lys	Asn	Leu	Arg	Cys	Phe					816
		260					265					270								
tac	gat	atg	gag	cag	gcc	atc	gcc	gaa	aac	gcc	gac	atg	aaa	aaa	cca					
Tyr	Asp	Met	Glu	Gln	Ala	Ile	Ala	Glu	Asn	Ala	Asp	Met	Lys	Lys	Pro					864
		275				280					285									
cca	cct	att	ctg	aaa	aat	tgc	gac	gaa	gtc	atc	ctc	acc	ggg	ttg	aga					
Pro	Pro	Ile	Leu	Lys	Asn	Cys	Asp	Glu	Val	Ile	Leu	Thr	Gly	Leu	Arg					912

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290	295	300	
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ttg ttc aaa acg gtc atc ctc ggg ttc agg aaa ccc atc acc act gaa Leu Phe Lys Thr Val Ile Leu Gly Phe Arg Lys Pro Ile Thr Thr Glu 340 345 350			1056
gtt ttc aca gaa atc acc gcc tca aaa gcg act cgg ggg gcc ttc ata Val Phe Thr Glu Ile Thr Ala Ser Lys Ala Thr Arg Gly Ala Phe Ile 355 360 365			1104
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tat ctc gag att cca ccg ccc cgc gtc gac gga ctc agc aga gac aac Tyr Leu Glu Ile Pro Pro Pro Arg Val Asp Gly Leu Ser Arg Asp Asn 385 390 395 400			1200
cag att aat caa gcg ctc ctc ctg gaa gag ttg cgc gcg acg gtc ccc Gln Ile Asn Gln Ala Leu Leu Leu Glu Glu Leu Arg Ala Thr Val Pro 405 410 415			1248
gtc acc gct aaa aaa ttc acc atc tac gcg ggc gtg tcg atg acg tac Val Thr Ala Lys Lys Phe Thr Ile Tyr Ala Gly Val Ser Met Thr Tyr 420 425 430			1296
ccg gac aac acg tac tat gac atc aag gcc atc gcc gaa agc agc gat Pro Asp Asn Thr Tyr Tyr Asp Ile Lys Ala Ile Ala Glu Ser Ser Asp 435 440 445			1344
ctg gtg ttc ctc aac ggg tac gac ctc ccg gga aag ccc gcc acc cgg Leu Val Phe Leu Asn Gly Tyr Asp Leu Pro Gly Lys Pro Ala Thr Arg 450 455 460			1392
ggg acc gtc ggc ccg acc gcc tgg gac atc ggc acg ggt tgc ggt atc Gly Thr Val Gly Pro Thr Ala Trp Asp Ile Gly Thr Gly Cys Gly Ile 465 470 475 480			1440
gag ggg gtc gag tgc ccc aac ccc acc gat tat cat ttc ctc aaa tac Glu Gly Val Glu Cys Pro Asn Pro Thr Asp Tyr His Phe Leu Lys Tyr 485 490 495			1488
ggg gtg agt tac tac acc tcg aga gtc ccc ccc gag aaa ctg tcc ttc Gly Val Ser Tyr Tyr Thr Ser Arg Val Pro Pro Glu Lys Leu Ser Phe 500 505 510			1536

500	505	510	
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atc ccg atg ggc gcg ata cgg tca ccg cag atg aaa ctc gcg gaa aaa Ile Pro Met Gly Ala Ile Arg Ser Pro Gln Met Lys Leu Ala Glu Lys 530 535 540			1632
atc agc tac ggc gat atc cgg aat aac gac atc gag tgc atc aag agt Ile Ser Tyr Gly Asp Ile Arg Asn Asn Asp Ile Glu Cys Ile Lys Ser 545 550 555 560			1680
cag cag cag atg tgc tgc acc aac cag gtg tac ctc atg ggt aat ccc Gln Gln Gln Met Cys Cys Thr Asn Gln Val Tyr Leu Met Gly Asn Pro 565 570 575			1728
gtg gcc atc agt tgg gac aac ggt gag acc gcc gtc gaa aag gcc gcc Val Ala Ile Ser Trp Asp Asn Gly Glu Thr Ala Val Glu Lys Ala Ala 580 585 590			1776
agg ctc agc cag gat tac ggc atc atg gag ttc cac acg atg tcc gtg Arg Leu Ser Gln Asp Tyr Gly Ile Met Glu Phe His Thr Met Ser Val 595 600 605			1824
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tac atc cac tct ccg ccc ccc tcc tcg atc acg acc aag acc gaa acc Tyr Ile His Ser Pro Pro Pro Ser Ser Ile Thr Thr Lys Thr Glu Thr 625 630 635 640			1920
ctg aaa ccc ccc acc tac cag atc ggg aag ggt ccc ctg gtc cac tgc Leu Lys Pro Pro Thr Tyr Gln Ile Gly Lys Gly Pro Leu Val His Cys 645 650 655			1968
ccg ggg atc atc gcc gtg gcc ggg gac ctg gtg ttc acc cag cac agc Pro Gly Ile Ile Ala Val Ala Gly Asp Leu Val Phe Thr Gln His Ser 660 665 670			2016
tac acc gcc ttc tcc agc ctc acc act ttc acg aac ctc ttt gtg gcc Tyr Thr Ala Phe Ser Ser Leu Thr Thr Phe Thr Asn Leu Phe Val Ala 675 680 685			2064
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ctc gaa cta gtt acc act gta ccc ggt ggc gcg gtc gac ctc aac acg Leu Glu Leu Val Thr Thr Val Pro Gly Gly Ala Val Asp Leu Asn Thr			2160

