

# SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> Preparation of an esterase

<130> 26073WO

<150> EP07013092

<151> 2007-07-04

<150> EP08000828

<151> 2008-01-17

<160> 45

<170> PatentIn version 3.3

<210> 1

<211> 1701

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (1)..(1701)

<223> Pig Liver Esterase

<400> 1

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tgg	gca	ggg	cag	cca	gcc	tcg	ccg	cct	gtt	gtg	gac	act	gcc	cag	ggc	96
Trp	Ala	Gly	Gln	Pro	Ala	Ser	Pro	Pro	Val	Val	Asp	Thr	Ala	Gln	Gly	
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cga	gtc	ctg	ggg	aag	tac	gtc	agc	tta	gaa	ggc	ctg	gca	cag	ccg	gtg	144
Arg	Val	Leu	Gly	Lys	Tyr	Val	Ser	Leu	Glu	Gly	Leu	Ala	Gln	Pro	Val	
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gcc	gtc	ttc	ctg	gga	gtc	cct	ttt	gcc	aag	ccc	cct	ctc	gga	tcc	ttg	192
Ala	Val	Phe	Leu	Gly	Val	Pro	Phe	Ala	Lys	Pro	Pro	Leu	Gly	Ser	Leu	
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agg	ttt	gct	ccg	ccg	cag	cct	gca	gaa	cca	tgg	agc	ttc	gtg	aag	aac	240
Arg	Phe	Ala	Pro	Pro	Gln	Pro	Ala	Glu	Pro	Trp	Ser	Phe	Val	Lys	Asn	
65					70					75				80		

acc	acc	tcc	tac	cct	ccc	atg	tgc	tgc	cag	gac	cca	gta	gtg	gag	cag	288
Thr	Thr	Ser	Tyr	Pro	Pro	Met	Cys	Cys	Gln	Asp	Pro	Val	Val	Glu	Gln	
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atg	acc	tca	gat	cta	ttt	acc	aac	gga	aag	gag	agg	ctc	act	ctg	gag	336
Met	Thr	Ser	Asp	Leu	Phe	Thr	Asn	Gly	Lys	Glu	Arg	Leu	Thr	Leu	Glu	
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ttt	tct	gaa	gac	tgt	ctc	tac	cta	aat	att	tac	acc	cct	gct	gac	ctg	384
Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Thr	Pro	Ala	Asp	Leu	
		115					120						125			

aca aag agg ggc aga ctg ccg gtg atg gtg tgg atc cac gga gga ggc Thr Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly 130 135 140	432
ctg gtg ttg ggc ggg gca cca atg tat gat ggg gtg gtg ctt gct gcg Leu Val Leu Gly Gly Ala Pro Met Tyr Asp Gly Val Val Leu Ala Ala 145 150 155 160	480
cat gaa aac gtg gtg gtg gtg gcc atc cag tac cgc ctg ggc atc tgg His Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp 165 170 175	528
gga ttc ttc agc aca ggg gat gaa cac agc cgg ggc aac tgg ggt cac Gly Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His 180 185 190	576
ttg gac cag gtg gcc gca ctg cac tgg gtc cag gag aac atc gcc aac Leu Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn 195 200 205	624
ttt gga ggc gac cca ggc tct gtg acc atc ttt gga gag tca gca gga Phe Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly 210 215 220	672
ggg gaa agt gtc tct gtt ctg gtg ttg tct ccc ttg gcc aag aac ctc Gly Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu 225 230 235 240	720
ttc cac cgg gcc atc tct gag agt ggc gtg gcc ctc act gtt gcc ctg Phe His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Val Ala Leu 245 250 255	768
gtc agg aag gac atg aag gct gca gct aag caa att gct gtc ctt gct Val Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala 260 265 270	816
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aag tcg gag gac gag ctc ttg gac tta acg ctg aag atg aaa ttt tta Lys Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Leu 290 295 300	912
act ctt gat ttt cat gga gac caa aga gag agc cat ccc ttc ctg ccc Thr Leu Asp Phe His Gly Asp Gln Arg Glu Ser His Pro Phe Leu Pro 305 310 315 320	960
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gct gag aag gat ttc aac act gtc ccc tac atc gtg gga atc aac aag Ala Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys 340 345 350	1056
caa gag ttt ggc tgg ctt ctg cca acg atg atg ggc ttc ccc ctc tct Gln Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser 355 360 365	1104