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705	710	715	720	
ttc ctt ccg acc acc tcc tcc ggg gac tac tca gtg ggc ctc ctc aac				2208
Phe Leu Pro Thr Thr Ser Ser Gly Asp Tyr Ser Val Gly Leu Leu Asn	725	730	735	
gga cgg ctg gtg cag ttc att ccc gag gtg cag gag tcc tgt cag gac				2256
Gly Arg Leu Val Gln Phe Ile Pro Glu Val Gln Glu Ser Cys Gln Asp	740	745	750	
acc aat tcc gag acc gtc aat cgc aag ccc tac gtg gag gta gac gag				2304
Thr Asn Ser Glu Thr Val Asn Arg Lys Pro Tyr Val Glu Val Asp Glu	755	760	765	
acc tac tac ctg tcg gag cca aaa atc aca gcg gac ggg atc atg atc				2352
Thr Tyr Tyr Leu Ser Glu Pro Lys Ile Thr Ala Asp Gly Ile Met Ile	770	775	780	
ccg gag ggg gtc cac ttt ttc atg acg gat gaa aag ctg tat gtg gac				2400
Pro Glu Gly Val His Phe Phe Met Thr Asp Glu Lys Leu Tyr Val Asp	785	790	800	
tac ctc aac ttc gcc acc acc tgc gtc aac tac aag atc gaa aac ctc				2448
Tyr Leu Asn Phe Ala Thr Thr Cys Val Asn Tyr Lys Ile Glu Asn Leu	805	810	815	
ccc agc tgc atc acg gtg acg tgc tcg agc gac ccg gga tgc atc aac				2496
Pro Ser Cys Ile Thr Val Thr Cys Ser Ser Asp Pro Gly Cys Ile Asn	820	825	830	
aga tac gcg gcc ata tgt tcc gag gcg gag agc gtg atc ggg gac gtg				2544
Arg Tyr Ala Ala Ile Cys Ser Glu Ala Glu Ser Val Ile Gly Asp Val	835	840	845	
cgc cgc agc aac aaa ctc atc ctg acg gca tac gac gac ctc tcg ctc				2592
Arg Arg Ser Asn Lys Leu Ile Leu Thr Ala Tyr Asp Asp Leu Ser Leu	850	855	860	
gag cac aag aag gcc aag atg ttt gcg cta cag ccc acc ggg gtc acc				2640
Glu His Lys Lys Ala Lys Met Phe Ala Leu Gln Pro Thr Gly Val Thr	865	870	875	
agg ggg aaa ttc atc ctc ggg acc gtg gcc ctg gcc gct gcc acc gcg				2688
Arg Gly Lys Phe Ile Leu Gly Thr Val Ala Leu Ala Ala Ala Thr Ala	885	890	895	
gcg gtc gtc cag tcc tct gtg gcc ctg ggc ctc gcc gtc acc acc gcc				2736
Ala Val Val Gln Ser Ser Val Ala Leu Gly Leu Ala Val Thr Thr Ala	900	905	910	
cag cga ctg gac acc atg att gac cag atg gag acg acc cgg gag gtc				2784
Gln Arg Leu Asp Thr Met Ile Asp Gln Met Glu Thr Thr Arg Glu Val				

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aag aac acg cag atg gtg aac gcc cgt ctg agc gag acc cag acc gcc Lys Asn Thr Gln Met Val Asn Ala Arg Leu Ser Glu Thr Gln Thr Ala 945 950 955 960			2880
atc aac aac cgt ttc acc atc atg gaa cat acc ttc aac cag ctg agc Ile Asn Asn Arg Phe Thr Ile Met Glu His Thr Phe Asn Gln Leu Ser 965 970 975			2928
agc gag ctc aag gac ctg agc acg acc atc aac gag aag ttc aag gtg Ser Glu Leu Lys Asp Leu Ser Thr Thr Ile Asn Glu Lys Phe Lys Val 980 985 990			2976
acc gtg ggc tac cag gtc tgg tac cag cag atg ctc agc ctc aac acc Thr Val Gly Tyr Gln Val Trp Tyr Gln Gln Met Leu Ser Leu Asn Thr 995 1000 1005			3024
atg ctc acc cag ggg gcc atc cag ctg tcg tac aag gtg ggg gtg Met Leu Thr Gln Gly Ala Ile Gln Leu Ser Tyr Lys Val Gly Val 1010 1015 1020			3069
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tgc ccc tcg ggg gtc acc ccc ttc gtg gag cac ccc ggg ctg gcc Cys Pro Ser Gly Val Thr Pro Phe Val Glu His Pro Gly Leu Ala 1040 1045 1050			3159
tac agg aag acg gtc gca gcg atc gtc tac gag gat gag aag ctc Tyr Arg Lys Thr Val Ala Ala Ile Val Tyr Glu Asp Glu Lys Leu 1055 1060 1065			3204
ttc atc gtg aac aaa ctc ccc tcc tcc ttc acc gcg ttc aat aag Phe Ile Val Asn Lys Leu Pro Ser Ser Phe Thr Ala Phe Asn Lys 1070 1075 1080			3249
gcc cgc ttc atc ccg acc ccc cgg gag atc ggc ggg gag atc tgc Ala Arg Phe Ile Pro Thr Pro Arg Glu Ile Gly Gly Glu Ile Cys 1085 1090 1095			3294
tgg ccg gac tac gac ctc tcc gcc gcc gac gga gag gtc cac tct Trp Pro Asp Tyr Asp Leu Ser Ala Ala Asp Gly Glu Val His Ser 1100 1105 1110			3339
tcc ata gag tgc gtg ggg cgc tat tgt gat gac ccg gta ccc gcc Ser Ile Glu Cys Val Gly Arg Tyr Cys Asp Asp Pro Val Pro Ala 1115 1120 1125			3384

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1115	1120	1125	
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atc tgc gcc ccc tgc ttc aaa gga gta tgt tac gac cgg gag tct Ile Cys Ala Pro Cys Phe Lys Gly Val Cys Tyr Asp Arg Glu Ser 1145 1150 1155			3474
aaa tcg gtg acg ttc aag aga ggc gag gtg acc gtg aag ctc ccc Lys Ser Val Thr Phe Lys Arg Gly Glu Val Thr Val Lys Leu Pro 1160 1165 1170			3519
gtg aaa acc gtc ccg gtg ttt gac aag ctc ccc ggg acg atc gct Val Lys Thr Val Pro Val Phe Asp Lys Leu Pro Gly Thr Ile Ala 1175 1180 1185			3564
gtg gaa cac ctg ctg gac acc ttc acg gtc ccg acg ctg ccc cct Val Glu His Leu Leu Asp Thr Phe Thr Val Pro Thr Leu Pro Pro 1190 1195 1200			3609
tac aag aac gtc agc atc gcc gtc aca ctg gag agc gtc gag ggg Tyr Lys Asn Val Ser Ile Ala Val Thr Leu Glu Ser Val Glu Gly 1205 1210 1215			3654
gat gtg cgc gac atg cgc gac acc ctg gcc cgg tac gaa aga gac Asp Val Arg Asp Met Arg Asp Thr Leu Ala Arg Tyr Glu Arg Asp 1220 1225 1230			3699
atg ggt att cta cgc gcc aga ggg gaa tcc tcg gcc acc ctg acc Met Gly Ile Leu Arg Ala Arg Gly Glu Ser Ser Ala Thr Leu Thr 1235 1240 1245			3744
aag gtc ctc atc acc atc atc atc atc atc atc ctc ctc atc ggg Lys Val Leu Ile Thr Ile Ile Ile Ile Ile Ile Leu Leu Ile Gly 1250 1255 1260			3789
ata ttc gcg ctc ctg tat ttc cta tac agg cgc aag gtc gcc acg Ile Phe Ala Leu Leu Tyr Phe Leu Tyr Arg Arg Lys Val Ala Thr 1265 1270 1275			3834
agc ggg tat gcc cgt ttg aac ttc ccc ggt gac gat gcc gtg cac Ser Gly Tyr Ala Arg Leu Asn Phe Pro Gly Asp Asp Ala Val His 1280 1285 1290			3879
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Ser Tyr Ser Glu Leu Asn Gly Val Pro Ile Pro Pro Asn Asn Arg Val
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Val Gly Arg Gln Tyr Val Cys Thr Ser Thr Gly Ala Gln Leu Arg Glu
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Glu Gly Arg Leu Ser Ser Thr Gly Asp Gly Val Cys Gln Tyr Tyr Cys
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Pro Asn Thr Asp Arg Leu Thr Leu Asn Gly Ile Thr Thr Phe Thr Gly
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Arg Asp Thr Met Glu Thr Thr Leu Leu Asn Pro Phe Val Tyr Glu Pro
 115 120 125

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

Asp Arg Leu Pro Ile Asn Glu Leu Ser Ile Lys Leu His Gly Ser Pro
 145 150 155 160

Gln Leu Lys Asn Ala Val Phe Gly His Gly Cys Thr Thr Thr Asn His
 165 170 175

Ser Arg Ser Thr Glu Cys Ala Val Ala Lys Leu Leu His Ile Ile Arg
 180 185 190

Asn Gly Gly Ile Pro Glu Asp Trp Met Val Thr Ala Val Arg Gly Glu
 195 200 205

Tyr Ala Cys Leu Leu Gly Tyr Ile Gly Ser Gly Arg Ile Ser Ile His
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Ser Ala Cys Trp Ile Gln Leu Gly Ala Asn Cys Tyr Lys Ser Phe Gly
 225 230 235 240

Lys Thr Glu Leu Cys Ile Asn Asp Arg Pro Lys Val Ala Gly Ile Thr
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Asp Phe Gln Asn Thr Pro Ser Asp Arg Lys Lys Asn Leu Arg Cys Phe
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Tyr Asp Met Glu Gln Ala Ile Ala Glu Asn Ala Asp Met Lys Lys Pro
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Pro Pro Ile Leu Lys Asn Cys Asp Glu Val Ile Leu Thr Gly Leu Arg
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Leu Glu Arg Arg Asp Asp Lys Trp Val Cys Glu Leu Thr Ala Ser Glu
 305 310 315 320

Lys Thr Thr Glu Trp His Arg Tyr Leu Asp Ile Leu Phe Phe Thr Ser
 325 330 335

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

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

Lys Ser Cys Gln Asp Ser Ile Ile Asn His Gly Phe Ser Gly Gly Ile
 370 375 380

Tyr Leu Glu Ile Pro Pro Pro Arg Val Asp Gly Leu Ser Arg Asp Asn
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Gln Ile Asn Gln Ala Leu Leu Leu Glu Glu Leu Arg Ala Thr Val Pro
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Val Thr Ala Lys Lys Phe Thr Ile Tyr Ala Gly Val Ser Met Thr Tyr
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Pro Asp Asn Thr Tyr Tyr Asp Ile Lys Ala Ile Ala Glu Ser Ser Asp
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Leu Val Phe Leu Asn Gly Tyr Asp Leu Pro Gly Lys Pro Ala Thr Arg
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Gly Thr Val Gly Pro Thr Ala Trp Asp Ile Gly Thr Gly Cys Gly Ile
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Glu Gly Val Glu Cys Pro Asn Pro Thr Asp Tyr His Phe Leu Lys Tyr
 485 490 495

Gly Val Ser Tyr Tyr Thr Ser Arg Val Pro Pro Glu Lys Leu Ser Phe
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Gly Phe Pro Leu Trp Gly Arg Gly Ser Arg Lys Glu Asn Gly Glu Trp
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Ile Pro Met Gly Ala Ile Arg Ser Pro Gln Met Lys Leu Ala Glu Lys
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Gln Gln Gln Met Cys Cys Thr Asn Gln Val Tyr Leu Met Gly Asn Pro
 565 570 575

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

Asn Leu Asp Thr Val Thr Gly Thr Ser Phe His Gln Ala Leu Glu Arg
 610 615 620

Tyr Ile His Ser Pro Pro Pro Ser Ser Ile Thr Thr Lys Thr Glu Thr
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Leu Lys Pro Pro Thr Tyr Gln Ile Gly Lys Gly Pro Leu Val His Cys
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Pro Gly Ile Ile Ala Val Ala Gly Asp Leu Val Phe Thr Gln His Ser
 660 665 670

Tyr Thr Ala Phe Ser Ser Leu Thr Thr Phe Thr Asn Leu Phe Val Ala
 675 680 685

Lys Val Thr Asp Leu Lys Thr Cys Val Lys Gly Asp Pro Gln Gly Lys
 690 695 700

Leu Glu Leu Val Thr Thr Val Pro Gly Gly Ala Val Asp Leu Asn Thr
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Phe Leu Pro Thr Thr Ser Ser Gly Asp Tyr Ser Val Gly Leu Leu Asn
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Gly Arg Leu Val Gln Phe Ile Pro Glu Val Gln Glu Ser Cys Gln Asp
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Pro Glu Gly Val His Phe Phe Met Thr Asp Glu Lys Leu Tyr Val Asp
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Glu His Lys Lys Ala Lys Met Phe Ala Leu Gln Pro Thr Gly Val Thr
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Ala Val Val Gln Ser Ser Val Ala Leu Gly Leu Ala Val Thr Thr Ala
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Gln Arg Leu Asp Thr Met Ile Asp Gln Met Glu Thr Thr Arg Glu Val
915 920 925