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Glu Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser	
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Tyr Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp	
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aag tat ttg ggg ggg aca gac gac ccc gtc aaa aag aaa gac ctg ttc	1248
Lys Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe	
405 410 415	
ctg gac ttg atg ggg gat gtg gtg ttt ggt gtc cca tct gtg acg gtg	1296
Leu Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val	
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gcc cgt caa cac aga gat gca gga gcc ccc acc tac atg tat gag ttt	1344
Ala Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe	
435 440 445	
cag tat cgc cca agc ttc tca tcg gac aag aaa ccc aag acg gtg atc	1392
Gln Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile	
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ggg gac cac ggg gat gag atc ttc tcc gtc ttt ggt ttt cca ctg tta	1440
Gly Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu	
465 470 475 480	
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Lys Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met	
485 490 495	
aaa ttc tgg gcc aac ttt gct cgc agt ggg aac ccc aat ggg gag ggg	1536
Lys Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly	
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ctg ccc cat tgg ccg atg tac gac cag gaa gaa ggg tac ctt cag atc	1584
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515 520 525	
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Gly Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala	
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Arg	Phe	Ala	Pro	Pro	Gln	Pro	Ala	Glu	Pro	Trp	Ser	Phe	Val	Lys	Asn				
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Thr	Thr	Ser	Tyr	Pro	Pro	Met	Cys	Cys	Gln	Asp	Pro	Val	Val	Glu	Gln				
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Met	Thr	Ser	Asp	Leu	Phe	Thr	Asn	Gly	Lys	Glu	Arg	Leu	Thr	Leu	Glu				
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Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Thr	Pro	Ala	Asp	Leu				
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Thr	Lys	Arg	Gly	Arg	Leu	Pro	Val	Met	Val	Trp	Ile	His	Gly	Gly	Gly				
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Leu	Val	Leu	Gly	Gly	Ala	Pro	Met	Tyr	Asp	Gly	Val	Val	Leu	Ala	Ala				
145					150					155					160				
His	Glu	Asn	Val	Val	Val	Val	Ala	Ile	Gln	Tyr	Arg	Leu	Gly	Ile	Trp				
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Gly	Phe	Phe	Ser	Thr	Gly	Asp	Glu	His	Ser	Arg	Gly	Asn	Trp	Gly	His				
			180					185					190						
Leu	Asp	Gln	Val	Ala	Ala	Leu	His	Trp	Val	Gln	Glu	Asn	Ile	Ala	Asn				
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Phe	Gly	Gly	Asp	Pro	Gly	Ser	Val	Thr	Ile	Phe	Gly	Glu	Ser	Ala	Gly				
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Gly	Glu	Ser	Val	Ser	Val	Leu	Val	Leu	Ser	Pro	Leu	Ala	Lys	Asn	Leu				
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Gly Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln  
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Thr Leu Asp Phe His Gly Asp Gln Arg Glu Ser His Pro Phe Leu Pro  
305 310 315 320

Thr Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu  
325 330 335

Ala Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys  
340 345 350

Gln Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser  
355 360 365

Glu Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser  
370 375 380

Tyr Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp  
385 390 395 400

Lys Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe  
405 410 415

Leu Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val  
420 425 430

Ala Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe  
435 440 445

Gln Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile  
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Gly Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu  
465 470 475 480

Lys Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met  
485 490 495

Lys Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly  
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Leu Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile  
515 520 525

Gly Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala  
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Ile Lys His Ala Glu Leu  
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gtc ttc ctg gga gtc cct ttt gcc aag ccc cct ctc gga tcc ttg agg Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg 50 55 60	192
ttt gct ccg ccg cag cct gca gaa cca tgg agc ttc gtg aag aac acc Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr 65 70 75 80	240
acc tcc tac cct ccc atg tgc tgc caa gag cca att ggg gga cag atg Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met 85 90 95	288
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gtg gtg ggc ggg gct tcc acc tat gat gga ctg gcc ctc gct gcg cat Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His 145 150 155 160	480
gaa aac gtg gtg gtg gtg gcc atc cag tac cgc ctg ggc atc tgg gga Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly 165 170 175	528
ttc ttc agc aca ggg gac gaa cac agc cgg ggc aac tgg ggt cac ttg Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu 180 185 190	576
gac cag gtg gcc gca ctg cac tgg gtc cag gag aac atc gcc aac ttt Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe 195 200 205	624
gga ggc gac cca ggc tct gtg acc atc ttt gga gag tca gca gga ggg Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly 210 215 220	672
gaa agt gtc tct gtt ctg gtg ttg tct ccc ttg gcc aag aac ctc ttc Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe 225 230 235 240	720
cac cgg gcc atc tct gag agt ggc gtg gcc ttc act gct ggc ctg gtc His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val 245 250 255	768
agg aag gac atg aag gct gca gct aag caa att gct gtc ctt gct ggg	816

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Cys	Lys	Thr	Thr	Thr	Ser	Ala	Val	Phe	Val	His	Cys	Leu	Arg	Gln	Lys		
		275					280					285					
tcg	gag	gac	gag	ctc	ttg	gac	tta	acg	ctg	aag	atg	aaa	ttt	ttc	gct	912	
Ser	Glu	Asp	Glu	Leu	Leu	Asp	Leu	Thr	Leu	Lys	Met	Lys	Phe	Phe	Ala		
	290					295					300						
ctt	gat	ttg	cat	gga	gac	ccc	aga	gag	agc	cat	ccc	ttc	ctg	acc	act	960	
Leu	Asp	Leu	His	Gly	Asp	Pro	Arg	Glu	Ser	His	Pro	Phe	Leu	Thr	Thr		
305					310					315					320		
gtg	gtg	gat	gga	gtg	ctg	ctg	ccc	aag	atg	cct	gaa	gag	att	ctg	gct	1008	
Val	Val	Asp	Gly	Val	Leu	Leu	Pro	Lys	Met	Pro	Glu	Glu	Ile	Leu	Ala		
				325					330					335			
gaa	aag	gat	ttc	aac	act	gtc	ccc	tac	atc	gtg	gga	atc	aac	aag	caa	1056	
Glu	Lys	Asp	Phe	Asn	Thr	Val	Pro	Tyr	Ile	Val	Gly	Ile	Asn	Lys	Gln		
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Gly	Lys	Leu	Asp	Gln	Lys	Thr	Ala	Thr	Ser	Leu	Leu	Trp	Lys	Ser	Tyr		
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Pro	Ile	Ala	Asn	Ile	Pro	Glu	Glu	Leu	Thr	Pro	Val	Ala	Thr	Asp	Lys		
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Tyr	Leu	Gly	Gly	Thr	Asp	Asp	Pro	Val	Lys	Lys	Lys	Asp	Leu	Phe	Leu		
				405					410					415			
gac	ttg	atg	ggg	gat	gtg	gtg	ttt	ggt	gtc	cca	tct	gtg	acg	gtg	gcc	1296	
Asp	Leu	Met	Gly	Asp	Val	Val	Phe	Gly	Val	Pro	Ser	Val	Thr	Val	Ala		
			420					425					430				
cgt	caa	cac	aga	gat	gca	gga	gcc	ccc	acc	tac	atg	tat	gag	ttt	cag	1344	
Arg	Gln	His	Arg	Asp	Ala	Gly	Ala	Pro	Thr	Tyr	Met	Tyr	Glu	Phe	Gln		
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tat	cgc	cca	agc	ttc	tca	tcg	gac	aag	aaa	ccc	aag	acg	gtg	atc	ggg	1392	
Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
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Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
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Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
				485				490						495			
ttc	tgg	gcc	aac	ttt	gct	cgc	agt	ggg	aac	ccc	aat	ggg	gag	ggg	ctg	1536	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		