Ile Ala Asn Phe Gly Glu Thr Thr Ala Ile Val Ser Ser Lys Leu Asp
930 935 940

Lys Asn Thr Gln Met Val Asn Ala Arg Leu Ser Glu Thr Gln Thr Ala
945 950 955 960

Ile Asn Asn Arg Phe Thr Ile Met Glu His Thr Phe Asn Gln Leu Ser
965 970 975

Ser Glu Leu Lys Asp Leu Ser Thr Thr Ile Asn Glu Lys Phe Lys Val
980 985 990

Thr Val Gly Tyr Gln Val Trp Tyr Gln Gln Met Leu Ser Leu Asn Thr
995 1000 1005

Met Leu Thr Gln Gly Ala Ile Gln Leu Ser Tyr Lys Val Gly Val
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Val Arg Asp Cys Phe Lys Ser Leu Met Gly Gly Thr Met Ala Gly
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Cys Pro Ser Gly Val Thr Pro Phe Val Glu His Pro Gly Leu Ala
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Tyr Arg Lys Thr Val Ala Ala Ile Val Tyr Glu Asp Glu Lys Leu
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Trp Pro Asp Tyr Asp Leu Ser Ala Ala Asp Gly Glu Val His Ser
1100 1105 1110

Ser Ile Glu Cys Val Gly Arg Tyr Cys Asp Asp Pro Val Pro Ala
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Ile Cys Ala Pro Cys Phe Lys Gly Val Cys Tyr Asp Arg Glu Ser
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Lys Ser Val Thr Phe Lys Arg Gly Glu Val Thr Val Lys Leu Pro
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Val Lys Thr Val Pro Val Phe Asp Lys Leu Pro Gly Thr Ile Ala
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Val Glu His Leu Leu Asp Thr Phe Thr Val Pro Thr Leu Pro Pro
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Tyr Lys Asn Val Ser Ile Ala Val Thr Leu Glu Ser Val Glu Gly
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Asp Val Arg Asp Met Arg Asp Thr Leu Ala Arg Tyr Glu Arg Asp
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Met Gly Ile Leu Arg Ala Arg Gly Glu Ser Ser Ala Thr Leu Thr
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Lys Val Leu Ile Thr Ile Ile Ile Ile Ile Ile Leu Leu Ile Gly
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Ile Phe Ala Leu Leu Tyr Phe Leu Tyr Arg Arg Lys Val Ala Thr
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Thr Lys Ile Leu Gln Asn Thr Gly Glu Phe Ala Lys Gly Thr Leu Ser
20 25 30

ggc att gaa tgg ttt atc aac aat gcc gcg gag cgt gag tcg ctc atc 144
Gly Ile Glu Trp Phe Ile Asn Asn Ala Ala Glu Arg Glu Ser Leu Ile
35 40 45

ctg ggg ggg gac ggg agt atc att tct cgg ggg gtg aga gga ccg gga 192
Leu Gly Gly Asp Gly Ser Ile Ile Ser Arg Gly Val Arg Gly Pro Gly
50 55 60

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gcc ctc atg agg ctc gtc tcc gtc ctc atg cgc ccc gag acg ctc ccc Ala Leu Met Arg Leu Val Ser Val Leu Met Arg Pro Glu Thr Leu Pro 100 105 110	336
cag gcg cag gcc gag ttt cac atg gtg ttc gag gtg acc gag cag cgt Gln Ala Gln Ala Glu Phe His Met Val Phe Glu Val Thr Glu Gln Arg 115 120 125	384
ctg gcg cag ccc gga aac ctc agc acc gtg gcg ggg ggc gcg tcc acc Leu Ala Gln Pro Gly Asn Leu Ser Thr Val Ala Gly Gly Ala Ser Thr 130 135 140	432
acc tcc tac gat ctc atc atc aac ctg gag cgc aag gtc gtc tcc atc Thr Ser Tyr Asp Leu Ile Ile Asn Leu Glu Arg Lys Val Val Ser Ile 145 150 155 160	480
gag atc gac tcc caa gag ata ttc tgc acc aat gac ccc ctc gtg atg Glu Ile Asp Ser Gln Glu Ile Phe Cys Thr Asn Asp Pro Leu Val Met 165 170 175	528
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ctg act ctc ctg gtg gag cac gca aag tac tgt gcc cgc cag ccg ctc Leu Thr Leu Leu Val Glu His Ala Lys Tyr Cys Ala Arg Gln Pro Leu 195 200 205	624
ctc gtg gag ctc tgt cag ctg aag gac gcc gcc aag aac aat gac tcc Leu Val Glu Leu Cys Gln Leu Lys Asp Ala Ala Lys Asn Asn Asp Ser 210 215 220	672
acc gag ggc gtc atc att tcg gtg tgc cag ctg gag aac ctg gtg tgc Thr Glu Gly Val Ile Ile Ser Val Cys Gln Leu Glu Asn Leu Val Cys 225 230 235 240	720
ggg gcg ctc aat cgc cag ccc cat aac ttc att tcc ctg atc cac acg Gly Ala Leu Asn Arg Gln Pro His Asn Phe Ile Ser Leu Ile His Thr 245 250 255	768
ggg ttg aaa atc atc gat gga acc ccc tcg aac agc gtg gtg gtg acc Gly Leu Lys Ile Ile Asp Gly Thr Pro Ser Asn Ser Val Val Val Thr 260 265 270	816

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acc tcc acc gtc ttc cgg aac ggg tcc ctc gat aac cgc ctc gcc tcc	864
Thr Ser Thr Val Phe Arg Asn Gly Ser Leu Asp Asn Arg Leu Ala Ser	
275 280 285	
ctg tcc ctc gag gcg ccc gca gcc ccg ctc acc tac agc gtg aac ggg	912
Leu Ser Leu Glu Ala Pro Ala Ala Pro Leu Thr Tyr Ser Val Asn Gly	
290 295 300	
gcg gtg ggg atg agc agc atc gcc cgc ttc ggg cgc ccc gtc ccc gag	960
Ala Val Gly Met Ser Ser Ile Ala Arg Phe Gly Arg Pro Val Pro Glu	
305 310 315 320	
ctg gcc ccg gga cgc ctg cag gtg tcc aac aag tac ccc aag atc tac	1008
Leu Ala Pro Gly Arg Leu Gln Val Ser Asn Lys Tyr Pro Lys Ile Tyr	
325 330 335	
aac ccg gag agc aag tcc gtc tac gga ctg gct gac gag cct cct gag	1056
Asn Pro Glu Ser Lys Ser Val Tyr Gly Leu Ala Asp Glu Pro Pro Glu	
340 345 350	
ccc ctg aag gtc gcg ggg gtg aac ctc ggt cac aac gaa cac atc ccg	1104
Pro Leu Lys Val Ala Gly Val Asn Leu Gly His Asn Glu His Ile Pro	
355 360 365	
gtg gtt ccg ctc gac gga acc aaa ttc tcg gcc gac ggg ggg atg agc	1152
Val Val Pro Leu Asp Gly Thr Lys Phe Ser Ala Asp Gly Gly Met Ser	
370 375 380	
gtg gag gac acg ctc acc cag ggt tgc gtg aag agg ctc ttc ttc acg	1200
Val Glu Asp Thr Leu Thr Gln Gly Cys Val Lys Arg Leu Phe Phe Thr	
385 390 395 400	
gtg ggg acc tgc ccg gtg gtg tat ggg agc gtg ccc ccc gaa agt ctg	1248
Val Gly Thr Cys Pro Val Val Tyr Gly Ser Val Pro Pro Glu Ser Leu	
405 410 415	
tac ggg gag agc gga aag tcc tcc gag ata acc ccg gag gcc atc gcc	1296
Tyr Gly Glu Ser Gly Lys Ser Ser Glu Ile Thr Pro Glu Ala Ile Ala	
420 425 430	
ctc cgg agc ccc tct tcc tcc tac atc atg aac cac gac cag ggt tgc	1344
Leu Arg Ser Pro Ser Ser Ser Tyr Ile Met Asn His Asp Gln Gly Cys	
435 440 445	
gcc gcc cag gag gta tcc ctg gag ctg ctg cac agg ctc tac tac gcg	1392
Ala Ala Gln Glu Val Ser Leu Glu Leu Leu His Arg Leu Tyr Tyr Ala	
450 455 460	
gat aac ccc gac gcc ttc gac gtg gga gtg ttt gcc aga aag ctg agg	1440
Asp Asn Pro Asp Ala Phe Asp Val Gly Val Phe Ala Arg Lys Leu Arg	
465 470 475 480	

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ggg gtc cag gcg atc cgc ctc ttt gat gag gag cag agt gcc gcc ctg Gly Val Gln Ala Ile Arg Leu Phe Asp Glu Glu Gln Ser Ala Ala Leu	1488
485 490 495	
tta ctg gaa aag acg tgg gag gcc aag gtg gag aac cag cag tcc gta Leu Leu Glu Lys Thr Trp Glu Ala Lys Val Glu Asn Gln Gln Ser Val	1536
500 505 510	
ttt gag ttc gac ccc cgg cac atg ttg atc aac cac cga gga gga agg Phe Glu Phe Asp Pro Arg His Met Leu Ile Asn His Arg Gly Gly Arg	1584
515 520 525	
gac gag ccc ggt ggc gtc aac gtg gtg gcc gtg gag ggg ggt gac gac Asp Glu Pro Gly Gly Val Asn Val Val Ala Val Glu Gly Gly Asp Asp	1632
530 535 540	
cgc gac gag ttc atc agg gcc atc ccc cgg gtc tgc atg tac aac tcc Arg Asp Glu Phe Ile Arg Ala Ile Pro Arg Val Cys Met Tyr Asn Ser	1680
545 550 555 560	
agt ccc atg agc atg ctg cag aac gag ttg gtg gga gtg ctc gcc acc Ser Pro Met Ser Met Leu Gln Asn Glu Leu Val Gly Val Leu Ala Thr	1728
565 570 575	
atg tac cag ctg gcg ccg ccc acc cag gag atg acc agg tac ctg tcc Met Tyr Gln Leu Ala Pro Pro Thr Gln Glu Met Thr Arg Tyr Leu Ser	1776
580 585 590	
atg atc aag acc gcc ctg gag gac gga acc gtg acg ggt ctc gag gac Met Ile Lys Thr Ala Leu Glu Asp Gly Thr Val Thr Gly Leu Glu Asp	1824
595 600 605	
gtt gct gcg ctg agg ctc atg ggc ctc acc ggc ggc gcc gag ata gac Val Ala Ala Leu Arg Leu Met Gly Leu Thr Gly Gly Ala Glu Ile Asp	1872
610 615 620	
gag gcc atg gtg cac cgc ctg ttc aac gcg ggg gag aac tac ctc ccg Glu Ala Met Val His Arg Leu Phe Asn Ala Gly Glu Asn Tyr Leu Pro	1920
625 630 635 640	
ctc tct gac ccc tac tgc cag ctc gtc ctg att gac aga ctg gag cgg Leu Ser Asp Pro Tyr Cys Gln Leu Val Leu Ile Asp Arg Leu Glu Arg	1968
645 650 655	
ttc atg cga ggc atc gac gcg ggg ggg gaa ttt tac cag gcc ctc ccc Phe Met Arg Gly Ile Asp Ala Gly Gly Glu Phe Tyr Gln Ala Leu Pro	2016
660 665 670	
gtc ctc agg gaa ctg gtg acg gtg atg cga ggc ggc gtg acc ggg gtc Val Leu Arg Glu Leu Val Thr Val Met Arg Gly Gly Val Thr Gly Val	2064
675 680 685	