500	505	510	
ccc cat tgg ccg atg tac gac	cag gaa gaa ggg tac ctt	cag atc ggc	1584
Pro His Trp Pro Met Tyr Asp	Gln Glu Glu Gly Tyr	Leu Gln Ile Gly	
515	520	525	
gtc aac acc cag gca gcc aag agg ctg aaa ggt gaa gaa gtg gcc ttc			1632
Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe			
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tgg aac gat ctc ctg tcc aag gag gca gca aag aag cca ccc aag ata			1680
Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile			
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aag cat gct gag ctg tga			1698
Lys His Ala Glu Leu			
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Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala			
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Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg			
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Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr			
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Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met			
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Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr			
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Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu			
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Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
165 170 175

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
180 185 190

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
195 200 205

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

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
225 230 235 240

His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val  
245 250 255

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
260 265 270

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
275 280 285

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Phe Ala  
290 295 300

Leu Asp Leu His Gly Asp Pro Arg Glu Ser His Pro Phe Leu Thr Thr  
305 310 315 320

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
325 330 335

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
340 345 350

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
355 360 365

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
370 375 380

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

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
 405 410 415

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
 420 425 430

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
 435 440 445

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
 450 455 460

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
 465 470 475 480

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
 485 490 495

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
 500 505 510

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
 515 520 525

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
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Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
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Lys His Ala Glu Leu  
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 gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
 Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
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 Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
 35 40 45

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Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr	
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act tcc tac cct cca atg tgt tgt caa gaa cca atc gga gga caa atg	240
Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met	
65 70 75 80	
ctt tca gac cta ttc act aac aga aag gaa agg ctt atc ccg gag ttc	288
Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe	
85 90 95	
tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca	336
Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr	
100 105 110	
aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg	384
Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu	
115 120 125	
gtt gtt ggc gga gca tcc act tat gac gga ttg gct ctt gcc gcg cac	432
Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His	
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gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga	480
Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly	
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ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta	528
Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu	
165 170 175	
gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc	576
Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe	
180 185 190	
gga ggt gat cca ggt tct gtt act att ttc gga gaa tca gca ggc gga	624
Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly	
195 200 205	
gag agt gtc tct gta ttg gtt tta tca cca tta gct aag aac ctt ttt	672
Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe	
210 215 220	
cat cgt gct att tcc gaa agt ggt gtt gct ttt acc gcc ggt ttg gtc	720
His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val	
225 230 235 240	
agg aag gat atg aag gcc gca gcc aag cag atc gct gtc ctt gca gga	768
Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly	
245 250 255	
tgc aaa act act act tcg gca gtc ttc gtg cat tgt ttg cgt caa aag	816
Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys	
260 265 270	
tcg gaa gat gaa ctt tta gac ctc acg ttg aag atg aaa ttc ttt gcc	864
Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Phe Ala	
275 280 285	
ctt gac tta cac gga gat cca agg gaa tct cac cct ttt ttg acc act	912

Leu	Asp	Leu	His	Gly	Asp	Pro	Arg	Glu	Ser	His	Pro	Phe	Leu	Thr	Thr	
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Val	Val	Asp	Gly	Val	Leu	Leu	Pro	Lys	Met	Pro	Glu	Glu	Ile	Leu	Ala	
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gag	aag	gac	ttt	aac	acc	gtc	cca	tac	att	gtt	gga	att	aac	aag	cag	1008
Glu	Lys	Asp	Phe	Asn	Thr	Val	Pro	Tyr	Ile	Val	Gly	Ile	Asn	Lys	Gln	
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gag	ttc	gga	tgg	ctt	ttg	cca	acg	atg	atg	gga	ttt	cct	ctt	tcc	gag	1056
Glu	Phe	Gly	Trp	Leu	Leu	Pro	Thr	Met	Met	Gly	Phe	Pro	Leu	Ser	Glu	
			340					345					350			
gga	aag	ttg	gat	caa	aag	acg	gct	acg	tca	ctt	ttg	tgg	aag	tcc	tac	1104
Gly	Lys	Leu	Asp	Gln	Lys	Thr	Ala	Thr	Ser	Leu	Leu	Trp	Lys	Ser	Tyr	
		355					360					365				
cca	att	gcc	aac	att	cct	gaa	gag	ttg	acc	cca	gtt	gct	acc	gat	aag	1152
Pro	Ile	Ala	Asn	Ile	Pro	Glu	Glu	Leu	Thr	Pro	Val	Ala	Thr	Asp	Lys	
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Tyr	Leu	Gly	Gly	Thr	Asp	Asp	Pro	Val	Lys	Lys	Lys	Asp	Leu	Phe	Leu	
385					390					395					400	
gat	ctg	atg	gga	gac	gtt	gtt	ttc	ggc	gtc	cca	tca	gtt	acg	gtt	gct	1248
Asp	Leu	Met	Gly	Asp	Val	Val	Phe	Gly	Val	Pro	Ser	Val	Thr	Val	Ala	
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cgt	cag	cat	agg	gac	gca	gga	gct	cca	act	tac	atg	tat	gag	ttc	caa	1296
Arg	Gln	His	Arg	Asp	Ala	Gly	Ala	Pro	Thr	Tyr	Met	Tyr	Glu	Phe	Gln	
			420					425					430			
tat	cgt	cca	tct	ttt	tca	tcg	gat	aag	aaa	cct	aag	acg	gtt	att	gga	1344
Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly	
		435					440					445				
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys	
	450					455					460					
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys	
465					470					475					480	
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu	
				485					490					495		
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly	
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gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe	
		515					520					525				
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile	