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atc tcc gtc ttt gag aag ctc ttc agc aac act gcc ttc agc atc tac	2112
Ile Ser Val Phe Glu Lys Leu Phe Ser Asn Thr Ala Phe Ser Ile Tyr	
690 695 700	
gat ccg gat gtc atg atc aac tct ctg tgc cag acc ccc cgg gga aca	2160
Asp Pro Asp Val Met Ile Asn Ser Leu Cys Gln Thr Pro Arg Gly Thr	
705 710 715 720	
ccc gag cag aat ctc ttc ctc aac gtg gtt tac ggg gcg atc ctc ccg	2208
Pro Glu Gln Asn Leu Phe Leu Asn Val Val Tyr Gly Ala Ile Leu Pro	
725 730 735	
ctg ttc tcc aac agg ctg gcg agg ctg gag gcc gac cgt cat ttc gcc	2256
Leu Phe Ser Asn Arg Leu Ala Arg Leu Glu Ala Asp Arg His Phe Ala	
740 745 750	
gcg gag gag gtc cac atc cag ggc ctg gtc tac aag tcg tac ggc ggg	2304
Ala Glu Glu Val His Ile Gln Gly Leu Val Tyr Lys Ser Tyr Gly Gly	
755 760 765	
gcg tgc ttc gtg ggg cgc tcg cac cgg ctt ccc gcc gcc agg atc gag	2352
Ala Cys Phe Val Gly Arg Ser His Arg Leu Pro Ala Ala Arg Ile Glu	
770 775 780	
atc ctc tgg gag gac gac atc ggg acc gcg gcc ccg gtg atc acc cgc	2400
Ile Leu Trp Glu Asp Asp Ile Gly Thr Ala Ala Pro Val Ile Thr Arg	
785 790 795 800	
cct ctg tgg aag cag cgg gtc gcg gcg ctg agg aac gcc ttc ggg ggg	2448
Pro Leu Trp Lys Gln Arg Val Ala Ala Leu Arg Asn Ala Phe Gly Gly	
805 810 815	
acc tgt ccc tac gtg ggg ttc ctg ggg ggg ctg cac tgc gcc acg cgc	2496
Thr Cys Pro Tyr Val Gly Phe Leu Gly Gly Leu His Cys Ala Thr Arg	
820 825 830	
ctg gac cgg gag acc gtg acc ggt cac ttt gac aag aag tac tac tcg	2544
Leu Asp Arg Glu Thr Val Thr Gly His Phe Asp Lys Lys Tyr Tyr Ser	
835 840 845	
ggg atg gcc tac atg tgc gtg cgg acc acc cgg ttc aac ggg cac ggg	2592
Gly Met Ala Tyr Met Cys Val Arg Thr Thr Arg Phe Asn Gly His Gly	
850 855 860	
atg tgt gtc atc ccg agg ggg tcg gcg cgc ctc atc acg gga aac atg	2640
Met Cys Val Ile Pro Arg Gly Ser Ala Arg Leu Ile Thr Gly Asn Met	
865 870 875 880	
tac gcg ggc acc ccg gta agc gag cct gtg gga aag tcg gtg tgg acg	2688
Tyr Ala Gly Thr Pro Val Ser Glu Pro Val Gly Lys Ser Val Trp Thr	
885 890 895	

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cag tgc atg gag ttc aag gtg gcg ccg tcc ggg atc gac aag ctg ggg Gln Cys Met Glu Phe Lys Val Ala Pro Ser Gly Ile Asp Lys Leu Gly 900 905 910	2736
gtg ctc atc ccc aat gtg cta tgt acg gag ctc aat ggc atg ggg gtc Val Leu Ile Pro Asn Val Leu Cys Thr Glu Leu Asn Gly Met Gly Val 915 920 925	2784
tcc ttc aat gtg aga gac ctc aac gcc atc gtc atc ctg gag gcc tac Ser Phe Asn Val Arg Asp Leu Asn Ala Ile Val Ile Leu Glu Ala Tyr 930 935 940	2832
aac ggc ttc acc cct gag agc aag acc acc tcg gcg cac gtt cac aac Asn Gly Phe Thr Pro Glu Ser Lys Thr Thr Ser Ala His Val His Asn 945 950 955 960	2880
atc ctc ccc atc tgc ggt cga tac gac gcc acc ggg gac atc aac tac Ile Leu Pro Ile Cys Gly Arg Tyr Asp Ala Thr Gly Asp Ile Asn Tyr 965 970 975	2928
gag cgc ccc gat atc atc acg cac cgc tac tcc cag tgc ccc act ctg Glu Arg Pro Asp Ile Ile Thr His Arg Tyr Ser Gln Cys Pro Thr Leu 980 985 990	2976
ctg cat cgc ctc gcc aac ggc ttc gat aag ctt cag agg gtg atc gag Leu His Arg Leu Ala Asn Gly Phe Asp Lys Leu Gln Arg Val Ile Glu 995 1000 1005	3024
gag agg cag ctt ccc ccc gag cac agt tac tct ctg gtc atc cag Glu Arg Gln Leu Pro Pro Glu His Ser Tyr Ser Leu Val Ile Gln 1010 1015 1020	3069
tcc acc ggc agg ggg aac gtc ttc gcg acg ctc ccc ccc gtg ctg Ser Thr Gly Arg Gly Asn Val Phe Ala Thr Leu Pro Pro Val Leu 1025 1030 1035	3114
cac acc gcc gag ctc atg acc gag cac gag atc ctg aag cgg acc His Thr Ala Glu Leu Met Thr Glu His Glu Ile Leu Lys Arg Thr 1040 1045 1050	3159
ctg gac gcc acc ccg gag gac agg aac ctg tac agg ccg acc ctg Leu Asp Ala Thr Pro Glu Asp Arg Asn Leu Tyr Arg Pro Thr Leu 1055 1060 1065	3204
ggg atc atc ttc tcc gat aac tat gtc atc gga aag aac ggg agc Gly Ile Ile Phe Ser Asp Asn Tyr Val Ile Gly Lys Asn Gly Ser 1070 1075 1080	3249
tat att ttt agg cag aac cag gac acc cag ccc ccc atg acc aga Tyr Ile Phe Arg Gln Asn Gln Asp Thr Gln Pro Pro Met Thr Arg 1085 1090 1095	3294