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                     20                      25                      30  
  
 Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
                     35                      40                      45  
  
 Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
                     50                      55                      60  
  
 Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met  
 65                      70                      75                      80  
  
 Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
                     85                      90                      95  
  
 Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
                     100                      105                      110  
  
 Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
                     115                      120                      125  
  
 Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
                     130                      135                      140  
  
 Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
 145                      150                      155                      160  
  
 Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
                     165                      170                      175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Phe Ala  
275 280 285

Leu Asp Leu His Gly Asp Pro Arg Glu Ser His Pro Phe Leu Thr Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln



420

425

430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
 435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
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Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
 465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
 485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
 500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
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 aagcctccac ttggatcttt gcgttttcgcc cctcctcaac cagcagagcc atgggtctttc 180  
 gttaagaaca ctacttcta ccctccaatg tgttgtcaag aaccaattgg aggtcaaag 240  
 ctttccgatc ttttactaa cagaaaggaa cgtcttattc ctgagttctc tgaggactgc 300  
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 cttgccgcac acgagaacgt tgttggtggt gctatccaat acagattggg tatctgggga 480  
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gcattgcatt gggccaaga aaacatcgct aacttcggag gtgacccagg ttctgttact	600
atcttcggtg aaagtgcagg aggtgagagt gtctctgtct tggttttatc cccacttgct	660
aagaaccttt tccaccgtgc tatctccgaa tccggtggtg ctttcaccgc cggtttggtc	720
agaaaggaca tgaaggccgc agccaagcag attgccgtcc ttgccggatg caagactact	780
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atgtacgacc aagaggaggg ataccttcaa atcgggtgtca aactcaagc cgctaagcgt	1560
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cctccaaaga ttaagcacgc tgaattgtaa	1650

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 <212> DNA  
 <213> artificial sequence

<220>  
 <223> primer

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 <220>  
 <223> primer  
  
 <400> 24  
 atttatacat atggggcagc cagcctcgcc gcctg 35

<210> 25  
 <211> 42  
 <212> DNA  
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 <400> 25  
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<210> 26  
 <211> 57  
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 <220>  
 <223> primer  
  
 <400> 26  
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<210> 27

<211> 38  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer  
  
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 <210> 28  
 <211> 71  
 <212> DNA  
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 <400> 28  
 gtaaattccc tacaatcctg ccattgtct gccacaact atggggatct tgtgtaggct 60  
 ggagctgctt c 71  
  
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 <211> 71  
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 <213> artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 29  
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 atcctcctta g 71  
  
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 <211> 74  
 <212> DNA  
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 <223> primer  
  
 <400> 30  
 cctattacgt ctgcgctac aatcgcggtg atcaacgata aggacacttt gtctgtgtag 60  
 gctggagctg cttc 74  
  
 <210> 31  
 <211> 75  
 <212> DNA  
 <213> artificial sequence  
  
 <220>  
 <223> primer

<400> 31  
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gaatatacctc cttag 75

<210> 32  
<211> 1629  
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<213> artificial sequence  
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<223> protein with esterase activity

<220>  
<221> CDS  
<222> (1)..(1629)  
<223> Bovine Liver Esterase

<400> 32  
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Met Gly Leu Ala Pro Ser Pro Pro Ile Val Asp Thr Ala Gln Gly Arg  
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gtt ctg ggg aag cac gtc agc cta aaa ggt ttc gca cag ccg gtg gcg 96  
Val Leu Gly Lys His Val Ser Leu Lys Gly Phe Ala Gln Pro Val Ala  
20 25 30  
gtt ttt ctg ggt gtc cca ttc gcc aaa ccg cct tta ggg tcc ttg cgt 144  
Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
35 40 45  
ttc gcc cca cct cag ccg gct gag ccg tgg acc ttt gtc aag aat acc 192  
Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Thr Phe Val Lys Asn Thr  
50 55 60  
att agc tat cca ccg atg tgc tcc caa gat cca gtg ggt gct cag ttg 240  
Ile Ser Tyr Pro Pro Met Cys Ser Gln Asp Pro Val Gly Ala Gln Leu  
65 70 75 80  
tta tcg gac ctg ttc acc aac cgc aaa gaa aac atc agt ctg act ttc 288  
Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Asn Ile Ser Leu Thr Phe  
85 90 95  
agc gag gat tgc ttg tat ctc aat atc tat acc ccg gca gat tta act 336  
Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110  
aaa cgt agc cgc ctg ccg gtg atg gtg tgg att cat ggt ggt gga ctg 384  
Lys Arg Ser Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125  
atg gtg ggc ggc gct tct acg tac gac ggg ctg gtc tta tcg gcg cac 432  
Met Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Val Leu Ser Ala His  
130 135 140  
gag aac gtg gtg gtg gtg acc atc cag tat cgt ctg ggc att tgg ggt 480  
Glu Asn Val Val Val Val Thr Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160



ttc ttt agc acg ggc gat gaa cat agt cgc ggg aac tgg ggc cat ttg	528
Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu	
165 170 175	
gat cag gtg gcg gct ctg cat tgg gtc cag gaa aac atc gcg aac ttc	576
Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe	
180 185 190	
ggc ggc gac cca ggc agc gtg acc atc ttt ggt gaa tcc gcc ggt gca	624
Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Ala	
195 200 205	
gag agt gtt agc atc tta gtg ctt tcc ccg ctg gcg cgt aat ttg ttt	672
Glu Ser Val Ser Ile Leu Val Leu Ser Pro Leu Ala Arg Asn Leu Phe	
210 215 220	
cat cgc gcg att agc gaa agc ggc gtg gcg ctg atc tcg acc ctg gtt	720
His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Ile Ser Thr Leu Val	
225 230 235 240	
aaa cgt gat tca aaa gcc gca gct gag caa atc gcc gtc atc gca ggc	768
Lys Arg Asp Ser Lys Ala Ala Ala Glu Gln Ile Ala Val Ile Ala Gly	
245 250 255	
tgt aag acc acc acc tct gcc gtc tta gta cat tgc ctg cgc cag aaa	816
Cys Lys Thr Thr Thr Ser Ala Val Leu Val His Cys Leu Arg Gln Lys	
260 265 270	
acg gaa gat gaa ttg ctg gaa atc acg ctg aag atg aaa ttc ttt gca	864
Thr Glu Asp Glu Leu Leu Glu Ile Thr Leu Lys Met Lys Phe Phe Ala	
275 280 285	
ctc gac ctt cat aag gat agt acg gaa agc cac ccg ttt ctg ccg acc	912
Leu Asp Leu His Lys Asp Ser Thr Glu Ser His Pro Phe Leu Pro Thr	
290 295 300	
gtg gtt gac ggc atg ctg ctg cct aaa atg ccg gaa gag atg ctg gcc	960
Val Val Asp Gly Met Leu Leu Pro Lys Met Pro Glu Glu Met Leu Ala	
305 310 315 320	
gag aaa aat ttt aac aac gtc ccg tat atg gtg ggt att aac aaa caa	1008
Glu Lys Asn Phe Asn Asn Val Pro Tyr Met Val Gly Ile Asn Lys Gln	
325 330 335	
gaa ttc ggc tgg atc atc cca ctg ttt atg agc tat ccg ctg ccg gag	1056
Glu Phe Gly Trp Ile Ile Pro Leu Phe Met Ser Tyr Pro Leu Pro Glu	
340 345 350	
gat aaa ctg gat cag aaa act gcg acg agt ctg ctg tgg cag agc tat	1104
Asp Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Gln Ser Tyr	
355 360 365	
tcc tta ttg agc atc cca gaa gaa ctg tcg ccg gtg gcc acg gat aaa	1152
Ser Leu Leu Ser Ile Pro Glu Glu Leu Ser Pro Val Ala Thr Asp Lys	
370 375 380	
tac cta ggt ggg act gat gat cct gtt aaa aag aaa gat ctg ttt ctg	1200
Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu	
385 390 395 400	
gat ctg atc gct gac gtt ctc ttc ggc gtc ccg tct gtc aat gtg gcg	1248

Asp	Leu	Ile	Ala	Asp	Val	Leu	Phe	Gly	Val	Pro	Ser	Val	Asn	Val	Ala		
				405					410					415			
cgg	cgc	cat	cgt	gac	gct	ggg	gcg	ccg	acc	tat	atg	tac	gaa	ttc	cag	1296	
Arg	Arg	His	Arg	Asp	Ala	Gly	Ala	Pro	Thr	Tyr	Met	Tyr	Glu	Phe	Gln		
			420					425					430				
tac	cgc	ccg	agc	ttt	agt	tca	gaa	ctg	aag	ccg	aaa	act	gtg	atc	ggc	1344	
Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Glu	Leu	Lys	Pro	Lys	Thr	Val	Ile	Gly		
			435				440					445					
gat	cac	ggc	gac	gaa	ctg	ttt	tcc	gtc	ttt	ggg	gca	cca	ttc	cta	aag	1392	
Asp	His	Gly	Asp	Glu	Leu	Phe	Ser	Val	Phe	Gly	Ala	Pro	Phe	Leu	Lys		
	450					455					460						
gac	ggc	gcg	tcg	gaa	gag	gaa	att	aat	ctg	agc	aaa	atg	gtg	atg	aag	1440	
Asp	Gly	Ala	Ser	Glu	Glu	Glu	Ile	Asn	Leu	Ser	Lys	Met	Val	Met	Lys		
465					470				475						480		
ttt	tgg	gcg	aac	ttc	gca	cgc	aat	ggg	aac	ccg	aat	ggc	gaa	ggc	tta	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Asn	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490					495				
cct	cac	tgg	cca	gct	tac	gat	cat	aaa	gag	ggc	tat	ttg	cag	atc	ggc	1536	
Pro	His	Trp	Pro	Ala	Tyr	Asp	His	Lys	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtt	aac	acg	cgt	gcg	gcc	gag	aaa	ctg	aag	gat	aaa	gag	gta	gca	ttt	1584	
Val	Asn	Thr	Arg	Ala	Ala	Glu	Lys	Leu	Lys	Asp	Lys	Glu	Val	Ala	Phe		
			515				520					525					
tgg	aat	gaa	ctg	ctg	agc	cgc	gaa	gtg	gca	cgt	cat	cat	acc	taa		1629	
Trp	Asn	Glu	Leu	Leu	Ser	Arg	Glu	Val	Ala	Arg	His	His	Thr				
	530					535					540						