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gcc ctc gct ccc aag atc ctc gga gag agc atg gtg aac ggc gtc 3339
Ala Leu Ala Pro Lys Ile Leu Gly Glu Ser Met Val Asn Gly Val
1100 1105 1110

tcc tac ggc gac atg gaa tac gga ttc gcc atc aag ctc gcc aag 3384
Ser Tyr Gly Asp Met Glu Tyr Gly Phe Ala Ile Lys Leu Ala Lys
1115 1120 1125

tac acc gga gtg tcc gtc tca gtg agg acc gac atc aac gcc tat 3429
Tyr Thr Gly Val Ser Val Ser Val Arg Thr Asp Ile Asn Ala Tyr
1130 1135 1140

taa 3432

<210> 13
<211> 1143
<212> PRT
<213> Herpes virus

<400> 13

Met Glu Pro Gln His Glu Ile Leu His Gln Leu Asp Thr Pro Ser Ile
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Thr Lys Ile Leu Gln Asn Thr Gly Glu Phe Ala Lys Gly Thr Leu Ser
20 25 30

Gly Ile Glu Trp Phe Ile Asn Asn Ala Ala Glu Arg Glu Ser Leu Ile
35 40 45

Leu Gly Gly Asp Gly Ser Ile Ile Ser Arg Gly Val Arg Gly Pro Gly
50 55 60

Leu Ala Ala Arg Asp Phe Gly Lys Lys Val Ile Val Pro Leu Met Lys
65 70 75 80

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

Ala Leu Met Arg Leu Val Ser Val Leu Met Arg Pro Glu Thr Leu Pro
100 105 110

Gln Ala Gln Ala Glu Phe His Met Val Phe Glu Val Thr Glu Gln Arg

115

120

125

Leu Ala Gln Pro Gly Asn Leu Ser Thr Val Ala Gly Gly Ala Ser Thr
 130 135 140

Thr Ser Tyr Asp Leu Ile Ile Asn Leu Glu Arg Lys Val Val Ser Ile
 145 150 155 160

Glu Ile Asp Ser Gln Glu Ile Phe Cys Thr Asn Asp Pro Leu Val Met
 165 170 175

Ala Gln Ala Ile Ala Ala Glu Leu Glu Ser Ala Glu Thr Thr Trp Asp
 180 185 190

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

Leu Val Glu Leu Cys Gln Leu Lys Asp Ala Ala Lys Asn Asn Asp Ser
 210 215 220

Thr Glu Gly Val Ile Ile Ser Val Cys Gln Leu Glu Asn Leu Val Cys
 225 230 235 240

Gly Ala Leu Asn Arg Gln Pro His Asn Phe Ile Ser Leu Ile His Thr
 245 250 255

Gly Leu Lys Ile Ile Asp Gly Thr Pro Ser Asn Ser Val Val Val Thr
 260 265 270

Thr Ser Thr Val Phe Arg Asn Gly Ser Leu Asp Asn Arg Leu Ala Ser
 275 280 285

Leu Ser Leu Glu Ala Pro Ala Ala Pro Leu Thr Tyr Ser Val Asn Gly
 290 295 300

Ala Val Gly Met Ser Ser Ile Ala Arg Phe Gly Arg Pro Val Pro Glu
 305 310 315 320

Leu Ala Pro Gly Arg Leu Gln Val Ser Asn Lys Tyr Pro Lys Ile Tyr

325

330

335

Asn Pro Glu Ser Lys Ser Val Tyr Gly Leu Ala Asp Glu Pro Pro Glu
 340 345 350

Pro Leu Lys Val Ala Gly Val Asn Leu Gly His Asn Glu His Ile Pro
 355 360 365

Val Val Pro Leu Asp Gly Thr Lys Phe Ser Ala Asp Gly Gly Met Ser
 370 375 380

Val Glu Asp Thr Leu Thr Gln Gly Cys Val Lys Arg Leu Phe Phe Thr
 385 390 395 400

Val Gly Thr Cys Pro Val Val Tyr Gly Ser Val Pro Pro Glu Ser Leu
 405 410 415

Tyr Gly Glu Ser Gly Lys Ser Ser Glu Ile Thr Pro Glu Ala Ile Ala
 420 425 430

Leu Arg Ser Pro Ser Ser Ser Tyr Ile Met Asn His Asp Gln Gly Cys
 435 440 445

Ala Ala Gln Glu Val Ser Leu Glu Leu Leu His Arg Leu Tyr Tyr Ala
 450 455 460

Asp Asn Pro Asp Ala Phe Asp Val Gly Val Phe Ala Arg Lys Leu Arg
 465 470 475 480

Gly Val Gln Ala Ile Arg Leu Phe Asp Glu Glu Gln Ser Ala Ala Leu
 485 490 495

Leu Leu Glu Lys Thr Trp Glu Ala Lys Val Glu Asn Gln Gln Ser Val
 500 505 510

Phe Glu Phe Asp Pro Arg His Met Leu Ile Asn His Arg Gly Gly Arg
 515 520 525

Asp Glu Pro Gly Gly Val Asn Val Val Ala Val Glu Gly Gly Asp Asp

530

535

540

Arg Asp Glu Phe Ile Arg Ala Ile Pro Arg Val Cys Met Tyr Asn Ser
 545 550 555 560

Ser Pro Met Ser Met Leu Gln Asn Glu Leu Val Gly Val Leu Ala Thr
 565 570 575

Met Tyr Gln Leu Ala Pro Pro Thr Gln Glu Met Thr Arg Tyr Leu Ser
 580 585 590

Met Ile Lys Thr Ala Leu Glu Asp Gly Thr Val Thr Gly Leu Glu Asp
 595 600 605

Val Ala Ala Leu Arg Leu Met Gly Leu Thr Gly Gly Ala Glu Ile Asp
 610 615 620

Glu Ala Met Val His Arg Leu Phe Asn Ala Gly Glu Asn Tyr Leu Pro
 625 630 635 640

Leu Ser Asp Pro Tyr Cys Gln Leu Val Leu Ile Asp Arg Leu Glu Arg
 645 650 655

Phe Met Arg Gly Ile Asp Ala Gly Gly Glu Phe Tyr Gln Ala Leu Pro
 660 665 670

Val Leu Arg Glu Leu Val Thr Val Met Arg Gly Gly Val Thr Gly Val
 675 680 685

Ile Ser Val Phe Glu Lys Leu Phe Ser Asn Thr Ala Phe Ser Ile Tyr
 690 695 700

Asp Pro Asp Val Met Ile Asn Ser Leu Cys Gln Thr Pro Arg Gly Thr
 705 710 715 720

Pro Glu Gln Asn Leu Phe Leu Asn Val Val Tyr Gly Ala Ile Leu Pro
 725 730 735

Leu Phe Ser Asn Arg Leu Ala Arg Leu Glu Ala Asp Arg His Phe Ala

740

745

750

Ala Glu Glu Val His Ile Gln Gly Leu Val Tyr Lys Ser Tyr Gly Gly
 755 760 765

Ala Cys Phe Val Gly Arg Ser His Arg Leu Pro Ala Ala Arg Ile Glu
 770 775 780

Ile Leu Trp Glu Asp Asp Ile Gly Thr Ala Ala Pro Val Ile Thr Arg
 785 790 795 800

Pro Leu Trp Lys Gln Arg Val Ala Ala Leu Arg Asn Ala Phe Gly Gly
 805 810 815

Thr Cys Pro Tyr Val Gly Phe Leu Gly Gly Leu His Cys Ala Thr Arg
 820 825 830

Leu Asp Arg Glu Thr Val Thr Gly His Phe Asp Lys Lys Tyr Tyr Ser
 835 840 845

Gly Met Ala Tyr Met Cys Val Arg Thr Thr Arg Phe Asn Gly His Gly
 850 855 860

Met Cys Val Ile Pro Arg Gly Ser Ala Arg Leu Ile Thr Gly Asn Met
 865 870 875 880