<210> 33  
 <211> 542  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 33

Met	Gly	Leu	Ala	Pro	Ser	Pro	Pro	Ile	Val	Asp	Thr	Ala	Gln	Gly	Arg
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Val	Leu	Gly	Lys	His	Val	Ser	Leu	Lys	Gly	Phe	Ala	Gln	Pro	Val	Ala
			20					25					30		
Val	Phe	Leu	Gly	Val	Pro	Phe	Ala	Lys	Pro	Pro	Leu	Gly	Ser	Leu	Arg
			35				40					45			
Phe	Ala	Pro	Pro	Gln	Pro	Ala	Glu	Pro	Trp	Thr	Phe	Val	Lys	Asn	Thr
	50					55					60				

Ile Ser Tyr Pro Pro Met Cys Ser Gln Asp Pro Val Gly Ala Gln Leu  
65 70 75 80

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

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Ser Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Met Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Val Leu Ser Ala His  
130 135 140

Glu Asn Val Val Val Val Thr Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Ala  
195 200 205

Glu Ser Val Ser Ile Leu Val Leu Ser Pro Leu Ala Arg Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Ile Ser Thr Leu Val  
225 230 235 240

Lys Arg Asp Ser Lys Ala Ala Ala Glu Gln Ile Ala Val Ile Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Leu Val His Cys Leu Arg Gln Lys  
260 265 270

Thr Glu Asp Glu Leu Leu Glu Ile Thr Leu Lys Met Lys Phe Phe Ala  
275 280 285

Leu Asp Leu His Lys Asp Ser Thr Glu Ser His Pro Phe Leu Pro Thr  
290 295 300

Val Val Asp Gly Met Leu Leu Pro Lys Met Pro Glu Glu Met Leu Ala  
305 310 315 320

Glu Lys Asn Phe Asn Asn Val Pro Tyr Met Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Ile Ile Pro Leu Phe Met Ser Tyr Pro Leu Pro Glu  
340 345 350

Asp Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Gln Ser Tyr  
355 360 365

Ser Leu Leu Ser Ile Pro Glu Glu Leu Ser Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Ile Ala Asp Val Leu Phe Gly Val Pro Ser Val Asn Val Ala  
405 410 415

Arg Arg His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Glu Leu Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Leu Phe Ser Val Phe Gly Ala Pro Phe Leu Lys  
450 455 460

Asp Gly Ala Ser Glu Glu Glu Ile Asn Leu Ser Lys Met Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Asn Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Ala Tyr Asp His Lys Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Arg Ala Ala Glu Lys Leu Lys Asp Lys Glu Val Ala Phe  
515 520 525

Trp Asn Glu Leu Leu Ser Arg Glu Val Ala Arg His His Thr  
530 535 540

<211> 1650  
<212> DNA  
<213> artificial sequence

<220>  
<223> protein with esterase activity

<220>  
<221> CDS  
<222> (1)..(1650)

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Met Gly Gln Pro Ala Ser Pro Pro Val Val Asp Thr Ala Gln Gly Arg  
1 5 10 15  
  
gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
20 25 30  
  
gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
35 40 45  
  
ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
50 55 60  
  
act tcc tac cct cca atg tgt tgt caa gat cca gtc gta gaa caa atg 240  
Thr Ser Tyr Pro Pro Met Cys Cys Gln Asp Pro Val Val Glu Gln Met  
65 70 75 80  
  
acg tca gac cta ttc act aac gga aag gaa agg ctt acc ctg gag ttc 288  
Thr Ser Asp Leu Phe Thr Asn Gly Lys Glu Arg Leu Thr Leu Glu Phe  
85 90 95  
  
tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110  
  
aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125  
  
gtt ctg ggc gga gca ccg atg tat gac gga gtg gtt ctt gcc gcg cac 432  
Val Leu Gly Gly Ala Pro Met Tyr Asp Gly Val Val Leu Ala Ala His  
130 135 140  
  
gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160  
  
ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175  
  
gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

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

Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
	515					520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

<210> 35  
 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 35

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

Thr Ser Asp Leu Phe Thr Asn Gly Lys Glu Arg Leu Thr Leu Glu Phe  
85 90 95

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Val Leu Gly Gly Ala Pro Met Tyr Asp Gly Val Val Leu Ala Ala His  
130 135 140

Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Val Ala Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Leu Thr  
275 280 285

Leu Asp Phe His Gly Asp Gln Arg Glu Ser His Pro Phe Leu Pro Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320



Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545

<211> 1650  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> protein with esterase activity

<220>  
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 <222> (1)..(1650)

<400> 36  
 atg gga caa cca gct tcg ccg cct gtc gtt gat acc gct caa gga cga 48  
 Met Gly Gln Pro Ala Ser Pro Pro Val Val Asp Thr Ala Gln Gly Arg  
 1 5 10 15

gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
 Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
 20 25 30

gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
 Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
 35 40 45

ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
 Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
 50 55 60

act tcc tac cct cca atg tgt tgt caa gat cca gtc gca gga caa atg 240  
 Thr Ser Tyr Pro Pro Met Cys Cys Gln Asp Pro Val Ala Gly Gln Met  
 65 70 75 80

acg tca gac cta ttc act aac gga aag gaa agg ctt atc ccg gag ttc 288  
 Thr Ser Asp Leu Phe Thr Asn Gly Lys Glu Arg Leu Ile Pro Glu Phe  
 85 90 95

tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
 Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
 100 105 110

aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
 Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
 115 120 125

gtt gtt ggc gga gca tcc act tat gac gga ttg gct ctt gcc gcg cac 432  
 Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
 130 135 140

gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
 Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
 145 150 155 160

ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
 Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
 165 170 175

gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
 Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
 180 185 190

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

Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
	515					520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

<210> 37  
 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 37

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

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

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Phe  
355 360 365

Pro Ile Thr Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545

<211> 1650  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> protein with esterase activity

<220>  
 <221> CDS  
 <222> (1)..(1650)