Tyr Ala Gly Thr Pro Val Ser Glu Pro Val Gly Lys Ser Val Trp Thr
 885 890 895

Gln Cys Met Glu Phe Lys Val Ala Pro Ser Gly Ile Asp Lys Leu Gly
 900 905 910

Val Leu Ile Pro Asn Val Leu Cys Thr Glu Leu Asn Gly Met Gly Val
 915 920 925

Ser Phe Asn Val Arg Asp Leu Asn Ala Ile Val Ile Leu Glu Ala Tyr
 930 935 940

Asn Gly Phe Thr Pro Glu Ser Lys Thr Thr Ser Ala His Val His Asn

945											950											955											960
Ile	Leu	Pro	Ile	Cys	Gly	Arg	Tyr	Asp	Ala	Thr	Gly	Asp	Ile	Asn	Tyr																		
				965					970					975																			
Glu	Arg	Pro	Asp	Ile	Ile	Thr	His	Arg	Tyr	Ser	Gln	Cys	Pro	Thr	Leu																		
				980					985					990																			
Leu	His	Arg	Leu	Ala	Asn	Gly	Phe	Asp	Lys	Leu	Gln	Arg	Val	Ile	Glu																		
				995					1000					1005																			
Glu	Arg	Gln	Leu	Pro	Pro	Glu	His	Ser	Tyr	Ser	Leu	Val	Ile	Gln																			
				1010					1015					1020																			
Ser	Thr	Gly	Arg	Gly	Asn	Val	Phe	Ala	Thr	Leu	Pro	Pro	Val	Leu																			
				1025					1030					1035																			
His	Thr	Ala	Glu	Leu	Met	Thr	Glu	His	Glu	Ile	Leu	Lys	Arg	Thr																			
				1040					1045					1050																			
Leu	Asp	Ala	Thr	Pro	Glu	Asp	Arg	Asn	Leu	Tyr	Arg	Pro	Thr	Leu																			
				1055					1060					1065																			
Gly	Ile	Ile	Phe	Ser	Asp	Asn	Tyr	Val	Ile	Gly	Lys	Asn	Gly	Ser																			
				1070					1075					1080																			
Tyr	Ile	Phe	Arg	Gln	Asn	Gln	Asp	Thr	Gln	Pro	Pro	Met	Thr	Arg																			
				1085					1090					1095																			
Ala	Leu	Ala	Pro	Lys	Ile	Leu	Gly	Glu	Ser	Met	Val	Asn	Gly	Val																			
				1100					1105					1110																			
Ser	Tyr	Gly	Asp	Met	Glu	Tyr	Gly	Phe	Ala	Ile	Lys	Leu	Ala	Lys																			
				1115					1120					1125																			
Tyr	Thr	Gly	Val	Ser	Val	Ser	Val	Arg	Thr	Asp	Ile	Asn	Ala	Tyr																			
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 tccagatgat ggaatcttca cggcgggtgta attccattag tgcccggacc gactggtggc 180
 ataaaagcct cagtcgcata ttcggctc 208

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 <213> Artificial

<220>
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<400> 15
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<210> 16
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<220>
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 gagccgaata tgcgactgag g 21

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<220>
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<400> 18
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<400> 20
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<220>

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<400> 22

atggtctgtc gctttcggag

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<210> 23

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<212> DNA

<213> Artificial

<220>

<223> primer

<400> 23

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<210> 24

<211> 20

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 24

ggggataacc accagttggg

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<210> 25

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<212> DNA

<213> Artificial

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<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 26

cttaccgcac tgcctaggcg ccag

24

<210> 27
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<220>
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<400> 27
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<210> 28
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<220>
 <223> primer

<400> 28
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<210> 29
 <211> 585
 <212> DNA
 <213> Herpes virus

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 aaactcatgg cacggaaaga ggaaaatgct cgcctactca aggatctcaa agatcctctg 180
 aagcgggcca tgaaggtttg ggaattgggg ggggacgcgg tggaccgcat ggaacgagat 240
 ttgaaacgga tgtgtgtcga tcccacgctc ccgaaactaa cccgatttac cgacatgac 300
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 gctaaaaatt atactctggc cctggcgcct aggcagtgcg gtaag 585

<210> 30
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 <212> DNA
 <213> Herpes virus

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 aaactcgtgg cgcggaaga ggaaaatgct cgcctgcttc aagatctcaa agatcctctg 180
 aagcgggcca tgaaggtttg ggaattgggg ggggacgcgg tggaccgcat ggaacgagat 240
 ttgaaacgga tgtgctgga cccactctc ccgaaactaa cccggtttac cgacatgac 300
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 gagctgatgc gaggcttttt catcgggctc gcccgaatc aattcgggga cgacctattc 420
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 aatcctctgt gcccttcgaa aattacatcg gagctcatcg actccacaat ggcgggttac 540
 gctaaaaatt atactctggc cctggcgcct aggcagtgcg gtaag 585

<210> 31
 <211> 20
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 <213> Artificial

<220>
 <223> probe sequence

<400> 31
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