<400> 38  
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 Met Gly Gln Pro Ala Ser Pro Pro Val Val Asp Thr Ala Gln Gly Arg  
 1 5 10 15

gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
 Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
 20 25 30

gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
 Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
 35 40 45

ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
 Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
 50 55 60

act tcc tac cct cca atg tgt tgt caa gat cca gtc gta gaa caa atg 240  
 Thr Ser Tyr Pro Pro Met Cys Cys Gln Asp Pro Val Val Glu Gln Met  
 65 70 75 80

acg tca gac cta ttc act aac gga aag gaa agg ctt acc ctg gag ttc 288  
 Thr Ser Asp Leu Phe Thr Asn Gly Lys Glu Arg Leu Thr Leu Glu Phe  
 85 90 95

tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
 Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
 100 105 110

aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
 Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
 115 120 125

gtt gtt ggc gga gca tcc act tat gac gga ttg gct ctt gcc gcg cac 432  
 Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
 130 135 140

gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
 Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
 145 150 155 160

ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
 Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
 165 170 175

gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
 Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
 180 185 190

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



Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
	515					520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

<210> 39  
 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 39

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

Thr Ser Asp Leu Phe Thr Asn Gly Lys Glu Arg Leu Thr Leu Glu Phe  
85 90 95

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
130 135 140

Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Phe Ala  
275 280 285

Leu Asp Leu His Gly Asp Pro Arg Glu Ser His Pro Phe Leu Thr Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545

<210> 40

<211> 1650  
<212> DNA  
<213> artificial sequence

<220>  
<223> protein with esterase activity

<220>  
<221> CDS  
<222> (1)..(1650)

<400> 40  
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gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
20 25 30  
  
gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
35 40 45  
  
ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
50 55 60  
  
act tcc tac cct cca atg tgt tgt caa gaa cca atc gga gga caa atg 240  
Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met  
65 70 75 80  
  
ctt tca gac cta ttc act aac aga aag gaa agg ctt atc ccg gag ttc 288  
Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
85 90 95  
  
tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110  
  
aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125  
  
gtt ctg ggc gga gca ccg atg tat gac gga gtg gtt ctt gcc gcg cac 432  
Val Leu Gly Gly Ala Pro Met Tyr Asp Gly Val Val Leu Ala Ala His  
130 135 140  
  
gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160  
  
ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175  
  
gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

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

Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
		515				520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

<210> 41  
 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 41

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

Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
85 90 95

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Val Leu Gly Gly Ala Pro Met Tyr Asp Gly Val Val Leu Ala Ala His  
130 135 140

Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Phe Ala  
275 280 285

Leu Asp Leu His Gly Asp Pro Arg Glu Ser His Pro Phe Leu Thr Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545

<210> 42



<211> 1650  
<212> DNA  
<213> artificial sequence

<220>  
<223> protein with esterase activity

<220>  
<221> CDS  
<222> (1)..(1650)

<400> 42  
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Met Gly Gln Pro Ala Ser Pro Pro Val Val Asp Thr Ala Gln Gly Arg  
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gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
20 25 30  
  
gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
35 40 45  
  
ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
50 55 60  
  
act tcc tac cct cca atg tgt tgt caa gaa cca atc gga gga caa atg 240  
Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met  
65 70 75 80  
  
ctt tca gac cta ttc act aac aga aag gaa agg ctt atc ccg gag ttc 288  
Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
85 90 95  
  
tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110  
  
aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125  
  
gtt gtt ggc gga gca tcc act tat gac gga ttg gct ctt gcc gcg cac 432  
Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
130 135 140  
  
gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160  
  
ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175  
  
gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

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

Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
	515					520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

<210> 43  
 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 43

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

Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
85 90 95

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
130 135 140

Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Val Ala Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Leu Ala  
275 280 285

Leu Asp Leu His Gly Asp Pro Arg Glu Ser His Pro Phe Leu Thr Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545

<210> 44

<211> 1650  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> protein with esterase activity

<220>  
 <221> CDS  
 <222> (1)..(1650)

<400> 44  
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 gtc ttg ggt aag tac gtc tct tta gag gga ttg gca caa ccg gtt gct 96  
 Val Leu Gly Lys Tyr Val Ser Leu Glu Gly Leu Ala Gln Pro Val Ala  
 20 25 30  
 gtc ttc ttg gga gtc cct ttt gct aag cca cct ctt gga tct ttg agg 144  
 Val Phe Leu Gly Val Pro Phe Ala Lys Pro Pro Leu Gly Ser Leu Arg  
 35 40 45  
 ttt gcc ccg ccg caa cca gca gag cca tgg tct ttc gtt aag aac act 192  
 Phe Ala Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Thr  
 50 55 60  
 act tcc tac cct cca atg tgt tgt caa gaa cca atc gga gga caa atg 240  
 Thr Ser Tyr Pro Pro Met Cys Cys Gln Glu Pro Ile Gly Gly Gln Met  
 65 70 75 80  
 ctt tca gac cta ttc act aac aga aag gaa agg ctt atc ccg gag ttc 288  
 Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
 85 90 95  
 tct gag gat tgc ctt tac cta aat att tac act cct gcc gat ttg aca 336  
 Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
 100 105 110  
 aag agg ggt agg ttg ccg gtt atg gtt tgg att cat gga gga ggt ttg 384  
 Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
 115 120 125  
 gtt gtt ggc gga gca tcc act tat gac gga ttg gct ctt gcc gcg cac 432  
 Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
 130 135 140  
 gag aac gtt gtt gtt gtt gct att caa tac cgt ttg ggt att tgg gga 480  
 Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
 145 150 155 160  
 ttt ttc tcc aca gga gat gag cat tcc cgt gga aac tgg ggc cat tta 528  
 Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
 165 170 175  
 gat caa gtt gct gca ttg cat tgg gtc caa gaa aac att gct aac ttc 576  
 Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
 180 185 190

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

Tyr	Arg	Pro	Ser	Phe	Ser	Ser	Asp	Lys	Lys	Pro	Lys	Thr	Val	Ile	Gly		
		435					440					445					
gat	cat	gga	gac	gaa	att	ttt	tcc	gtc	ttc	ggc	ttc	cca	ttg	ctc	aaa	1392	
Asp	His	Gly	Asp	Glu	Ile	Phe	Ser	Val	Phe	Gly	Phe	Pro	Leu	Leu	Lys		
	450					455				460							
ggt	gac	gct	cca	gag	gaa	gaa	gtc	agt	ctt	tct	aag	acg	gtt	atg	aaa	1440	
Gly	Asp	Ala	Pro	Glu	Glu	Glu	Val	Ser	Leu	Ser	Lys	Thr	Val	Met	Lys		
465					470				475					480			
ttt	tgg	gct	aac	ttc	gcc	cgt	agt	gga	aac	cct	aat	gga	gaa	gga	ttg	1488	
Phe	Trp	Ala	Asn	Phe	Ala	Arg	Ser	Gly	Asn	Pro	Asn	Gly	Glu	Gly	Leu		
			485					490						495			
cct	cac	tgg	ccg	atg	tac	gat	caa	gag	gag	gga	tac	ctt	caa	att	ggt	1536	
Pro	His	Trp	Pro	Met	Tyr	Asp	Gln	Glu	Glu	Gly	Tyr	Leu	Gln	Ile	Gly		
			500					505					510				
gtc	aac	act	caa	gca	gct	aag	agg	ttg	aaa	ggc	gag	gag	gtt	gct	ttt	1584	
Val	Asn	Thr	Gln	Ala	Ala	Lys	Arg	Leu	Lys	Gly	Glu	Glu	Val	Ala	Phe		
	515					520				525							
tgg	aac	gac	ctg	ttg	tcc	aag	gaa	gca	gca	aag	aag	cca	cct	aag	ata	1632	
Trp	Asn	Asp	Leu	Leu	Ser	Lys	Glu	Ala	Ala	Lys	Lys	Pro	Pro	Lys	Ile		
	530					535				540							
aag	cac	gcc	gaa	ttg	taa											1650	
Lys	His	Ala	Glu	Leu													
545																	

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 <211> 549  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Synthetic Construct

<400> 45

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



Leu Ser Asp Leu Phe Thr Asn Arg Lys Glu Arg Leu Ile Pro Glu Phe  
85 90 95

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr  
100 105 110

Lys Arg Gly Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu  
115 120 125

Val Val Gly Gly Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His  
130 135 140

Glu Asn Val Val Val Val Ala Ile Gln Tyr Arg Leu Gly Ile Trp Gly  
145 150 155 160

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu  
165 170 175

Asp Gln Val Ala Ala Leu His Trp Val Gln Glu Asn Ile Ala Asn Phe  
180 185 190

Gly Gly Asp Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly  
195 200 205

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe  
210 215 220

His Arg Ala Ile Ser Glu Ser Gly Val Ala Phe Thr Ala Gly Leu Val  
225 230 235 240

Arg Lys Asp Met Lys Ala Ala Ala Lys Gln Ile Ala Val Leu Ala Gly  
245 250 255

Cys Lys Thr Thr Thr Ser Ala Val Phe Val His Cys Leu Arg Gln Lys  
260 265 270

Ser Glu Asp Glu Leu Leu Asp Leu Thr Leu Lys Met Lys Phe Leu Thr  
275 280 285

Leu Asp Phe His Gly Asp Gln Arg Glu Ser His Pro Phe Leu Pro Thr  
290 295 300

Val Val Asp Gly Val Leu Leu Pro Lys Met Pro Glu Glu Ile Leu Ala  
305 310 315 320

Glu Lys Asp Phe Asn Thr Val Pro Tyr Ile Val Gly Ile Asn Lys Gln  
325 330 335

Glu Phe Gly Trp Leu Leu Pro Thr Met Met Gly Phe Pro Leu Ser Glu  
340 345 350

Gly Lys Leu Asp Gln Lys Thr Ala Thr Ser Leu Leu Trp Lys Ser Tyr  
355 360 365

Pro Ile Ala Asn Ile Pro Glu Glu Leu Thr Pro Val Ala Thr Asp Lys  
370 375 380

Tyr Leu Gly Gly Thr Asp Asp Pro Val Lys Lys Lys Asp Leu Phe Leu  
385 390 395 400

Asp Leu Met Gly Asp Val Val Phe Gly Val Pro Ser Val Thr Val Ala  
405 410 415

Arg Gln His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu Phe Gln  
420 425 430

Tyr Arg Pro Ser Phe Ser Ser Asp Lys Lys Pro Lys Thr Val Ile Gly  
435 440 445

Asp His Gly Asp Glu Ile Phe Ser Val Phe Gly Phe Pro Leu Leu Lys  
450 455 460

Gly Asp Ala Pro Glu Glu Glu Val Ser Leu Ser Lys Thr Val Met Lys  
465 470 475 480

Phe Trp Ala Asn Phe Ala Arg Ser Gly Asn Pro Asn Gly Glu Gly Leu  
485 490 495

Pro His Trp Pro Met Tyr Asp Gln Glu Glu Gly Tyr Leu Gln Ile Gly  
500 505 510

Val Asn Thr Gln Ala Ala Lys Arg Leu Lys Gly Glu Glu Val Ala Phe  
515 520 525

Trp Asn Asp Leu Leu Ser Lys Glu Ala Ala Lys Lys Pro Pro Lys Ile  
530 535 540

Lys His Ala Glu Leu  
545